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(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE
EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene
expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in
the Fetal liver and their use in methods for detecting gene expression.

HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

CROSS REFERENCE TO RELATED APPLICATIONS

5

The present application is a continuation-in-part of U.S.
patent application serial nos. 09/632,366, filed August 3,
2000 and 09/608,408, filed June 30, 2000; claims the
benefit under 35 U.S.C. s 119(e) of U.S. provisional patent
10 application serial nos. 60/236,359, filed September 27,
2000, 60/234,687, filed September 21, 2000, 60/207,456,
filed May 26, 2000, and 60/180,312, filed February 4, 2000;
and further claims the benefit under 35 U.S.C. s 119(a) of
UK patent application no. 0024263.6, filed October 4, 2000,
15 the disclosures of which are incorporated herein by
reference in their entireties.

REFERENCE TO SEQUENCE LISTING AND INCORPORATION BY
REFERENCE THEREOF

20

The present application includes a Sequence Listing in
electronic format, filed pursuant to PCT Administrative
Instructions 801 - 806 on a single CD-R disc, in
triplicate, containing a file named pto_FETAL_LIVER.txt,
25 created 24 January 2001, having 25,630,231 bytes. The
Sequence Listing contained in said file on said disc is
incorporated herein by reference in its entirety.

Field of the Invention

30

The present invention relates to genome-derived
single exon microarrays useful for verifying the expression
of regions of genomic DNA predicted to encode protein. In
particular, the present invention relates to unique genome-
35 derived single exon nucleic acid probes expressed in human

Fetal liver and single exon nucleic acid microarrays that include such probes.

Background of the Invention

5 For almost two decades following the invention of general techniques for nucleic acid sequencing, Sanger et al., *Proc. Natl. Acad. Sci. USA* 70(4):1209-13 (1973); Gilbert et al., *Proc. Natl. Acad. Sci. USA* 70(12):3581-4 (1973), these techniques were used principally as tools to
10 further the understanding of proteins - known or suspected - about which a basic foundation of biological knowledge had already been built. In many cases, the cloning effort that preceded sequence identification had been both informed and directed by that antecedent
15 biological understanding.

For example, the cloning of the T cell receptor for antigen was predicated upon its known or suspected cell type-specific expression, by its suspected membrane association, and by the predicted assembly of its gene via
20 T cell-specific somatic recombination. Subsequent sequencing efforts at once confirmed and extended understanding of this family of proteins. Hedrick et al., *Nature* 308(5955):153-8 (1984).

More recently, however, the development of high
25 throughput sequencing methods and devices, in concert with large public and private undertakings to sequence the human and other genomes, has altered this investigational paradigm: today, sequence information often precedes understanding of the basic biology of the encoded protein
30 product.

One of the approaches to large-scale sequencing is predicated upon the proposition that expressed sequences - that is, those accessible through isolation of mRNA - are of greatest initial interest. This "expressed
35 sequence tag" ("EST") approach has already yielded vast

amounts of sequence data (see for example Adams et al.,
Science 252:1651 (1991); Williamson, *Drug Discov. Today*
4:115 (1999)). For nucleic acids sequenced by this
approach, often the only biological information that is
5 known a priori with any certainty is the likelihood of
biologic expression itself. By virtue of the species and
tissue from which the mRNA had originally been obtained,
most such sequences are also annotated with the identity of
the species and at least one tissue in which expression
10 appears likely.

More recently, the pace of genomic sequencing has
accelerated dramatically. When genomic DNA serves as the
initial substrate for sequencing efforts, expression cannot
be presumed; often the only a priori biological information
15 about the sequence includes the species and chromosome (and
perhaps chromosomal map location) of origin.

With the ever-accelerating pace of sequence
accumulation by directed, EST, and genomic sequencing
approaches - and in particular, with the accumulation of
20 sequence information from multiple genera, from multiple
species within genera, and from multiple individuals within
a species - there is an increasing need for methods that
rapidly and effectively permit the functions of nucleic
sequences to be elucidated. And as such functional
25 information accumulates, there is a further need for
methods of storing such functional information in
meaningful and useful relationship to the sequence itself;
that is, there is an increasing need for means and
apparatus for annotating raw sequence data with known or
30 predicted functional information.

Although the increase in the pace of genomic
sequencing is due in large part to technological changes in
sequencing strategies and instrumentation, Service, *Science*
280:995 (1998); Pennisi, *Science* 283: 1822-1823 (1999),
35 there is an important functional motivation as well.

While it was understood that the EST approach would rarely be able to yield sequence information about the noncoding portions of the genome, it now also appears the EST approach is capable of capturing only a fraction of a genome's actual expression complexity.

For example, when the *C. elegans* genome was fully sequenced, gene prediction algorithms identified over 19,000 potential genes, of which only 7,000 had been found by EST sequencing. *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998). Analogously, the recently completed sequence of chromosome 2 of *Arabidopsis* predicts over 4000 genes, Lin et al., *Nature*, 402:761 (1999), of which only about 6% had previously been identified via EST sequencing efforts. Although the human genome has the greatest depth of EST coverage, it is still woefully short of surrendering all of its genes. One recent estimate suggests that the human genome contains more than 146,000 genes, which would at this point leave greater than half of the genes undiscovered. It is now predicted that many genes, perhaps 20 to 50%, will only be found by genomic sequencing.

There is, therefore, a need for methods that permit the functional regions of genomic sequence – and most importantly, but not exclusively, regions that function to encode genes – to be identified.

Much of the coding sequence of the human genome is not homologous to known genes, making detection of open reading frames ("ORFs") and predictions of gene function difficult. Computational methods exist for predicting coding regions in eukaryotic genomes. Gene prediction programs such as GRAIL and GRAIL II, Uberbacher et al., *Proc. Natl. Acad. Sci. USA* 88(24):11261-5 (1991); Xu et al., *Genet. Eng.* 16:241-53 (1994); Uberbacher et al., *Methods Enzymol.* 266:259-81 (1996); GENEFINDER, Solovyev et al., *Nucl. Acids. Res.* 22:5156-63 (1994); Solovyev et al.,

Ismb 5:294-302 (1997); and GENESCAN, Burge et al., *J. Mol. Biol.* 268:78-94 (1997), predict many putative genes without known homology or function. Such programs are known, however, to give high false positive rates. Burset et al., *Genomics* 34:353-367 (1996). Using a consensus obtained by a plurality of such programs is known to increase the reliability of calling exons from genomic sequence. Ansari-Lari et al., *Genome Res.* 8(1):29-40 (1998)

Identification of functional genes from genomic data remains, however, an imperfect art. For example, in reporting the full sequence of human chromosome 21, the Chromosome 21 Mapping and Sequencing Consortium reports that prior bioinformatic estimates of human gene number may need to be revised substantially downwards. *Nature* 405:311-199 (2000); Reeves, *Nature* 405:283-284 (2000).

Thus, there is a need for methods and apparatus that permit the functions of the regions identified bioinformatically - and specifically, that permit the expression of regions predicted to encode protein - readily to be confirmed experimentally.

Recently, the development of nucleic acid microarrays has made possible the automated and highly parallel measurement of gene expression. Reviewed in Schena (ed.), DNA Microarrays : A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); *Nature Genet.* 21(1)(suppl):1 - 60 (1999); Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

It is common for microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, such as those from the I.M.A.G.E. consortium, Lennon et al., *Genomics* 33(1):151-2 (1996), or from the construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas

et al., *Cancer Res.* (in press). Such microarrays by definition can measure expression only of those genes found in EST libraries, and thus have not been useful as probes for genes discovered solely by genomic sequencing.

5 The utility of using whole genome nucleic acid microarrays to answer certain biological questions has been demonstrated for the yeast *Saccharomyces cerevisiae*. De Risi et al., *Science* 278:680 (1997). The vast majority of yeast nuclear genes, approximately 95% however, are single
10 exon genes, i.e., lack introns, Lopez et al., *RNA* 5:1135-1137 (1999); Goffeau et al., *Science* 274:563-67 (1996), permitting coding regions more readily to be identified. Whole genome nucleic acid microarrays have not generally
15 eukaryotic genomes, and in particular from those averaging more than one intron per gene.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition,
20 onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies. There is a need for methods and apparatus that permit prediction of
25 diseases of the liver, particularly those diseases with polygenic etiology, from diagnosis of fetal liver.

Summary of the Invention

30 The present invention solves these and other problems in the art by providing methods and apparatus for predicting, confirming, and displaying functional information derived from genomic sequence. The present invention also provides apparatus for verifying the
35 expression of putative genes identified within genomic

sequence.

In particular, the invention provides novel genome-derived single exon nucleic acid microarrays useful for verifying the expression of putative genes identified within genomic sequence.

The present invention also provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

Accordingly, in a first aspect of the invention, there is provided a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver, comprising a plurality of single exon nucleic acid probes according to any one of the nucleotide sequences set out in SEQ ID NOS: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.

By plurality is meant at least two, suitably at least 20, most suitably at least 100, preferably at least 1000 and, most preferably, upto 5000.

In one embodiment of the first aspect, each of said plurality of probes is separately and addressably amplifiable.

In an alternative embodiment, each of said plurality of probes is separately and addressably isolatable from said plurality.

In a preferred embodiment, each of said plurality of probes is amplifiable using at least one common primer. Preferably, each of said plurality of probes is amplifiable using a first and a second common primer.

In yet another embodiment, said set of single exon nucleic acid probes comprises between 50 - 20,000 probes, for example, 50 - 5000.

Suitably, said set of single exon nucleic acid

probes comprises at least 50 - 1000 discrete single exon nucleic acid probes having a sequence as set out in any of SEQ ID NOS.: 1 - 25,129 or a complimentary sequence, or a portion of such a sequence.

5 Preferably, the average length of the single exon nucleic acid probes is between 200 and 500 bp. It is preferred that the average length should be at least 200bp, suitably at least 250bp, most suitably at least 300bp, preferably at least 400bp and, most preferably, 500 bp.

10 In another embodiment, the single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence. It is preferred that at least 50%, suitably at least 60%, most suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said
15 single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

 In another preferred embodiment, said single exon nucleic acid lack homopolymeric stretches of A or T. It is preferred that at least 50%, suitably at least 60%, most
20 suitably at least 70%, preferably at least 75%, more preferably at least 80, 85, 90, 95 or 99% of said single exon nucleic acid probes lack homopolymeric stretches of A or T.

 Preferably, a spatially-addressable set of single
25 exon nucleic acid probes in accordance with the first aspect of the invention is addressably disposed upon a substrate.

 Suitable substrates include a filter membrane which may, preferably, be nitrocellulose or nylon. The
30 nylon may preferably, be positively-charged. Other suitable substrates include glass, amorphous silicon, crystalline silicon, and plastic. Further suitable materials include polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride,
35 polytetrafluoroethylene, polystyrene, polycarbonate,

polyacetal, polysulfone, celluloseacetate,
cellulosenitrate, nitrocellulose, and mixtures thereof.

In a second aspect of the invention, there is
provided a microarray comprising a spatially addressable
5 set of single exon nucleic acid probes in accordance with
the first aspect of the invention.

In one embodiment, a genome-derived single-exon
microarray is packaged together with such an ordered set of
amplifiable probes corresponding to the probes, or one or
10 more subsets of probes, thereon. In alternative
embodiments, the ordered set of amplifiable probes is
packaged separately from the genome-derived single exon
microarray.

In another aspect, the invention provides genome-
15 derived single exon nucleic acid probes useful for gene
expression analysis, and particularly for gene expression
analysis by microarray. In particular embodiments of this
aspect, the present invention provides human single-exon
probes that include specifically-hybridizable fragments of
20 SEQ ID Nos. 12,674 - 25,129, wherein the fragment
hybridizes at high stringency to an expressed human gene.
In particular embodiments, the invention provides single
exon probes comprising SEQ ID Nos. 1 - 12,673.

Accordingly, in a third aspect of the invention,
25 there is provided a single exon nucleic acid probe for
measuring human gene expression in a sample derived from
human Fetal liver which is a nucleic acid molecule
comprising a nucleotide sequence as set out in any of SEQ
ID NOS.: 1 - 12,673 or a complementary sequence or a
30 fragment thereof wherein said probe hybridizes at high
stringency to a nucleic acid expressed in the human Fetal
liver.

In one embodiment, a single exon nucleic acid
probe in accordance with the third aspect comprises a
35 nucleotide sequence as set out in any of SEQ ID NOS.:

12,674 - 25,129 or a complementary sequence or a fragment thereof.

In a fourth aspect of the invention, there is provided a single exon nucleic acid probe for measuring
5 human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any of SEQ ID NOs.: 25,130 - 37,156 or a complementary sequence or a fragment thereof wherein said probe
10 hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

Preferably, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention comprises between at least 15 and 50 contiguous
15 nucleotides of said SEQ ID NO:. It is preferred that the single exon nucleic acid probe comprises at least 15, suitably at least 20, more suitably at least 25 or preferably at least 50 contiguous nucleotides of said SEQ ID NO:.

20 In another preferred embodiment, a single exon nucleic acid probe in accordance with the third or fourth aspects of the invention is between 3kb and 25kb in length. It is preferred that said probe is no more than 3kb, suitably no more than 5kb, more suitably no more than 10kb,
25 preferably 15kb, more preferably 20kb or, most preferably, no more than 20kb in length.

Preferably, a single exon nucleic acid probe in accordance with either the fifth or sixth aspect of the invention is DNA, preferably single-stranded DNA, RNA or
30 PNA.

In another embodiment of either the third or fourth aspect of the invention, a single exon nucleic acid probe is detectably labeled. Suitable detectable labels include a radionuclide, a fluorescent label or a first
35 member of a specific binding pair. Suitable fluorescent

labels include dyes such as cyanine dyes, preferably Cy3 and Cy5 although other suitable dyes will be known to those skilled in the art.

In a particularly preferred embodiment, a single
5 exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks prokaryotic and bacteriophage vector sequence. In yet another embodiment, a single exon nucleic acid probe in accordance with either the third or fourth aspect of the invention lacks
10 homopolymeric stretches of A or T.

In a fifth aspect of the invention, there is provided an amplifiable nucleic acid composition, comprising:

the single exon nucleic acid probe in accordance
15 with either of the third or fourth aspects of the invention; and at least one nucleic acid primer;

wherein said at least one primer is sufficient to prime enzymatic amplification of said probe.

In an sixth aspect of the invention, there is
20 provided a method of measuring gene expression in a sample derived from human Fetal liver, comprising:

contacting the single exon microarray in
accordance with the second aspect of the invention, with a first collection of detectably labeled nucleic acids, said
25 first collection of nucleic acids derived from mRNA of human Fetal liver; and then

measuring the label detectably bound to each probe of said microarray.

In a seventh aspect of the invention, there is
30 provided a method of identifying exons in a eukaryotic genome, comprising:

algorithmically predicting at least one exon from genomic sequence of said eukaryote; and then

detecting specific hybridization of detectably
35 labeled nucleic acids to a single exon probe,

wherein said detectably labeled nucleic acids are derived from mRNA from the Fetal liver of said eukaryote, said probe is a single exon probe having a fragment identical in sequence to, or complementary in sequence to, said predicted exon, said probe is included within a single exon microarray in accordance with the first aspect of the invention, and said fragment is selectively hybridizable at high stringency.

In a eighth aspect of the invention, there is provided a method of assigning exons to a single gene, comprising:

identifying a plurality of exons from genomic sequence in accordance with the seventh aspect of the invention; and then measuring the expression of each of said exons in a plurality of tissues and/or cell types using hybridization to single exon microarrays having a probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

In an ninth aspect of the invention, there is provided a nucleic acid sequence as set out in any of SEQ ID NOS: 1 - 25,129 wherein said sequence encodes a peptide.

In a tenth aspect of the invention, there is provided a peptide encoded by a sequence comprising a sequence as set out in any of SEQ ID NOS: 12,674 - 25,129, or a complementary sequence or coding portion thereof.

In a preferred embodiment, a peptide may be encoded by a sequence comprising a sequence set out in any of SEQ ID NOS.: 1 -12,673.

In a further aspect, the invention provides peptides comprising an amino acid sequence translated from the DNA fragments, said amino acid sequences comprising SEQ

ID NOS.: 25,130 - 37,156.

Accordingly in a eleventh aspect of the invention there is provided a peptide comprising a sequence as set out in any of SEQ ID NOS: 25,130 - 37,156, or fragment thereof.

In another aspect, the invention provides means for displaying annotated sequence, and in particular, for displaying sequence annotated according to the methods and apparatus of the present invention. Further, such display can be used as a preferred graphical user interface for electronic search, query, and analysis of such annotated sequence.

15 Detailed Description of the Invention

Definitions

As used herein, the term "microarray" and phrase "nucleic acid microarray" refer to a substrate-bound collection of plural nucleic acids, hybridization to each of the plurality of bound nucleic acids being separately detectable. The substrate can be solid or porous, planar or non-planar, unitary or distributed.

As so defined, the term "microarray" and phrase "nucleic acid microarray" include all the devices so called in Schena (ed.), DNA Microarrays: A Practical Approach (Practical Approach Series), Oxford University Press (1999) (ISBN: 0199637768); Nature Genet. 21(1)(suppl):1 - 60 (1999); and Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376). As so defined, the term "microarray" and phrase "nucleic acid microarray" further include substrate-bound collections of plural nucleic acids in which the nucleic acids are distributably disposed on a plurality of beads, rather than on a unitary

planar substrate, as is described; *inter alia*, in Brenner
et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000);
in such case, the term "microarray" and phrase "nucleic
acid microarray" refer to the plurality of beads in
5 aggregate.

As used herein with respect to a nucleic acid
microarray, the term "probe" refers to the nucleic acid
that is, or is intended to be, bound to the substrate; in
such context, the term "target" thus refers to nucleic acid
10 intended to be bound thereto by Watson-Crick
complementarity. As used herein with respect to solution
phase hybridization, the term "probe" refers to the nucleic
acid of known sequence that is detectably labeled.

As used herein, the expression "probe comprising
15 SEQ ID NO.", and variants thereof, intends a nucleic acid
probe, at least a portion of which probe has either (i) the
sequence directly as given in the referenced SEQ ID NO., or
(ii) a sequence complementary to the sequence as given in
the referenced SEQ ID NO., the choice as between sequence
20 directly as given and complement thereof dictated by the
requirement that the probe hybridize to mRNA.

As used herein, the term "open reading frame" and
the equivalent acronym "ORF" refer to that portion of an
exon that can be translated in its entirety into a sequence
25 of contiguous amino acids i.e. a nucleic acid sequence
that, in at least one reading frame, does not possess stop
codons; the term does not require that the ORF encode the
entirety of a natural protein.

As used herein, the term "amplicon" refers to a
30 PCR product amplified from human genomic DNA, containing
the predicted exon.

As used herein the term "exon" refers to the
consensus prediction of the various exon and gene
predicting algorithms i.e. a nucleic acid sequence
35 bioinformatically predicted to encode a portion of a

natural protein.

As used herein, the term "peptide" refers to a sequence of amino acids. The sequences referred to as PEPTIDE SEQ ID NOS.: are the predicted peptide sequences that would be translated from one of the exons, or a portion thereof set out in exon SEQ ID NOS.: The codons encoding the peptide are wholly contained within the exon.

As used herein, a "portions" of a defined nucleotide sequence or sequences can be and, preferably, are fragments unique to that sequence or to one or a combination of those sequences. A fragment unique to a nucleic acid molecule is one that is a signature for the larger nucleic acid molecule.

As used herein, the phrase "expression of a probe" and its linguistic variants means that the ORF present within the probe, or its complement, is present within a target mRNA.

As used herein, "stringent conditions" refers to parameters well known to those skilled in the art. When a nucleic acid molecule is said to be hybridisable to another of a given sequence under "stringent conditions" it is meant that it is homologous to the given sequence.

As used herein, the phrase "specific binding pair" intends a pair of molecules that bind to one another with high specificity. Binding pairs are said to exhibit specific binding when they exhibit avidity of at least 10^7 , preferably at least 10^8 , more preferably at least 10^9 liters/mole. Nonlimiting examples of specific binding pairs are: antibody and antigen; biotin and avidin; and biotin and streptavidin.

As used herein with respect to the visual display of annotated genomic sequence, the term "rectangle" means any geometric shape that has at least a first and a second border, wherein the first and second borders each are capable of mapping uniquely to a point of another visual

object of the display.

As used herein, a "Mondrian" means a visual display in which a single genomic sequence is annotated with predicted and experimentally confirmed functional
5 information.

Brief Description of the Drawings

10 The present invention is further illustrated with reference to the following non-limiting figures and examples in which:

FIG. 1 illustrates a process for predicting functional regions from genomic sequence, confirming the
15 functional activity of such regions experimentally, and associating and displaying the data so obtained in meaningful and useful relationship to the original sequence data;

FIG. 2 further elaborates that portion of the
20 process schematized in FIG. 1 for predicting functional regions from genomic sequence;

FIG. 3 illustrates a Mondrian visual display;

FIG. 4 presents a Mondrian showing a hypothetical annotated genomic sequence;

25 FIG. 5 is a histogram showing the distribution of ORF length and PCR products as obtained, with ORF length shown in black and PCR product length shown in dotted lines;

FIG. 6 is a histogram showing the distribution,
30 among exons predicted according to the methods described, of expression as measured using simultaneous two color hybridization to a genome-derived single exon microarray. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or
35 more but not all tested tissues ("1" - "9"), or expressed

in all tissues tested ("10");

FIG. 7 is a pictorial representation of the expression of verified sequences that showed expression with signal intensity greater than 3 in at least one tissue, with: FIG. 7A showing the expression as measured by microarray hybridization in each of the 10 measured tissues, and the expression as measured "bioinformatically" by query of EST, NR and SwissProt databases; with FIG. 7B showing the legend for display of physical expression (ratio) in FIG. 7A; and with FIG. 7C showing the legend for scoring EST hits as depicted in FIG. 7A;

FIG. 8 shows a comparison of normalized CY3 signal intensity for arrayed sequences that were identical to sequences in existing EST, NR and SwissProt databases or that were dissimilar (unknown), where black denotes the signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (1×10^{-30}) ("unknown") and a dotted line denotes sequence-verified spots with a BLAST expect ("E") value of less than $1e-30$ (1×10^{-30}) ("known");

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000), containing the carbamyl phosphate synthetase gene (AF154830.1); and

FIG. 10 is a Mondrian of BAC A049839.

Methods and Apparatus for Predicting, Confirming, Annotating, and Displaying Functional Regions From Genomic Sequence Data

30

FIG. 1 is a flow chart illustrating in broad outline a process for predicting functional regions from genomic sequence, confirming and characterizing the functional activity of such regions experimentally, and then associating and displaying the information so obtained

in meaningful and useful relationship to the original sequence data.

The initial input into process 10 of the present invention is drawn from one or more databases 100
5 containing genomic sequence data. Because genomic sequence is usually obtained from subgenomic fragments, the sequence data typically will be stored in a series of records corresponding to these subgenomic sequenced fragments. Some fragments will have been catenated to form larger
10 contiguous sequences ("contigs"); others will not. A finite percentage of sequence data in the database will typically be erroneous, consisting *inter alia* of vector sequence, sequence created from aberrant cloning events, sequence of artificial polylinkers, and sequence that was
15 erroneously read.

Each sequence record in database 100 will minimally contain as annotation a unique sequence identifier (accession number), and will typically be annotated further to identify the date of accession,
20 species of origin, and depositor. Because database 100 can contain nongenomic sequence, each sequence will typically be annotated further to permit query for genomic sequence. Chromosomal origin, optionally with map location, can also be present. Data can be, and over time increasingly will
25 be, further annotated with additional information, in part through use of the present invention, as described below. Annotation can be present within the data records, in information external to database 100 and linked to the records thereto, or through a combination of the two.

30 Databases useful as genomic sequence database 100 in the present invention include GenBank, and particularly include several divisions thereof, including the htgs(draft), NT (nucleotide, command line), and NR (nonredundant) divisions. GenBank is produced by the
35 National Institutes of Health and is maintained by the

National Center for Biotechnology Information (NCBI).
Databases of genomic sequence from species other than
human, such as mouse, rat, *Arabidopsis*, *C. elegans*, *C.*
briggsii, *Drosophila*, zebra fish, and other higher
5 eukaryotic organisms will also prove useful as genomic
sequence database 100.

Genomic sequence obtained by query of genomic
sequence database 100 is then input into one or more
processes 200 for identification of regions therein that
10 are predicted to have a biological function as specified by
the user. Such functions include, but are not limited to,
encoding protein, regulating transcription, regulating
message transport after transcription into mRNA, regulating
message splicing after transcription into mRNA, of
15 regulating message degradation after transcription into
mRNA, and the like. Other functions include directing
somatic recombination events, contributing to chromosomal
stability or movement, contributing to allelic exclusion or
X chromosome inactivation, and the like.

20 The particular genomic sequence to be input into
process 200 will depend upon the function for which
relevant sequence is to be identified as well as upon the
approach chosen for such identification. Process step 200
can be iterated to identify different functions within a
25 given genomic region. In such case, the input often will
be different for the several iterations.

Sequences predicted to have the requisite
function by process 200 are then input into process 300,
where a subset of the input sequences suitable for
30 experimental confirmation is identified. Experimental
confirmation can involve physical and/or bioinformatic
assay. Where the subsequent experimental assay is
bioinformatic, rather than physical, there are fewer
constraints on the sequences that can be tested, and in
35 this latter case therefore process 300 can output the

entirety of the input sequence.

The subset of sequences output from process 300 is then used in process 400 for experimental verification and characterization of the function predicted in process 200, which experimental verification can, and often will, include both physical and bioinformatic assay.

Process 500 annotates the sequence data with the functional information obtained in the physical and/or bioinformatic assays of process 400. Such annotation can be done using any technique that usefully relates the functional information to the sequence, as, for example, by incorporating the functional data into the sequence data record itself, by linking records in a hierarchical or relational database, by linking to external databases, by a combination thereof, or by other means well known within the database arts. The data can even be submitted for incorporation into databases maintained by others, such as GenBank, which is maintained by NCBI.

As further noted in FIG. 1, additional annotation can be input into process 500 from external sources 600.

The annotated data is then displayed in process 800, either before, concomitantly with, or after optional storage 700 on nontransient media, such as magnetic disk, optical disc, magneto-optical disk, flash memory, or the like.

FIG. 1 shows that the experimental data output from process 400 can be used in each preceding step of process 10: e.g., facilitating identification of functional sequences in process 200, facilitating identification of an experimentally suitable subset thereof in process 300, and facilitating creation of physical and/or informational substrates for, and performance of subsequent assay, of functional sequences in process 400.

Information from each step can be passed directly to the succeeding process, or stored in permanent or

interim form prior to passage to the succeeding process. Often, data will be stored after each, or at least a plurality, of such process steps. Any or all process steps can be automated.

5 FIG. 2 further elaborates the prediction of functional sequence within genomic sequence according to process 200.

Genomic sequence database 100 is first queried 20 for genomic sequence.

10 The sequence required to be returned by query 20 will depend, in the first instance, upon the function to be identified.

For example, genomic sequences that function to encode protein can be identified *inter alia* using gene
15 prediction approaches, comparative sequence analysis approaches, or combinations of the two. In gene prediction analysis, sequence from one genome is input into process 200 where at least one, preferably a plurality, of algorithmic methods are applied to identify putative coding
20 regions. In comparative sequence analysis, by contrast, corresponding, e.g., syntenic, sequence from a plurality of sources, typically a plurality of species, is input into process 200, where at least one, possibly a plurality, of algorithmic methods are applied to compare the sequences
25 and identify regions of least variability.

The exact content of query 20 will also depend upon the database queried. For example, if the database contains both genomic and nongenomic sequence, perhaps derived from multiple species, and the function to be
30 determined is protein coding regions in human genomic sequence, the query will accordingly require that the sequence returned be genomic and derived from humans.

Query 20 can also incorporate criteria that compel return of sequence that meets operative requirements
35 of the subsequent analytical method. Alternatively, or in

addition, such operative criteria can be enforced in subsequent preprocess step 24.

For example, if the function sought to be identified is protein coding, query 20 can incorporate
5 criteria that return from genomic sequence database 100 only those sequences present within contigs sufficiently long as to have obviated substantial fragmentation of any given exon among a plurality of separate sequence fragments.

10 Such criteria can, for example, consist of a required minimal individual genomic sequence fragment length, such as 10 kb, more typically 20 kb, 30 kb, 40kb, and preferably 50 kb or more, as well as an optional further or alternative requirement that sequence from any
15 given clone, such as a bacterial artificial chromosome ("BAC"), be presented in no more than a finite maximal number of fragments, such as no more than 20 separate pieces, more typically no more than 15 fragments, even more typically no more than about 10 - 12 fragments.

20 Results using the present invention have shown that genomic sequence from bacterial artificial chromosomes (BACs) is sufficient for gene prediction analysis according to the present invention if the sequence is at least 50 kb in length, and if additionally the sequence from any given
25 BAC is presented in fewer than 15, and preferably fewer than 10, fragments. Accordingly, query 20 can incorporate a requirement that data accessioned from BAC sequencing be in fewer than 15, preferably fewer than 10, fragments.

An additional criterion that can be incorporated
30 into the query can be the date, or range of dates, of sequence accession. Although the process has been described above as if genomic sequence database 100 were static, it is of course understood that the genomic sequence databases need not be static, and indeed are
35 typically updated on a frequent, even hourly, basis. Thus,

as further described in Examples 1 and 2, *infra*, it is possible to query the database for newly added sequence, either newly added after an absolute date, or newly added relative to a prior analysis performed using the methods and apparatus of the present invention. In this way, the process herein described can incorporate a dynamic, temporal component.

One utility of such temporal limitation is to identify, from newly accessioned genomic sequence, the presence of novel genes, particularly those not previously identified by EST sequencing (or other sequencing efforts that are similarly based upon gene expression). As further described in Example 1, such an approach has shown that newly accessioned human genomic sequence, when analyzed for sequences that function to encode protein, readily identifies genes that are novel over those in existing EST and other expression databases. This makes the methods of the present invention extremely powerful gene discovery tools. And as would be appreciated, such gene discovery can be performed using genomic sequence from species other than human.

If query 20 incorporates multiple criteria, such as above-described, the multiple criteria can be performed as a series of separate queries or as a single query, depending in part upon the query language, the complexity of the query, and other considerations well known in the database arts.

If query 20 returns no genomic sequence meeting the query criteria, the negative result can be reported by process 22, and process 200 (and indeed, entire process 10) ended 23, as shown. Alternatively, or in addition to report and termination of the initial inquiry, a new query 20 can be generated that takes into account the initial negative result.

When query 20 returns sequence meeting the query

criteria, the returned sequence is then passed to optional preprocessing 24, suitable and specific for the desired analytical approach and the particular analytical methods thereof to be used in process 25.

5 Preprocessing 24 can include processes suitable for many approaches and methods thereof, as well as processes specifically suited for the intended subsequent analysis.

 Preprocessing 24 suitable for most approaches and
10 methods will include elimination of sequence irrelevant to, or that would interfere with, the subsequent analysis. Such sequence includes repetitive sequence, such as Alu repeats and LINE elements, vector sequence, artificial sequence, such as artificial polylinkers, and the like.
15 Such removal can readily be performed by identification and subsequent masking of the undesired sequence.

 Identification can be effected by comparing the genomic sequence returned by query 20 with public or private databases containing known repetitive sequence,
20 vector sequence, artificial sequence, and other artifactual sequence. Such comparison can readily be done using programs well known in the art, such as CROSS_MATCH, or by proprietary sequence comparison programs the engineering of which is well within the skill in the art.

25 Alternatively, or in addition, undesirable, including artifactual, sequence can be identified algorithmically without comparison to external databases and thereafter removed. For example, synthetic polylinker sequence can be identified by an algorithm that identifies
30 a significantly higher than average density of known restriction sites. As another example, vector sequence can be identified by algorithms that identify nucleotide or codon usage at variance with that of the bulk of the genomic sequence.

35 Once identified, undesired sequence can be

removed. Removal can usefully be done by masking the undesired sequence as, for example, by converting the specific nucleotide references to one that is unrecognized by the subsequent bioinformatic algorithms, such as "X".

- 5 Alternatively, but at present less preferred, the undesired sequence can be excised from the returned genomic sequence, leaving gaps.

Preprocessing 24 can further include selection from among duplicative sequences of that one sequence of
10 highest quality. Higher quality can be measured as a lower percentage of, fewest number of, or least densely clustered occurrence of ambiguous nucleotides, defined as those nucleotides that are identified in the genomic sequence using symbols indicating ambiguity. Higher quality can
15 also or alternatively be valued by presence in the longest contig.

Preprocessing 24 can, and often will, also include formatting of the data as specifically appropriate for passage to the analytical algorithms of process 25.
20 Such formatting can and typically will include, *inter alia*, addition of a unique sequence identifier, either derived from the original accession number in genomic sequence database 100, or newly applied, and can further include additional annotation. Formatting can include conversion
25 from one to another sequence listing standard, such as conversion to or from FASTA or the like, depending upon the input expected by the subsequent process.

Preprocessing, which can be optional depending upon the function desired to be identified and the
30 informational requirements of the methods for effecting such identification, is followed by sequence processing 25, where sequences with the desired function are identified within the genomic sequence.

As mentioned above, such functions can include,
35 but are not limited to, encoding protein, regulating

transcription, regulating message transport after transcription into mRNA, regulating message splicing after transcription, of regulating message degradation, and the like. Other functions include directing somatic
5 recombination events, contributing to chromosomal stability or movement, contributing to allelic exclusion or X chromosome inactivation, or the like.

The methods of the present invention are particularly useful for gene discovery, that is, for
10 identifying, from genomic sequence, regions that function to encode genes, and in a particularly useful embodiment, for identifying regions that function to encode genes not hitherto identified by expression-based or directed cloning and sequencing. In conjunction with verification using the
15 novel single exon microarrays of the present invention, as further described below, the methods herein described become powerful gene discovery tools.

Accordingly, in a preferred embodiment of the present invention, process 25 is used to identify putative
20 coding regions. Two preferred approaches in process 25 for identifying sequence that encodes putative genes are gene prediction and comparative sequence analysis.

Gene prediction can be performed using any of a number of algorithmic methods, embodied in one or more
25 software programs, that identify open reading frames (ORFs) using a variety of heuristics, such as GRAIL, DICTION, and GENEFINDER. Comparative sequence analysis similarly can be performed using any of a variety of known programs that identify regions with lower sequence variability.

30 As further described in Example 1, below, gene finding software programs yield a range of results. For the newly accessioned human genomic sequence input in Example 1, for example, GRAIL identified the greatest percentage of genomic sequence as putative coding region,
35 2% of the data analyzed; GENEFINDER was second, calling 1%;

and DICTION yielded the least putative coding region, with 0.8% of genomic sequence called as coding region.

Increased reliability can be obtained when consensus is required among several such methods. Although
5 discussed herein particularly with respect to exon calling, consensus among methods will in general increase reliability of predicting other functions as well.

Thus, as indicated by query 26, sequence processing 25, optionally with preprocessing 24, can be
10 repeated with a different method, with consensus among such iterations determined and reported in process 27.

Process 27 compares the several outputs for a given input genomic sequence and identifies consensus among the separately reported results. The consensus itself, as
15 well as the sequence meeting that consensus, is then stored in process 29a, displayed in process 29b, and/or output to process 300 for subsequent identification of a subset thereof suitable for assay.

Multiple levels of consensus can be calculated
20 and reported by process 27. For example, as further described in Example 1, *infra*, process 27 can report consensus as between all specific pairs of methods of gene prediction, as consensus among any one or more of the pairs of methods of gene prediction, or as among all of the gene
25 prediction algorithms used. Thus, in Example 1, process 27 reported that GRAIL and GENEFINDER programs agreed on 0.7% of genomic sequence, that GRAIL and DICTION agreed on 0.5% of genomic sequence, and that the three programs together agreed on 0.25% of the data analyzed. Put another way,
30 0.25% of the genomic sequence was identified by all three of the programs as containing putative coding region.

Furthermore, consensus can be required among different approaches to identifying a chosen function.

For example, if the function desired to be
35 identified is coding of protein sequence, and a first used

approach to exon calling is gene prediction, the process can be repeated on the same input sequence, or subset thereof, with another approach, such as comparative sequence analysis. In such a case, where comparative
5 sequence analysis follows gene prediction, the comparison can be performed not only on genomic nucleic acid sequence, but additionally or alternatively can be performed on the predicted amino acid sequence translated from the ORFs prior identified by the gene prediction approach.

10 Although shown as an iterative process, the multiple analyses required to achieve consensus can be done in series, in parallel, or some combination thereof.

Predicted functional sequence, optionally representing a consensus among a plurality of methods and
15 approaches for determination thereof, is passed to process 300 for identification of a subset thereof for functional assay.

In the preferred embodiment of the methods of the present invention, wherein the function sought to be
20 identified is protein coding, process 300 is used to identify a subset thereof suitable for experimental verification by physical and/or bioinformatic approaches.

For example, putative ORFs identified in process 200 can be classified, or binned, bioinformatically into
25 putative genes. This binning can be based *inter alia* upon consideration of the average number of exons/gene in the species chosen for analysis, upon density of exons that have been called on the genomic sequence, and other empirical rules. Thereafter, one or more among the gene-
30 specific ORFs can be chosen for subsequent use in gene expression assay.

Where such subsequent gene expression assay uses amplified nucleic acid, considerations such as desired amplicon length, primer synthesis requirements, putative
35 exon length, sequence GC content, existence of possible

secondary structure, and the like can be used to identify and select those ORFs that appear most likely successfully to amplify. Where subsequent gene expression assay relies upon nucleic acid hybridization, whether or not using
5 amplified product, further considerations involving hybridization stringency can be applied to identify that subset of sequences that will most readily permit sequence-specific discrimination at a chosen hybridization and wash stringency. One particular such consideration is avoidance
10 of putative exons that span repetitive sequence; such sequence can hybridize spuriously to nonspecific message, reducing specific signal in the hybridization.

For bioinformatic assay, there are fewer constraints on the sequences that can be tested
15 experimentally, and in this latter case therefore process 300 can output the entirety of the input sequence.

The subset of sequences identified by process 300 as suitable for use in assay is then used in process 400 to create the physical and/or informational substrate for
20 experimental verification of the predictions made in process 200, and thereafter to assay those substrates.

As mentioned, the methods of the present invention are particularly useful for identifying potential coding regions within genomic sequence. In a preferred
25 embodiment of process 400, therefore, the expression of the sequences predicted to encode protein is verified. The combination of the predictive and experimental methods provides a powerful gene discovery engine.

Thus, in another aspect, the present invention
30 provides methods and apparatus for verifying the expression of putative genes identified within genomic sequence. In particular, the invention provides a novel method of verifying gene expression in which expression of predicted ORFs is measured and confirmed using a novel type of
35 nucleic acid microarray, the genome-derived single exon

nucleic acid microarrays of the present invention.

Putative ORFs as predicted by a consensus of gene calling, particularly gene prediction, algorithms in process 200, and as further identified as suitable by process 300, are amplified from genomic DNA using the polymerase chain reaction (PCR). Although PCR is conveniently used, other amplification approaches can also be used.

Amplification schemes can be designed to capture the entirety of each predicted ORF in an amplicon with minimal additional (that is, intronic or intergenic) sequence. Because ORFs predicted from human genomic sequence using the methods of the present invention differ in length, such an approach results in amplicons of varying length.

However, most predicted ORFs are shorter than 500 bp in length, and although amplicons of at least about 100 or 200 base pairs can be immobilized as probes on nucleic acid microarrays, early experimental results using the methods of the present invention have suggested that longer amplicons, at least about 400 or 500 base pairs, are more effective. Furthermore, certain advantages derive from application to the microarray of amplicons of defined size.

Therefore, amplification schemes can alternatively, and preferably, be designed to amplify regions of defined size, preferably at least about 300, 400 or 500 bp, centered about each predicted ORF. Such an approach results in a population of amplicons of limited size diversity, but that typically contain intronic and/or intergenic nucleic acid in addition to putative ORF.

Conversely, somewhat fewer than 10% of ORFs predicted from human genomic sequence according to the methods of the present invention exceed 500 bp in length. Portions of such extended ORFs, preferably at least about 300, 400 or 500 bp in length, can be amplified. However, it

has been discovered that the percentage success at amplifying pieces of such ORFs is low, and that such putative exons are more effectively amplified when larger fragments, at least about 1000 or 1500 bp, and even as large as 2000 bp are amplified.

The putative ORFs selected in process 300 are thus input into one or more primer design programs, such as PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>), with a goal of amplifying at least about 500 base pairs of genomic sequence centered within or about ORFs predicted to be no more than about 500 bp, or at least about 1000 - 1500 bp of genomic sequence for ORFs predicted to exceed 500 bp in length, and the primers synthesized by standard techniques. Primers with the requisite sequences can be purchased commercially or synthesized by standard techniques.

Conveniently, a first predetermined sequence can be added commonly to the ORF-specific 5' primer and a second, typically different, predetermined sequence commonly added to each 3' ORF-unique primer. This serves to immortalize the amplicon, that is, serves to permit further amplification of any amplicon using a single set of primers complementary respectively to the common 5' and common 3' sequence elements. The presence of these "universal" priming sequences further facilitates later sequence verification, providing a sequence common to all amplicons at which to prime sequencing reactions. The common 5' and 3' sequences further serve to add a cloning site should any of the ORFs warrant further study.

Such predetermined sequence is usefully at least about 10, 12 or 15 nt in length, and usually does not exceed about 25 nt in length. The "universal" priming sequences used in the examples presented *infra* were each 16 nt long.

The genomic DNA to be used as substrate for

amplification will come from the eukaryotic species from which the genomic sequence data had originally been obtained, or a closely related species, and can conveniently be prepared by well known techniques from somatic or germline tissue or cultured cells of the organism. See, e.g., Short Protocols in Molecular Biology : A Compendium of Methods from Current Protocols in Molecular Biology, Ausubel et al. (eds.), 4th edition (April 1999), John Wiley & Sons (ISBN: 047132938X) and Maniatis et al., Molecular Cloning : A Laboratory Manual, 2nd edition (December 1989), Cold Spring Harbor Laboratory Press (ISBN: 0879693096). Many such prepared genomic DNAs are available commercially, with the human genomic DNAs additionally having certification of donor informed consent.

Although the intronic and intergenic material flanking putative coding regions in the amplicons could potentially interfere with hybridizations during microarray experiments, we have found, surprisingly, that differential expression ratios are not significantly affected. Rather, the predominant effect of exon size is to alter the absolute signal intensity, rather than its ratio. Equally surprising, the art had suggested that single exon probes would not provide sufficient signal intensity for high stringency hybridization analyses; we find that such probes not only provide adequate signal, but have substantial advantages, as herein described.

After partial purification, as by size exclusion spin column, with or without confirmation as to amplicon quality as by gel electrophoresis, each amplicon (single exon probe) is disposed in an array upon a support substrate.

Methods for creating microarrays by deposition and fixation of nucleic acids onto support substrates are well known in the art (Reviewed by Schena et al., see

above).

Typically, the support substrate will be glass, although other materials, such as amorphous or crystalline silicon or plastics. Such plastics include

5 polymethylacrylic, polyethylene, polypropylene, polyacrylate, polymethylmethacrylate, polyvinylchloride, polytetrafluoroethylene, polystyrene, polycarbonate, polyacetal, polysulfone, celluloseacetate, cellulosenitrate, nitrocellulose, or mixtures thereof, can

10 also be used. Typically, the support will be rectangular, although other shapes, particularly circular disks and even spheres, present certain advantages. Particularly advantageous alternatives to glass slides as support substrates for array of nucleic acids are optical discs, as

15 described in WO 98/12559.

The amplified nucleic acids can be attached covalently to a surface of the support substrate or, more typically, applied to a derivatized surface in a chaotropic agent that facilitates denaturation and adherence by

20 presumed noncovalent interactions, or some combination thereof.

Robotic spotting devices useful for arraying nucleic acids on support substrates can be constructed using public domain specifications (The MGuide, version

25 2.0, <http://cmgm.stanford.edu/pbrown/mguide/index.html>), or can conveniently be purchased from commercial sources (MicroArray GenII Spotter and MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Spotting can also be effected by printing methods, including those using

30 ink jet technology.

As is well known in the art, microarrays typically also contain immobilized control nucleic acids. For controls useful in providing measurements of background signal for the genome-derived single exon microarrays of

35 the present invention, a plurality of *E. coli* genes can

readily be used. As further described in Example 1, 16 or 32 *E. coli* genes suffice to provide a robust measure of background noise in such microarrays.

As is well known in the art, the amplified
5 product disposed in arrays on a support substrate to create a nucleic acid microarray can consist entirely of natural nucleotides linked by phosphodiester bonds, or alternatively can include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as
10 complementary binding can be obtained in the hybridization. If enzymatic amplification is used to produce the immobilized probes, the amplifying enzyme will impose certain further constraints upon the types of nucleic acid analogs that can be generated.

15 Although particularly described herein as using high density microarrays constructed on planar substrates, the methods of the present invention for confirming the expression of ORFs predicted from genomic sequence can use any of the known types of microarrays, as herein defined,
20 including lower density planar arrays, and microarrays on nonplanar, nonunitary, distributed substrates.

For example, gene expression can be confirmed using hybridization to lower density arrays, such as those constructed on membranes, such as nitrocellulose, nylon,
25 and positively-charged derivatized nylon membranes.

Further, gene expression can also be confirmed using nonplanar, bead-based microarrays such as are described in Brenner et al., *Proc. Natl. Acad. Sci. USA* 97(4):166501670 (2000); U.S. Patent No. 6,057,107; and U.S. Patent No.
30 5,736,330. In theory, a packed collection of such beads provides in aggregate a higher density of nucleic acid probe than can be achieved with spotting or lithography techniques on a single planar substrate.

Planar microarrays on solid substrates, however,
35 provide certain useful advantages, including high

throughput and compatibility with existing readers. For example, each standard microscope slide can include at least 1000, typically at least 2000, preferably 5000 and upto 10,000 - 50,000 or more nucleic acid probes of
5 discrete sequence. The number of sequences deposited will depend on their required application.

Each putative gene can be represented in the array by a single predicted ORF. Alternatively, genes can be represented by more than one predicted ORF. For
10 purposes of measuring differential splicing, more than one predicted ORF will be provided for a putative gene. And as is well known in the art, each probe of defined sequence, representing a single predicted ORF, can be deposited in a plurality of locations on a single microarray to provide
15 redundancy of signal.

The genome-derived single exon microarrays described above differ in several fundamental and advantageous ways from microarrays presently used in the gene expression art, including (1) those created by
20 deposition of mRNA-derived nucleic acids, (2) those created by *in situ* synthesis of oligonucleotide probes, and (3) those constructed from yeast genomic DNA.

Most nucleic acid microarrays that are in use for study of eukaryotic gene expression have as immobilized
25 probes nucleic acids that are derived - either directly or indirectly - from expressed message. As discussed above, it is common, for example, for such microarrays to be derived from cDNA/EST libraries, either from those previously described in the literature, see Lennon et al.,
30 or from the *de novo* construction of "problem specific" libraries targeted at a particular biological question, R.S. Thomas et al., *Cancer Res.* (in press). Such microarrays are herein collectively denominated "EST microarrays".

35 Such EST microarrays by definition can measure

expression only of those genes found in EST libraries, shown herein to represent only a fraction of expressed genes. Furthermore, such libraries - and thus microarrays based thereupon - are biased by the tissue or cell type of message origin, by the expression levels of the respective genes within the tissues, and by the ability of the message successfully to have been reverse-transcribed and cloned.

Thus, as further discussed in Example 1, the methods of the present invention enable sequences that do not appear in EST or other expression databases to be determined - subsequently arrayed for expression measurements could not, therefore, have been represented as probes on an EST microarray. And as further demonstrated in the examples, *infra*, the remaining population of genes identified from genomic sequence by the methods of the present invention - that is, the one third of sequences that had previously been accessioned in EST or other expression databases - are biased toward genes with higher expression levels.

Representation of a message in an EST and/or cDNA library depends upon the successful reverse transcription, optionally but typically with subsequent successful cloning, of the message. This introduces substantial bias into the population of probes available for arraying in EST microarrays.

In contrast, neither reverse transcription nor cloning is required to produce the probes arrayed on the genome-derived single exon microarrays of the present invention. And although the ultimate deposition of a probe on the genome-derived single exon microarray of the present invention depends upon a successful amplification from genomic material, *a priori* knowledge of the sequence of the desired amplicon affords greater opportunity to recover any given probe sequence recalcitrant to amplification than is afforded by the requirement for successful reverse

transcription and cloning of unknown message in EST approaches.

Thus, the genome-derived single exon microarrays of the present invention present a far greater diversity of probes for measuring gene expression, with far less bias, than do EST microarrays presently used in the art.

As a further consequence of their ultimate origin from expressed message, the probes in EST microarrays often contain poly-A (or complementary poly-T) stretches derived from the poly-A tail of mature mRNA. These homopolymeric stretches contribute to cross-hybridization, that is, to a spurious signal occasioned by hybridization to the homopolymeric tail of a labeled cDNA that lacks sequence homology to the gene-specific portion of the probe.

In contrast, the probes arrayed in the genome-derived single exon microarrays of the present invention lack homopolymeric stretches derived from message polyadenylation, and thus can provide more specific signal. Typically, at least about 50, 60 or 75% of the probes on the genome-derived single exon microarrays of the present invention lack homopolymeric regions consisting of A or T, where a homopolymeric region is defined for purposes herein as stretches of 25 or more, typically 30 or more, identical nucleotides.

A further distinction, which also affects the specificity of hybridization, is occasioned by the typical derivation of EST microarray probes from cloned material. Because much of the probe material disposed as probes on EST microarrays is excised or amplified from plasmid, phage, or phagemid vectors, EST microarrays typically include a fair amount of vector sequence, more so when the probes are amplified, rather than excised, from the vector.

In contrast, the vast majority of probes in the genome-derived single exon microarrays of the present invention contain no prokaryotic or bacteriophage vector

sequence, having been amplified directly or indirectly from genomic DNA. Typically, therefore, at least about 50, 60, 70 or 80% or more of individual exon-including probes disposed on a genome-derived single exon microarray of the present invention lack vector sequence, and particularly lack sequences drawn from plasmids and bacteriophage. Preferably, at least about 85, 90 or more than 90% of exon-including probes in the genome-derived single exon microarray of the present invention lack vector sequence.

10 With attention to removal of vector sequences through preprocessing 24, percentages of vector-free exon-including probes can be as high as 95 - 99%. The substantial absence of vector sequence from the genome-derived single exon microarrays of the present invention results in greater

15 specificity during hybridization, since spurious cross-hybridization to a probe vector sequence is reduced.

As a further consequence of excision or amplification of probes from vectors in construction of EST microarrays, the probes arrayed thereon often contain

20 artificial sequence, derived from vector polylinker multiple cloning sites, at both 5' and 3' ends. The probes disposed upon the genome-derived single exon microarrays need have no such artificial sequence appended thereto.

As mentioned above, however, the ORF-specific

25 primers used to amplify putative ORFs can include artificial sequences, typically 5' to the ORF-specific primer sequence, useful for "universal" (that is, independent of ORF sequence) priming of subsequent amplification or sequencing reactions. When such

30 "universal" 5' and/or 3' priming sequences are appended to the amplification primers, the probes disposed upon the genome-derived single exon microarray will include artificial sequence similar to that found in EST microarrays. However, the genome-derived single exon

35 microarray of the present invention can be made without

such sequences, and if so constructed, presents an even smaller amount of nonspecific sequence that would contribute to nonspecific hybridization.

Yet another consequence of typical use of cloned material as probes in EST microarrays is that such microarrays contain probes that result from cloning artifacts, such as chimeric molecules containing coding region of two separate genes. Derived from genomic material, typically not thereafter cloned, the probes of the genome-derived single exon microarrays of the present invention lack such cloning artifacts, and thus provide greater specificity of signal in gene expression measurements.

A further consequence of the cloned origin of probes on many EST microarrays is that the individual probes often have disparate sizes, which can cause the optimal hybridization stringency to vary among probes on a single microarray. In contrast, as discussed above, the probes arrayed on the genome-derived single exon microarrays of the present invention can readily be designed to have a narrow distribution in sizes, with the range of probe sizes no greater than about 10% of the average size, typically no greater than about 5% of the average probe size.

Because of their origin from fully- or partially-spliced message, probes disposed upon EST arrays will often include multiple exons. The percentage of such exon-spanning probes in an EST microarray can be calculated, on average, based upon the predicted number of exons/gene for the given species and the average length of the immobilized probes. For human genes, the near-complete sequence of human chromosome 22, Dunham *et al.*, *Nature* 402(6761):489-95 (1999), predicts that human genes average 5.5 exons/gene. Even with probes of 200 - 500 bp, the vast majority of human EST microarray probes include more than one exon.

In contrast, by virtue of their origin from algorithmically identified ORFs in genomic sequence, the probes in the genome-derived single exon microarrays of the present invention can consist of individual exons. Thus, 5 in contrast to EST microarrays, at least about 50, 60, 70, 75, 80, 85, 95 or 99% of probes deposited in the genome-derived microarray of the present invention consist of, or include, no more than one predicted ORF.

This provides the ability, not readily achieved 10 using EST microarrays, to use the genome-derived single exon microarrays of the present invention to measure tissue-specific expression of individual exons, which in turn allows differential splicing events to be detected and characterized, and in particular, allows the correlation of 15 differential splicing to tissue-specific expression patterns.

Furthermore, the exons that are represented in EST microarrays are often biased toward the 3' or 5' end of their respective genes, since sequencing strategies used 20 for EST identification are so biased. In contrast, no such 3' or 5' bias necessarily inheres in the selection of exons for disposition on the genome-derived single exon microarrays of the present invention.

Conversely, the probes provided on the genome- 25 derived single exon microarrays of the present invention typically, but need not necessarily, include intronic and/or intergenic sequence that is absent from EST microarrays, which are derived from mature mRNA. Typically, at least about 50, 60, 70, 80 or 90% of the 30 exon-including probes on the genome-derived single exon microarrays of the present invention include sequence drawn from noncoding regions. As discussed above, the additional presence of noncoding region does not significantly interfere with measurement of gene expression, and provides 35 the additional opportunity to assay prespliced RNA, and

thus measure such phenomena such as nuclear export control.

The genome-derived single exon microarrays of the present invention are also quite different from *in situ* synthesis microarrays, where probe size is severely
5 constrained by inadequacies in the photolithographic synthesis process.

Typically, probes arrayed on *in situ* synthesis microarrays are limited to a maximum of about 25 bp. As a well known consequence, hybridization to such chips must be
10 performed at low stringency. In order, therefore, to achieve unambiguous sequence-specific hybridization results, the *in situ* synthesis microarray requires substantial redundancy, with concomitant programmed arraying for each probe of probe analogues with altered
15 (*i.e.*, mismatched) sequence.

In contrast, the longer probe length of the genome-derived single exon microarrays of the present invention allows much higher stringency hybridization and wash. Typically, therefore, exon-including probes on the
20 genome-derived single exon microarrays of the present invention average at least about 100, 200, 300, 400 or 500 bp in length. By obviating the need for substantial probe redundancy, this approach permits a higher density of probes for discrete exons or genes to be arrayed on the
25 microarrays of the present invention than can be achieved for *in situ* synthesis microarrays.

A further distinction is that the probes in *in situ* synthesis microarrays typically are covalently linked to the substrate surface. In contrast, the probes disposed
30 on the genome-derived microarray of the present invention typically are, but need not necessarily be, bound noncovalently to the substrate.

Furthermore, the short probe size on *in situ* microarrays causes large percentage differences in the
35 melting temperature of probes hybridized to their

complementary target sequence, and thus causes large percentage differences in the theoretically optimum stringency across the array as a whole.

In contrast, the larger probe size in the
5 microarrays of the present invention create lower percentage differences in melting temperature across the range of arrayed probes.

A further significant advantage of the microarrays of the present invention over *in situ*
10 synthesized arrays is that the quality of each individual probe can be confirmed before deposition. In contrast, the quality of probes cannot be assessed on a probe-by-probe basis for the *in situ* synthesized microarrays presently being used.

15 The genome-derived single exon microarrays of the present invention are also distinguished over, and present substantial benefits over, the genome-derived microarrays from lower eukaryotes such as yeast. Lashkari et al., *Proc. Natl. Acad. Sci. USA* 94:13057-13062 (1997).

20 Only about 220 - 250 of the 6100 or so nuclear genes in *Saccharomyces cerevisiae* - that is, only about 4 - 5% - have standard, spliceosomal, introns, Lopez et al., *Nucl. Acids Res.* 28:85-86 (2000); Spingola et al., *RNA* 5(2):221-34 (1999). Furthermore, the entire yeast genome
25 has already been sequenced. These two facts permit the ready amplification and disposition of single-ORF amplicons on such microarray without the requirement for antecedent use of gene prediction and/or comparative sequence analyses.

30 Thus, a significant aspect of the present invention is the ability to identify and to confirm expression of predicted coding regions in genomic sequence drawn from eukaryotic organisms that have a higher percentage of genes having introns than do yeast such as
35 *Saccharomyces cerevisiae*, particularly in genomic sequence

drawn from eukaryotes in which at least about 10, 20 or 50% of protein-encoding genes have introns. In preferred embodiments, the methods and apparatus of the present invention are used to identify and confirm expression of
5 novel genes from genomic sequence of eukaryotes in which the average number of introns per gene is at least about one, two or three or more.

After the physical substrate is prepared, experimental verification of predicted function is
10 performed.

In a preferred embodiment of the present invention, where the function sought to be identified in genomic sequence is protein coding, experimental verification is performed by measuring expression of the
15 putative ORFs, typically through nucleic acid hybridization experiments, and in particularly preferred embodiments, through hybridization to genome-derived single exon microarrays prepared as above- described.

Expression is conveniently measured and expressed
20 for each probe in the microarray as a ratio of the expression measured concurrently in a plurality of mRNA sources, according to techniques well known in the microarray art, Reviewed in Schena et al., and as further described in Example 2, below. The mRNA source for the
25 reference against which specific expression is measured can be drawn from a homogeneous mRNA source, such as a single cultured cell-type, or alternatively can be heterogeneous, as from a pool of mRNA derived from multiple tissues and/or cell types, as further described in Example 2, *infra*.

30 mRNA can be prepared by standard techniques, see Ausubel et al. and Maniatis et al., or purchased commercially. The mRNA is then typically reverse-transcribed in the presence of labeled nucleotides: the index source (that in which expression is desired to be
35 measured) is reverse transcribed in the presence of

nucleotides labeled with a first label, typically a fluorophore (fluorochrome; fluor; fluorescent dye); the reference source is reverse transcribed in the presence of a second label, typically a fluorophore, typically
5 fluorometrically-distinguishable from the first label. As further described in Example 2, *infra*, Cy3 and Cy5 dyes prove particularly useful in these methods. After partial purification of the index and reference targets, hybridization to the probe array is conducted according to
10 standard techniques, typically under a coverslip.

After wash, microarrays are conveniently scanned using a commercial microarray scanning device, such as a Gen3 Scanner (Molecular Dynamics, Sunnyvale, CA). Data on expression is then passed, with or without interim storage,
15 to process 500, where the results for each probe are related to the original sequence.

Often, hybridization of target material to the genome-derived single exon microarray will identify certain of the probes thereon as of particular interest. Thus, it
20 is often desirable that the user be able readily to obtain sufficient quantities of an individual probe, either for subsequent arrayed deposition upon an additional support substrate, often as part of a microarray having a plurality of probes so identified, or alternatively or additionally
25 as a solitary solid-phase or solution-phase probe, for further use.

Thus, in another aspect, the present invention provides compositions and kits for the ready production of nucleic acids identical in sequence to, or substantially
30 identical in sequence to, probes on the genome-derived single exon microarrays of the present invention.

In this aspect, a small quantity of each probe is disposed, typically without attachment to substrate, in a spatially-addressable ordered set, typically one per well
35 of a microtiter dish. Although a 96 well microtiter plate

can be used, greater efficiency is obtained using higher density arrays, such as are provided by microtiter plates having 384, 864, 1536, 3456, 6144, or 9600 wells, and although microtiter plates having physical depressions
5 (wells) are conveniently used, any device that permits addressable withdrawal of reagent from fluidly-noncommunicating areas can be used.

In this aspect of the invention, therefore, a fluidly noncommunicating addressable ordered set of
10 individual probes, corresponding to those on a genome-derived single exon microarray, is provided, with each probe in sufficient quantity to permit amplification, such as by PCR. As earlier mentioned, the ORF-specific
5' primers used for genomic amplification can have a first
15 common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this preferred embodiment, the use of a single set of 5' and 3' primers to amplify any one of the probes from the
20 amplifiable ordered set.

Each discrete amplifiable probe can also be packaged with amplification primers, solutes, buffers, etc., and can be provided in dry (e.g., lyophilized) form or wet, in the latter case typically with addition of
25 agents that retard evaporation.

In another aspect of the present invention, a genome-derived single-exon microarray is packaged together with such an ordered set of amplifiable probes
corresponding to the probes, or one or more subsets of
30 probes, thereon. In alternative embodiments, the ordered set of amplifiable probes is packaged separately from the genome-derived single exon microarray.

In some embodiments, the microarray and/or ordered probe set are further packaged with recordable
35 media that provide probe identification and addressing

information, and that can additionally contain annotation information, such as gene expression data. Such recordable media can be packaged with the microarray, with the ordered probe set, or with both.

5 If the microarray is constructed on a substrate that incorporates recordable media, such as is described in international patent application no. WO 98/12559, then separate packaging of the genome-derived single exon microarray and the bioinformatic information is not
10 required.

The amount of amplifiable probe material should be sufficient to permit at least one amplification sufficient for subsequent hybridization assay.

Although the use of high density genome-derived
15 microarrays on solid planar substrates is presently a preferred approach for the physical confirmation and characterization of the expression of sequences predicted to encode protein, other types of microarrays (as herein defined) can also be used.

20 Furthermore, as earlier mentioned, experimental verification of the function predicted from genomic sequence in process 200 can be bioinformatic, rather than, or additional to, physical verification.

For example, where the function desired to be
25 identified is protein coding, the predicted ORFs can be compared bioinformatically to sequences known or suspected of being expressed.

Thus, the sequences output from process 300 (or process 200), can be used to query expression databases,
30 such as EST databases, SNP ("single nucleotide polymorphism") databases, known cDNA and mRNA sequences, SAGE ("serial analysis of gene expression") databases, and more generalized sequence databases that allow query for expressed sequences. Such query can be done by any
35 sequence query algorithm, such as BLAST ("basic local

alignment search tool"). The results of such query -
including information on identical sequences and
information on nonidentical sequences that have diffuse or
focal regions of sequence homology to the query sequence -
5 can then be passed directly to process 500, or used to
inform analyses subsequently undertaken in process 200,
process 300, or process 400.

Experimental data, whether obtained by physical
or bioinformatic assay in process 400, is passed to process
10 500 where it is usefully related to the sequence data
itself, a process colloquially termed "annotation". Such
annotation can be done using any technique that usefully
relates the functional information to the sequence, as, for
example, by incorporating the functional data into the
15 record itself, by linking records in a hierarchical or
relational database, by linking to external databases, or
by a combination thereof. Such database techniques are
well within the skill in the art.

The annotated sequence data can be stored
20 locally, uploaded to genomic sequence database 100, and/or
displayed 800.

The methods and apparatus of the present
invention rapidly produce functional information from
genomic sequence. Coupled with the escalating pace at
25 which sequence now accumulates, the rapid pace of sequence
annotation produces a need for methods of displaying the
information in meaningful ways.

FIG. 3 shows visual display 80 presenting a
single genomic sequence annotated according to the present
30 invention. Because of its nominal resemblance to artistic
works of Piet Mondrian, visual display 80 is alternatively
described herein as a "Mondrian".

Each of the visual elements of display 80 is
aligned with respect to the genomic sequence being
35 annotated (hereinafter, the "annotated sequence"). Given

the number of nucleotides typically represented in an annotated sequence, representation of individual nucleotides would rarely be readable in hard copy output of display 80. Typically, therefore, the annotated sequence
5 is schematized as rectangle 89, extending from the left border of display 80 to its right border. By convention herein, the left border of rectangle 89 represents the first nucleotide of the sequence and the right border of rectangle 89 represents the last nucleotide of the
10 sequence.

As further discussed below, however, the Mondrian visual display of annotated sequence can serve as a convenient graphical user interface for computerized representation, analysis, and query of information stored
15 electronically. For such use, the individual nucleotides can conveniently be linked to the X axis coordinate of rectangle 89. This permits the annotated sequence at any point within rectangle 89 readily to be viewed, either automatically - for example, by time-delayed appearance of
20 a small overlaid window upon movement of a cursor or other pointer over rectangle 89 - or through user intervention, as by clicking a mouse or other pointing device at a point in rectangle 89.

Visual display 80 is generated after user
25 specification of the genomic sequence to be displayed. Such specification can consist of or include an accession number for a single clone (e.g., a single BAC accessioned into GenBank), wherein the starting and stopping nucleotides are thus absolutely identified, or
30 alternatively can consist of or include an anchor or fulcrum point about which a chosen range of sequence is anchored, thus providing relative endpoints for the sequence to be displayed. For example, the user can anchor such a range about a given chromosomal map location, gene
35 name, or even a sequence returned by query for similarity

or identity to an input query sequence. When visual display 80 is used as a graphical user interface to computerized data, additional control over the first and last displayed nucleotide will typically be dynamically selectable, as by use of standard zooming and/or selection tools.

Field 81 of visual display 80 is used to present the output from process 200, that is, to present the bioinformatic prediction of those sequences having the desired function within the genomic sequence. Functional sequences are typically indicated by at least one rectangle 83 (83a, 83b, 83c), the left and right borders of which respectively indicate, by their X-axis coordinates, the starting and ending nucleotides of the region predicted to have function.

Where a single bioinformatic method or approach identifies a plurality of regions having the desired function, a plurality of rectangles 83 is disposed horizontally in field 81. Where multiple methods and/or approaches are used to identify function, each such method and/or approach can be represented by its own series of horizontally disposed rectangles 83, each such horizontally disposed series of rectangles offset vertically from those representing the results of the other methods and approaches.

Thus, rectangles 83a in FIG. 3 represent the functional predictions of a first method of a first approach for predicting function, rectangles 83b represent the functional predictions of a second method and/or second approach for predicting that function, and rectangles 83c represent the predictions of a third method and/or approach.

Where the function desired to be identified is protein coding, field 81 is used to present the bioinformatic prediction of sequences encoding protein.

For example, rectangles 83a can represent the results from GRAIL or GRAIL II, rectangles 83b can represent the results from GENEFINDER, and rectangles 83c can represent the results from DICTION.

5 Optionally, and preferably, rectangles 83 collectively representing predictions of a single method and/or approach are identically colored and/or textured, and are distinguishable from the color and/or texture used for a different method and/or approach.

10 Alternatively, or in addition, the color, hue, density, or texture of rectangles 83 can be used further to report a measure of the bioinformatic reliability of the prediction. For example, many gene prediction programs will report a measure of the reliability of prediction.
15 Thus, increasing degrees of such reliability can be indicated, e.g., by increasing density of shading. Where display 80 is used as a graphical user interface, such measures of reliability, and indeed all other results output by the program, can additionally or alternatively be
20 made accessible through linkage from individual rectangles 83, as by time-delayed window ("tool tip" window), or by pointer (e.g., mouse)-activated link.

 As earlier described, increased predictive reliability can be achieved by requiring consensus among
25 methods and/or approaches to determining function. Thus, field 81 can include a horizontal series of rectangles 83 that indicate one or more degrees of consensus in predictions of function.

 Although FIG. 3 shows three series of
30 horizontally disposed rectangles in field 81, display 80 can include as few as one such series of rectangles and as many as can discriminably be displayed, depending upon the number of methods and/or approaches used to predict a given function.

35 Furthermore, field 81 can be used to show

predictions of a plurality of different functions.

However, the increased visual complexity occasioned by such display makes more useful the ability of the user to select a single function for display. When display 80 is used as
5 a graphical user interface for computer query and analysis, such function can usefully be indicated and user-selectable, as by a series of graphical buttons or tabs (not shown in FIG. 3).

Rectangle 89 is shown in FIG. 3 as including
10 interposed rectangle 84. Rectangle 84 represents the portion of annotated sequence for which predicted functional information has been assayed physically, with the starting and ending nucleotides of the assayed material indicated by the X axis coordinates of the left and right
15 borders of rectangle 84. Rectangle 85, with optional inclusive circles 86 (86a, 86b, and 86c) displays the results of such physical assay.

Although a single rectangle 84 is shown in FIG. 3, physical assay is not limited to just one region of
20 annotated genomic sequence. It is expected that an increasing percentage of regions predicted to have function by process 200 will be assayed physically, and that display 80 will accordingly, for any given genomic sequence, have an increasing number of rectangles 84 and 85, representing
25 an increased density of sequence annotation.

Where the function desired to be identified is protein coding, rectangle 84 identifies the sequence of the probe used to measure expression. In embodiments of the present invention where expression is measured using
30 genome-derived single exon microarrays, rectangle 84 identifies the sequence included within the probe immobilized on the support surface of the microarray. As noted supra, such probe will often include a small amount of additional, synthetic, material incorporated during
35 amplification and designed to permit reamplification of the

probe, which sequence is typically not shown in display 80.

Rectangle 87 is used to present the results of bioinformatic assay of the genomic sequence. For example, where the function desired to be identified is protein coding, process 400 can include bioinformatic query of expression databases with the sequences predicted in process 200 to encode exons. And as earlier discussed, because bioinformatic assay presents fewer constraints than does physical assay, often the entire output of process 200 can be used for such assay, without further subsetting thereof by process 300. Therefore, rectangle 87 typically need not have separate indicators therein of regions submitted for bioinformatic assay; that is, rectangle 87 typically need not have regions therein analogous to rectangles 84 within rectangle 89.

Rectangle 87 as shown in FIG. 3 includes smaller rectangles 880 and 88. Rectangles 880 indicate regions that returned a positive result in the bioinformatic assay, with rectangles 88 representing regions that did not return such positive results. Where the function desired to be predicted and displayed is protein coding, rectangles 880 indicate regions of the predicted exons that identify sequence with significant similarity in expression databases, such as EST, SNP, SAGE databases, with rectangles 88 indicating genes novel over those identified in existing expression data bases.

Rectangles 880 can further indicate, through color, shading, texture, or the like, additional information obtained from bioinformatic assay.

For example, where the function assayed and displayed is protein coding, the degree of shading of rectangles 880 can be used to represent the degree of sequence similarity found upon query of expression databases. The number of levels of discrimination can be as few as two (identity, and similarity, where similarity

has a user-selectable lower threshold). Alternatively, as many different levels of discrimination can be indicated as can visually be discriminated.

Where display 80 is used as a graphical user interface, rectangles 880 can additionally provide links directly to the sequences identified by the query of expression databases, and/or statistical summaries thereof. As with each of the precedingly-discussed uses of display 80 as a graphical user interface, it should be understood that the information accessed via display 80 need not be resident on the computer presenting such display, which often will be serving as a client, with the linked information resident on one or more remotely located servers.

Rectangle 85 displays the results of physical assay of the sequence delimited by its left and right borders.

Rectangle 85 can consist of a single rectangle, thus indicating a single assay, or alternatively, and increasingly typically, will consist of a series of rectangles (85a, 85b, 85c) indicating separate physical assays of the same sequence.

Where the function assayed is gene expression, and where gene expression is assayed as herein described using simultaneous two-color fluorescent detection of hybridization to genome-derived single exon microarrays, individual rectangles 85 can be colored to indicate the degree of expression relative to control. Conveniently, shades of green can be used to depict expression in the sample over control values, and shades of red used to depict expression less than control, corresponding to the spectra of the Cy3 and Cy5 dyes conventionally used for respective labeling thereof. Additional functional information can be provided in the form of circles 86 (86a, 86b, 86c), where the diameter of the circle can be used to

indicate expression intensity. As discussed *infra*, such relative expression (expression ratios) and absolute expression (signal intensity) can be expressed using normalized values.

5 Where display 80 is used as a graphical user interface, rectangle 85 can be used as a link to further information about the assay. For example, where the assay is one for gene expression, each rectangle 85 can be used to link to information about the source of the hybridized
10 mRNA, the identity of the control, raw or processed data from the microarray scan, or the like.

FIG. 4 is rendition of display 80 representing gene prediction and gene expression for a hypothetical BAC, showing conventions used in the Examples presented *infra*.
15 BAC sequence ("Chip seq.") 89 is presented, with the physically assayed region thereof (corresponding to rectangle 84 in FIG. 3) shown in white. Algorithmic gene predictions are shown in field 81, with predictions by GRAIL shown, predictions by GENEFINDER, and predictions by
20 DICTION shown. Within rectangle 87, regions of sequence that, when used to query expression databases, return identical or similar sequences ("EST hit") are shown as white rectangles (corresponding to rectangles 880 in FIG. 3), gray indicates low homology, and black indicates
25 unknowns (where black and gray would correspond to rectangles 88 in FIG. 3).

Although FIGS. 3 and 4 show a single stretch of sequence, uninterrupted from left to right, longer sequences are usefully represented by vertical stacking of
30 such individual Mondrians, as shown in FIGS. 9 and 10.

Single Exon Probes Useful For Measuring Gene Expression

The methods and apparatus of the present
35 invention rapidly produce functional information from

genomic sequence. Where the function to be identified is protein coding, the methods and apparatus of the present invention rapidly identify and confirm the expression of portions of genomic sequence that function to encode protein. As a direct result, the methods and apparatus of the present invention rapidly yield large numbers of single-exon nucleic acid probes, the majority from previously unknown genes, each of which is useful for measuring and/or surveying expression of a specific gene in one or more tissues or cell types.

It is, therefore, another aspect of the present invention to provide genome-derived single exon nucleic acid probes useful for gene expression analysis, and particularly for gene expression analysis by microarray.

Using the methods and genome-derived single-exon microarrays of the present invention, we have for example readily identified a large number of unique ORFs from human genomic sequence. Using single exon probes that encompass these ORFs, we have demonstrated, through microarray hybridization analysis, the expression of 12,673 of these ORFs in Fetal liver.

As would immediately be appreciated by one of skill in the art, each single exon probe having demonstrable expression in Fetal liver is currently available for use in measuring the level of its ORF's expression in Fetal liver.

Diseases of the liver are a significant cause of human morbidity and mortality. Increasingly, genetic factors are being found that contribute to predisposition, onset, and/or aggressiveness of most, if not all, of these diseases; although causative mutations in single genes have been identified for some, these disorders are believed for the most part to have polygenic etiologies.

For example, cirrhosis is a major public health problem. In the industrialized world, it is among the top

ten causes of death; among patients aged 45 to 65, it is the third leading cause of death. The high prevalence is largely the result of alcohol abuse, but other major contributors include chronic hepatitis, biliary disease and iron overload. Approximately 10-15% are cryptogenic.

Cirrhosis is a broad description encompassing the common end stage of many forms of liver injury. Many patients with cirrhosis will remain asymptomatic for years, while others show generalized weakness, anorexia, malaise, and weight loss or, occasionally, more severe symptoms.

The progression from fibrosis, an early consequence of liver disease, to cirrhosis, and the specific histologic morphology that characterizes cirrhosis depend on the extent of injury, the presence of continuing damage, and the response of the liver to damage. The liver may be injured acutely and severely (e.g. necrosis with hepatitis), moderately over months or years (e.g. biliary tract obstruction and chronic active hepatitis), or modestly but continuously (e.g. alcohol abuse).

During the repair process, new vessels connecting the hepatic artery and portal vein to the hepatic venules form within the fibrous sheath that surrounds the surviving nodules of liver cells. These vessels restore the intrahepatic circulatory pathway, but provide relatively low-volume, high-pressure drainage that is less efficient than normal and results in increased portal vein pressure (portal hypertension). Thus, cirrhosis is not static and its features depend on the disease activity and stage.

As cirrhosis is the end stage of many forms of liver disease, many genes have been identified that can contribute to the development of cirrhosis. These include, e.g., the genes responsible for Wilson disease (Online Mendelian Inheritance of Man ("OMIM") 277900), type IV glycogen storage disease (OMIM 232500), galactosemia (OMIM

230400), and a deficiency of alpha-1-antitrypsin (OMIM 107400). There is substantial evidence, however, for as yet uncharacterized loci which cause cirrhosis.

For example, Iber and Maddrey, Prog. Liver Dis. 5 2: 290-302 (1965), reviewed 13 previously reported families and 8 new to this study, each with 2 or more affected members. They pointed out that, with a single exception, the multiple cases were in the same generation. Within a given family, the age of onset, clinical course, and biopsy 10 findings were very similar, but there were wide differences between families.

Kalra et al., Hum. Hered. 32:170-175 (1982) studied the families of 220 cases of Indian childhood cirrhosis and 70 families of age-matched controls. The 15 hypotheses of autosomal recessive, partial sex-linkage, and doubly recessive inheritance were found untenable and the authors concluded that multifactorial inheritance was most plausible. Lefkowitz et al., New Eng. J. Med. 307:271-277 (1982) described 4 white American sibs who died between 20 ages 4.5 and 6 years of cirrhosis that closely resembled that of the childhood cirrhosis of Asiatic Indians.

Another example of uncharacterized loci which cause cirrhosis are those related to the risk of alcoholism.

25 Cloninger, Science 236:410-416 (1987), defined two separate types of alcoholism. According to these definitions, type 1 alcohol abuse has its usual onset after the age of 25 years and is characterized by severe psychological dependence and guilt. Type 1 occurs in both 30 men and women and requires both genetic and environmental factors to become manifest. By contrast, type 2 alcohol abuse has its onset before the age of 25; persons with this type of alcoholism are characterized by their inability to abstain from alcohol and by frequent aggressive and 35 antisocial behavior. Type 2 alcoholism is rarely found in

women and is much more heritable.

Despite considerable effort to identify genes related to the risk of alcoholism, relatively few genes have been identified. Some of this work has suggested a
5 relationship between the metabolism of dopamine and alcoholism. Blum et al., J.A.M.A. 263:2055-2060 (1990) and Bolos et al., J.A.M.A. 264:3156-3160 (1990) investigated the relationship of the dopamine D2 receptor (DRD2; OMIM 126450) to alcoholism, but the sample size was small and
10 their results were inconclusive. However, Tiihonen et al., Molec. Psychiat. 4, 286-289 (1999), found a markedly higher frequency in a population of type 1 alcoholics of the low activity allele of the enzyme catechol-O-methyltransferase (COMT, OMIM 116790), which has a crucial role in the
15 metabolism of dopamine, suggesting a role for dopamine metabolism in increased risk of alcoholism. For a brief review of recent progress toward the identification of genes related to risk for alcoholism see Buck, Genome 9:927-928 (1998).

20 As another example, multiple genes have been shown to predispose to hyperlipoproteinemia or hyperlipidemia. Much attention has been focused on these disorders because there is a strong association of hyperlipidemia, especially hypercholesterolemia, with
25 development of coronary artery disease. Coronary artery disease accounts for at least 25% of all deaths in the United States. Coronary artery disease results when the arteries supplying the heart muscle become occluded by plaques composed of lipids like cholesterol, blood clotting
30 components and blood cells.

The major plasma lipids circulate bound to proteins as macromolecular complexes called lipoproteins. Although closely interrelated, the major lipoprotein classes - chylomicron, very-low-density lipoprotein (VLDL),
35 low-density lipoprotein (LDL), and high-density lipoprotein

(HDL) - are usually classified in terms of physicochemical properties (e.g., density after centrifugation).

Chylomicrons, the largest lipoproteins, carry exogenous triglyceride from the intestine via the thoracic duct to the venous system and into peripheral sites. VLDL carries endogenous triglyceride primarily from the liver to the same peripheral sites for storage or use. Lipases quickly degrade the triglyceride in VLDL to produce intermediate density lipoproteins (IDL) and within 2 to 6 h, IDL is degraded further to generate LDL, which has a plasma half-life of 2 to 3 days. While the overall fate of LDL is unclear, the liver is responsible for removing approximately 70% and active receptor sites have been found on the surfaces of hepatocytes.

Several monogenic conditions that lead to elevated levels of one or more serum lipoproteins have been defined and the responsible gene identified, including, e.g., hyperlipoproteinemia type I (OMIM 238600), familial hypercholesterolemia (OMIM 143890), and familial defective apolipoprotein B (OMIM 107730). However, in many cases the etiology is unknown and there is strong evidence for additional uncharacterized loci.

For example, Zuliani et al., *Arterioscler. Thromb. Vasc. Biol.* 19:802-809 (1999) identified a Sardinian family with a recessive form of hypercholesterolemia with the clinical features of familial hypercholesterolemia (OMIM 603813), and found that previously identified genes were not responsible for this disorder. They proposed that in this new lipid disorder, a recessive defect causes a selective impairment of the LDL receptor function in the liver. Ciccarese et al., *Am. J. Hum. Genet.* 66:453-460 (2000) recently mapped this novel disease locus.

Another example is designated familial combined hyperlipidemia (OMIM 144250) which affects approximately 1-

2% of the population in the Western world. This disorder can have its basis in mutation in several novel genes, two of which have been mapped to chromosome 1 (Pajukanta et al., Nature Genet. 18:369-373 (1998)) and chromosome 11
5 (Aouizerat et al., Am. J. Hum. Genet. 65, 397-412 (1999)). The high frequency of this disorder suggests that most, if not all, hyperlipidemias are of multifactorial genetic etiology.

As yet a further example, primary schlerosing
10 cholangitis (PSC) is a disorder characterized by a patchy obliterative inflammatory fibrosis of the large bile ducts. Chronic inflammation leads to extensive bile duct strictures, cholestasis, and gradual progression to biliary cirrhosis. PSC occurs most often in young men and is
15 commonly associated with inflammatory bowel disease, especially ulcerative colitis. The onset is usually insidious, with gradual, progressive fatigue, pruritus, and jaundice. There is no specific therapy for sclerosing cholangitis, and liver transplantation is the only apparent
20 cure.

The etiology of PSC is not known, but both genetic and immunologic abnormalities have been implicated. However, the frequency of HLA-B8 and HLA-DT2, which are associated with a number of autoimmune diseases, is higher
25 in PSC than normal individuals. Prochazka et al., New Eng. J. Med. 322:1842-1844 (1990) found that 100% of 29 patients with primary sclerosing cholangitis carried the HLA-DRw52a antigen, which is normally present in 35% of the population.

30 As a still further example, sarcoidosis is a disease of unknown cause characterized by non-caseating granulomas in one or more organ systems. These granulomas may resolve completely or proceed to fibrosis. The disorder is systemic, but the liver is affected in approximately 75%
35 of cases. Sarcoidosis occurs mainly in persons aged 20 to

40 yr and is most common in Northern Europeans and American blacks. The lifetime risk of developing sarcoidosis is particularly high among Swedish men (1.15%), Swedish women (1.6%), and African Americans (2.4%).

5 The much greater frequency in African Americans relative to the United States population overall suggests a genetic contribution to etiology. Early research studying familial aggregation indicated that the disease may have a nongenetic basis because the family pattern did not conform
10 to a simple Mendelian mode of inheritance (Allison, Sth. Med. J. 57: 27-32 (1964)). However, Headings et al., Ann. N.Y. Acad. Sci. 278:377-385 (1976) favored multifactorial genetic inheritance of susceptibility. Nowack et al., Arch. Intern. Med. 147:481-483 (1987), found an unusually
15 high frequency of HLA-DR5 in a study of 440 patients with sarcoidosis in Marburg, Germany. They also concluded that the role of an environmental or infectious agent triggering sarcoidosis cannot be envisaged without considering genetically linked cofactors.

20 Other significant diseases of liver are also believed to have a genetic, typically polygenic, etiologic component. These diseases include, e.g., primary biliary cirrhosis, Zellweger syndrome, cholestasis-lymphedema syndrome, Alstrom syndrome, primary pulmonary
25 hypertension, Berardinelli-Seip congenital lipodystrophy, iron overload in Africa, neonatal cholestatic hepatitis, autosomal recessive KID syndrome, familial hypotransferrinemia, type I congenital dyserythropoietic anemia, porphyria variegata, Finnish lactic acidosis with
30 hepatic hemosiderosis, Rotor syndrome, essential hypertension, ARC syndrome, type II conjugated hyperbilirubinemia, Lambert syndrome, ichthyosis congenita with biliary atresia, Kabuki make-up syndrome, Meckel
35 storage diseases, polycystic kidney and hepatic disease,

isolated Caroli disease, trisomy 18-like syndrome, Osler-Rendu-Weber syndrome 3, fatal intrahepatic cholestasis, Coach syndrome, type C Niemann-Pick disease, hereditary persistence of fetal hemoglobin and hepatocellular cancer.

5 Altered responses to a variety of infectious agents that target the liver, especially acute viral hepatitis, have also been shown or are suspected to have genetic bases or contributions. In addition to differential susceptibility to primary infectious agents, 10 these altered responses include predisposition to complicating conditions following contact with particular infectious agents. These include, e.g., development of hepatocellular carcinoma 2 correlated with Hepatitis B infection, and severe hepatic fibrosis following 15 *Schistosoma mansoni* infection.

The central role of the liver in drug metabolism results in exposure of this organ to a large variety of potentially toxic chemical agents and metabolites. These include naturally occurring plant alkaloids and mycotoxins, 20 industrial chemicals, and, additionally, pharmacologic agents used in treating disease. The range of manifestations of toxin- and drug-induced liver disease are virtually as broad as the range of acute and chronic disorders and have also been shown or suspected to have 25 genetic bases or contributions.

Such interactions between drugs and genotype have been shown in the response, e.g., to the anticonvulsant phenytoin, which can cause severe hepatitis-like disease in individuals who are impaired in the ability to detoxify a 30 metabolite of phenytoin in the liver, and in the response to the drug sodium valproate, which can produce severe hepatotoxicity in certain individuals. The abnormal responses to both of these drugs are believed to be influenced by underlying genetic factors.

35 The human genome-derived single exon nucleic acid

probes and microarrays of the present invention are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of human liver, particularly those diseases with polygenic etiology. With each of the single
5 exon probes described herein shown to be expressed at detectable levels in human liver, and with about 2/3 of the probes identifying novel genes, the single exon microarrays of the present invention provide exceptionally high informational content for such studies.

10 For example, diagnosis (including differential diagnosis among clinically indistinguishable disorders, such as cirrhosis), staging, and/or grading of a disease can be based upon the quantitative relatedness of a patient gene expression profile to one or more reference expression
15 profiles known to be characteristic of a given liver disease, or to specific grades or stages thereof.

In one embodiment, the patient gene expression profile is generated by hybridizing nucleic acids obtained directly or indirectly from transcripts expressed in the
20 patient's liver to the genome-derived single exon microarray of the present invention. Reference profiles are obtained similarly, using nucleic acids obtained directly or indirectly from transcripts expressed by liver of individuals with known liver disease. Methods for
25 quantitatively relating gene expression profiles, without regard to the function of the protein encoded by the gene, are disclosed in WO 99/58720, incorporated herein by reference in its entirety.

In another approach, the genome-derived single
30 exon probes and microarrays of the present invention can be used to interrogate genomic DNA, rather than pools of expressed message; this latter approach permits predisposition to and/or prognosis of liver disease to be assessed through the massively parallel determination of
35 altered copy number, deletion, or mutation in the patient's

genome of exons known to be expressed in human liver. The algorithms set forth in WO 99/58720 can be applied to such genomic profiles without regard to the function of the protein encoded by the interrogated gene.

5 The utility is specific to the probe; at sufficiently high hybridization stringency, which stringencies are well known in the art - see Ausubel et al. and Maniatis et al. - each probe reports the level of expression of message specifically containing that ORF.

10 It should be appreciated, however, that the probes of the present invention, for which expression in the Fetal liver has been demonstrated are useful for both measurement in the Fetal liver and for survey of expression in other tissues.

15 Significant among such advantages is the presence of probes for novel genes.

 As mentioned above and further detailed in Examples 1 and 2, the methods described enable ORFs which are not present in existing expression databases to be
20 identified. And the fewer the number of tissues in which the ORF can be shown to be expressed, the more likely the ORF will prove to be part of a novel gene: as further discussed in Example 2, ORFs whose expression was measurable in only a single of the tested tissues were
25 represented in existing expression databases at a rate of only 11%, whereas 36% of ORFs whose expression was measurable in 9 tissues were present in existing expression databases, and fully 45% of those ORFs expressed in all ten tested tissues were present in existing expressed sequence
30 databases.

 Either as tools for measuring gene expression or tools for surveying gene expression, the genome-derived single exon probes of the present invention have significant advantages over the cDNA or EST-based probes
35 that are currently available for achieving these utilities.

The genome-derived single exon probes of the present invention are useful in constructing genome-derived single exon microarrays; the genome-derived single exon microarrays, in turn, are useful devices for measuring and
5 for surveying gene expression in the human.

Gene expression analysis using microarrays - conventionally using microarrays having probes derived from expressed message - is well-established as useful in the biological research arts (see Lockhart et al. *Nature* 405,
10 827-836).

Microarrays have been used to determine gene expression profiles in cells in response to drug treatment (see, for example, Kaminski et al., "Global Analysis of Gene Expression in Pulmonary Fibrosis Reveals Distinct
15 Programs Regulating Lung Inflammation and Fibrosis," *Proc. Natl. Acad. Sci. USA* 97(4):1778-83 (2000); Bartosiewicz et al., "Development of a Toxicological Gene Array and Quantitative Assessment of This Technology," *Arch. Biochem. Biophys.* 376(1):66-73 (2000)), viral infection (see for
20 example, Geiss et al., "Large-scale Monitoring of Host Cell Gene Expression During HIV-1 Infection Using cDNA Microarrays," *Virology* 266(1):8-16 (2000)) and during cell processes such as differentiation, senescence and apoptosis (see, for example, Shelton et al., "Microarray Analysis of
25 Replicative Senescence," *Curr. Biol.* 9(17):939-45 (1999); Voehringer et al., "Gene Microarray Identification of Redox and Mitochondrial Elements That Control Resistance or Sensitivity to Apoptosis," *Proc. Natl. Acad. Sci. USA* 97(6):2680-5 (2000)).

30 Microarrays have also been used to determine abnormal gene expression in diseased tissues (see, for example, Alon et al., "Broad Patterns of Gene Expression Revealed by Clustering Analysis of Tumor and Normal Colon Tissues Probed by Oligonucleotide Arrays," *Proc. Natl. Acad. Sci. USA* 96(12):6745-50 (1999); Perou et al.,
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"Distinctive Gene Expression Patterns in Human Mammary Epithelial Cells and Breast Cancers, *Proc. Natl. Acad. Sci. USA* 96(16):9212-7 (1999); Wang et al., "Identification of Genes Differentially Over-expressed in Lung Squamous Cell Carcinoma Using Combination of cDNA Subtraction and Microarray Analysis," *Oncogene* 19(12):1519-28 (2000); Whitney et al., "Analysis of Gene Expression in Multiple Sclerosis Lesions Using cDNA Microarrays," *Ann. Neurol.* 46(3):425-8 (1999)), in drug discovery screens (see, for example, Scherf et al., "A Gene Expression Database for the Molecular Pharmacology of Cancer," *Nat. Genet.* 24(3):236-44 (2000)) and in diagnosis to determine appropriate treatment strategies (see, for example, Sgroi et al., "In vivo Gene Expression Profile Analysis of Human Breast Cancer Progression," *Cancer Res.* 59(22):5656-61 (1999)).

In microarray-based gene expression screens of pharmacological drug candidates upon cells, each probe provides specific useful data. In particular, it should be appreciated that even those probes that show no change in expression are as informative as those that do change, serving, in essence, as negative controls.

For example, where gene expression analysis is used to assess toxicity of chemical agents on cells, the failure of the agent to change a gene's expression level is evidence that the drug likely does not affect the pathway of which the gene's expressed protein is a part. Analogously, where gene expression analysis is used to assess side effects of pharmacological agents - whether in lead compound discovery or in subsequent screening of lead compound derivatives - the inability of the agent to alter a gene's expression level is evidence that the drug does not affect the pathway of which the gene's expressed protein is a part.

WO 99/58720 provides methods for quantifying the relatedness of a first and second gene expression profile

and for ordering the relatedness of a plurality of gene expression profiles. The methods so described permit useful information to be extracted from a greater percentage of the individual gene expression measurements
5 from a microarray than methods previously used in the art.

Other uses of microarrays are described in Gerhold et al., *Trends Biochem. Sci.* 24(5):168-173 (1999) and Zweiger, *Trends Biotechnol.* 17(11):429-436 (1999); Schena et al.

10 The invention particularly provides genome-derived single-exon probes known to be expressed in Fetal liver. The individual single exon probes can be provided in the form of substantially isolated and purified nucleic acid, typically, but not necessarily, in a quantity
15 sufficient to perform a hybridization reaction.

Such nucleic acid can be in any form directly hybridizable to the message that contains the probe's ORF, such as double stranded DNA, single-stranded DNA complementary to the message, single-stranded RNA
20 complementary to the message, or chimeric DNA/RNA molecules so hybridizable. The nucleic acid can alternatively or additionally include either nonnative nucleotides, alternative internucleotide linkages, or both, so long as complementary binding can be obtained. For example, probes
25 can include phosphorothioates, methylphosphonates, morpholino analogs, and peptide nucleic acids (PNA), as are described, for example, in U.S. Patent Nos. 5,142,047; 5,235,033; 5,166,315; 5,217,866; 5,184,444; 5,861,250.

Usefully, however, such probes are provided in a
30 form and quantity suitable for amplification, where the amplified product is thereafter to be used in the hybridization reactions that probe gene expression. Typically, such probes are provided in a form and quantity suitable for amplification by PCR or by other well known
35 amplification technique. One such technique additional to

PCR is rolling circle amplification, as is described, *inter alia*, in U.S. Patent Nos. 5,854,033 and 5,714,320 and international patent publications WO 97/19193 and WO 00/15779. As is well understood, where the probes are
5 to be provided in a form suitable for amplification, the range of nucleic acid analogues and/or internucleotide linkages will be constrained by the requirements and nature of the amplification enzyme.

Where the probe is to be provided in form
10 suitable for amplification, the quantity need not be sufficient for direct hybridization for gene expression analysis, and need be sufficient only to function as an amplification template, typically at least about 1, 10 or 100 pg or more.

15 Each discrete amplifiable probe can also be packaged with amplification primers, either in a single composition that comprises probe template and primers, or in a kit that comprises such primers separately packaged therefrom. As earlier mentioned, the ORF-specific
20 5' primers used for genomic amplification can have a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification can have a second, different, common sequence added thereto, thus permitting, in this embodiment, the use of a single set of 5' and 3'
25 primers to amplify any one of the probes. The probe composition and/or kit can also include buffers, enzyme, etc., required to effect amplification.

As mentioned earlier, when intended for use on a genome-derived single exon microarray of the present
30 invention, the genome-derived single exon probes of the present invention will typically average at least about 100, 200, 300, 400 or 500 bp in length, including (and typically, but not necessarily centered about) the ORF. Furthermore, when intended for use on a genome-derived
35 single exon microarray of the present invention, the

genome-derived single exon probes of the present invention will typically not contain a detectable label.

When intended for use in solution phase hybridization, however – that is, for use in a hybridization reaction in which the probe is not first bound to a support substrate (although the target may indeed be so bound) – length constraints that are imposed in microarray-based hybridization approaches will be relaxed, and such probes will typically be labeled.

10 In such case, the only functional constraint that dictates the minimum size of such probe is that each such probe must be capable of specifically identifying in a hybridization reaction the exon from which it is drawn. In theory, a probe of as little as 17 nucleotides is capable
15 of uniquely identifying its cognate sequence in the human genome. For hybridization to expressed message – a subset of target sequence that is much reduced in complexity as compared to genomic sequence – even fewer nucleotides are required for specificity.

20 Therefore, the probes of the present invention can include as few as 20, 25 or 50 bp or ORF, or more. In particular embodiments, the ORF sequences are given in SEQ ID NOS. 12,674 – 25,129, respectively, for probe SEQ ID NOS. 1 – 12,673. The minimum amount of ORF required to be
25 included in the probe of the present invention in order to provide specific signal in either solution phase or microarray-based hybridizations can readily be determined for each of ORF SEQ ID NOS. 12,674 – 25,129 individually by routine experimentation using standard high stringency
30 conditions.

Such high stringency conditions are described, *inter alia*, in Ausubel et al. and Maniatis et al. For microarray-based hybridization, standard high stringency conditions can usefully be 50% formamide, 5X SSC, 0.2 µg/µl
35 poly(dA), 0.2 µg/µl human c_ot1 DNA, and 0.5 % SDS, in a

humid oven at 42°C overnight, followed by successive washes of the microarray in 1X SSC, 0.2% SDS at 55°C for 5 minutes, and then 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. For solution phase hybridization, standard high stringency conditions can usefully be aqueous hybridization at 65°C in 6X SSC. Lower stringency conditions, suitable for cross-hybridization to mRNA encoding structurally- and functionally-related proteins, can usefully be the same as the high stringency conditions but with reduction in temperature for hybridization and washing to room temperature (approximately 25°C).

When intended for use in solution phase hybridization, the maximum size of the single exon probes of the present invention is dictated by the proximity of other expressed exons in genomic DNA: although each single exon probe can include intergenic and/or intronic material contiguous to the ORF in the human genome, each probe of the present invention will include portions of only one expressed exon.

Thus, each single exon probe will include no more than about 25 kb of contiguous genomic sequence, more typically no more than about 20 kb of contiguous genomic sequence, more usually no more than about 15 kb, even more usually no more than about 10 kb. Usually, probes that are maximally about 5 kb will be used, more typically no more than about 3 kb.

It will be appreciated that the Sequence Listing appended hereto presents, by convention, only that strand of the probe and ORF sequence that can be directly translated reading from 5' to 3' end. As would be well understood by one of skill in the art, single stranded probes must be complementary in sequence to the ORF as present in an mRNA; it is well within the skill in the art to determine such complementary sequence. It will further be understood that double stranded probes can be used in

both solution-phase hybridization and microarray-based hybridization if suitably denatured.

Thus, it is an aspect of the present invention to provide single-stranded nucleic acid probes that have
5 sequence complementary to those described herein above and below, and double-stranded probes one strand of which has sequence complementary to the probes described herein.

The probes can, but need not, contain intergenic and/or intronic material that flanks the ORF, on one or
10 both sides, in the same linear relationship to the ORF that the intergenic and/or intronic material bears to the ORF in genomic DNA. The probes do not, however, contain nucleic acid derived from more than one expressed ORF.

And when intended for use in solution
15 hybridization, the probes of the present invention can usefully have detectable labels. Nucleic acid labels are well known in the art, and include, *inter alia*, radioactive labels, such as ^3H , ^{32}P , ^{33}P , ^{35}S , ^{125}I , ^{131}I ; fluorescent labels, such as Cy3, Cy5, Cy5.5, Cy7, SYBR[®]

20 Green and other labels described in Haugland, *Handbook of Fluorescent Probes and Research Chemicals*, 7th ed., Molecular Probes Inc., Eugene, OR (2000), or fluorescence resonance energy transfer tandem conjugates thereof; labels suitable for chemiluminescent and/or
25 enhanced chemiluminescent detection; labels suitable for ESR and NMR detection; and labels that include one member of a specific binding pair, such as biotin, digoxigenin, or the like.

The probes, either in quantity sufficient for
30 hybridization or sufficient for amplification, can be provided in individual vials or containers.

Alternatively, such probes can usefully be packaged as a plurality of such individual genome-derived single exon probes.

35 When provided as a collection of plural

individual probes, the probes are typically made available in amplifiable form in a spatially-addressable ordered set, typically one per well of a microtiter dish. Although a 96 well microtiter plate can be used, greater efficiency is
5 obtained using higher density arrays.

If, as earlier mentioned, the ORF-specific 5' primers used for genomic amplification had a first common sequence added thereto, and the ORF-specific 3' primers used for genomic amplification had a second,
10 different, common sequence added thereto, a single set of 5' and 3' primers can be used to amplify all of the probes from the amplifiable ordered set.

Such collections of genome-derived single exon probes can usefully include a plurality of probes chosen
15 for the common attribute of expression in the human Fetal liver.

In such defined subsets, typically at least 50, 60, 75, 80, 85, 90 or 95% or more of the probes will be chosen by their expression in the defined tissue or cell
20 type.

The single exon probes of the present invention, as well as fragments of the single exon probes comprising selectively hybridizable portions of the probe ORF, can be used to obtain the full length cDNA that includes the ORF
25 by (i) screening of cDNA libraries; (ii) rapid amplification of cDNA ends ("RACE"); or (iii) other conventional means, as are described, *inter alia*, in Ausubel et al. and Maniatis et al.

It is another aspect of the present invention to
30 provide genome-derived single exon nucleic acid microarrays useful for gene expression analysis, where the term "microarray" has the meaning given in the definitional section of this description, *supra*.

The invention particularly provides genome-
35 derived single-exon nucleic acid microarrays comprising a

plurality of probes known to be expressed in human Fetal liver. In preferred embodiments, the present invention provides human genome-derived single exon microarrays comprising a plurality of probes drawn from the group
5 consisting of SEQ ID NOS.: 1 - 12,673.

When used for gene expression analysis, the genome-derived single exon microarrays provide greater physical informational density than do the genome-derived single exon microarrays that have lower percentages of
10 probes known to be expressed commonly in the tested tissue. At a fixed probe density, for example, a given microarray surface area of the defined subset genome-derived single exon microarray can yield a greater number of expression measurements. Alternatively, at a given probe density, the
15 same number of expression measurements can be obtained from a smaller substrate surface area. Alternatively, at a fixed probe density and fixed surface area, probes can be provided redundantly, providing greater reliability in signal measurement for any given probe. Furthermore, with
20 a higher percentage of probes known to be expressed in the assayed tissue, the dynamic range of the detection means can be adjusted to reveal finer levels discrimination among the levels of expression.

Although particularly described with respect to
25 their utility as probes of gene expression, particularly as probes to be included on a genome-derived single exon microarray, each of the nucleic acids having SEQ ID NOS.: 1 - 12,673 contains an open-reading frame, set forth respectively in SEQ ID NOS.: 12,674 - 25,129, that encodes
30 a protein domain. Thus, each of SEQ ID NOS. 1 - 12,673 can be used, or that portion thereof in SEQ ID NOS. 12,674 - 25,129 used, to express a protein domain by standard in vitro recombinant techniques. See Ausubel et al. and Maniatis et al.

35 Additionally, kits are available commercially

that readily permit such nucleic acids to be expressed as protein in bacterial cells, insect cells, or mammalian cells, as desired (e.g., HAT™ Protein Expression & Purification System, ClonTech Laboratories, Palo Alto, CA; 5 Adeno-X™ Expression System, ClonTech Laboratories, Palo Alto, CA; Protein Fusion & Purification (pMAL™) System, New England Biolabs, Beverley, MA)

Furthermore, shorter peptides can be chemically synthesized using commercial peptide synthesizing equipment 10 and well known techniques. Procedures are described, *inter alia*, in Chan et al. (eds.), Fmoc Solid Phase Peptide Synthesis: A Practical Approach (Practical Approach Series, (Paper)), Oxford Univ. Press (March 2000) (ISBN: 0199637245); Jones, Amino Acid and Peptide Synthesis 15 (Oxford Chemistry Primers, No 7) , Oxford Univ. Press (August 1992) (ISBN: 0198556683); and Bodanszky, Principles of Peptide Synthesis (Springer Laboratory), Springer Verlag (December 1993) (ISBN: 0387564314).

It is, therefore, another aspect of the invention 20 to provide peptides comprising an amino acid sequence translated from SEQ ID NOS.: 12,674 - 25,129. Such amino acid sequences are set out in SEQ ID NOS: 25,130 - 37,156. Any such recombinantly-expressed or synthesized peptide of at least 8, and preferably at least about 15, amino acids, 25 can be conjugated to a carrier protein and used to generate antibody that recognizes the peptide. Thus, it is a further aspect of the invention to provide peptides that have at least 8, preferably at least 15, consecutive amino acids.

30

The following examples are offered by way of illustration and not by way of limitation.

EXAMPLE 1

35 Preparation of Single Exon Microarrays from ORFs Predicted

in Human Genomic Sequence

Bioinformatics Results

All human BAC sequences in fewer than 10 pieces
5 that had been accessioned in a five month period
immediately preceding this study were downloaded from
GenBank. This corresponds to ~2200 clones, totaling ~350
MB of sequence, or approximately 10% of the human genome.

After masking repetitive elements using the
10 program CROSS_MATCH, the sequence was analyzed for open
reading frames using three separate gene finding programs.
The three programs predict genes using independent
algorithmic methods developed on independent training sets:
GRAIL uses a neural network, GENEFINDER uses a hidden
15 Markoff model, and DICTION, a program proprietary to
Genetics Institute, operates according to a different
heuristic. The results of all three programs were used to
create a prediction matrix across the segment of genomic
DNA.

20 The three gene finding programs yielded a range
of results. GRAIL identified the greatest percentage of
genomic sequence as putative coding region, 2% of the data
analyzed. GENEFINDER was second, calling 1%, and DICTION
yielded the least putative coding region, with 0.8% of
25 genomic sequence called as coding region.

The consensus data were as follows. GRAIL and
GENEFINDER agreed on 0.7% of genomic sequence, GRAIL and
DICTION agreed on 0.5% of genomic sequence, and the three
programs together agreed on 0.25% of the data analyzed.
30 That is, 0.25% of the genomic sequence was identified by
all three of the programs as containing putative coding
region.

ORFs predicted by any two of the three programs
("consensus ORFs") were assorted into "gene bins" using two
35 criteria: (1) any 7 consecutive exons within a 25 kb window

were placed together in a bin as likely contributing to a single gene, and (2) all ORFs within a 25 kb window were placed together in a bin as likely contributing to a single gene if fewer than 7 exons were found within the 25 kb window.

PCR

The largest ORF from each gene bin that did not span repetitive sequence was then chosen for amplification, as were all consensus ORFs longer than 500 bp. This method approximated one exon per gene; however, a number of genes were found to be represented by multiple elements.

Previously, we had determined that DNA fragments fewer than 250 bp in length do not bind well to the amino-modified glass surface of the slides used as support substrate for construction of microarrays; therefore, amplicons were designed in the present experiments to approximate 500 bp in length.

Accordingly, after selecting the largest ORF per gene bin, a 500 bp fragment of sequence centered on the ORF was passed to the primer picking software, PRIMER3 (available online for use at <http://www-genome.wi.mit.edu/cgi-bin/primer/>). A first additional sequence was commonly added to each ORF-unique 5' primer, and a second, different, additional sequence was commonly added to each ORF-unique 3' primer, to permit subsequent reamplification of the amplicon using a single set of "universal" 5' and 3' primers, thus immortalizing the amplicon. The addition of universal priming sequences also facilitates sequence verification, and can be used to add a cloning site should some ORFs be found to warrant further study.

The ORFs were then PCR amplified from genomic DNA, verified on agarose gels, and sequenced using the universal primers to validate the identity of the amplicon

to be spotted in the microarray.

Primers were supplied by Operon Technologies (Alameda, CA). PCR amplification was performed by standard techniques using human genomic DNA (Clontech, Palo Alto, CA) as template. Each PCR product was verified by SYBR[®] green (Molecular Probes, Inc., Eugene, OR) staining of agarose gels, with subsequent imaging by Fluorimager (Molecular Dynamics, Inc., Sunnyvale, CA). PCR amplification was classified as successful if a single band appeared.

The success rate for amplifying ORFs of interest directly from genomic DNA using PCR was approximately 75%. FIG. 5 graphs the distribution of predicted ORF (exon) length and distribution of amplified PCR products, with ORF length shown in red and PCR product length shown in blue (which may appear black in the figure). Although the range of ORF sizes is readily seen to extend to beyond 900 bp, the mean predicted exon size was only 229 bp, with a median size of 150 bp (n=9498). With an average amplicon size of 475 ± 25 bp, approximately 50% of the average PCR amplification product contained predicted coding region, with the remaining 50% of the amplicon containing either intron, intergenic sequence, or both.

Using a strategy predicated on amplifying about 500 bp, it was found that long exons had a higher PCR failure rate. To address this, the bioinformatics process was adjusted to amplify 1000, 1500 or 2000 bp fragments from exons larger than 500 bp. This improved the rate of successful amplification of exons exceeding 500 bp, constituting about 9.2% of the exons predicted by the gene finding algorithms.

Approximately 75% of the probes disposed on the array (90% of those that successfully PCR amplified) were sequence-verified by sequencing in both the forward and reverse direction using MegaBACE sequencer (Molecular

Dynamics, Inc., Sunnyvale, CA), universal primers, and standard protocols.

Some genomic clones (BACs) yielded very poor PCR and sequencing results. The reasons for this are unclear, but may be related to the quality of early draft sequence or the inclusion of vector and host contamination in some submitted sequence data.

Although the intronic and intergenic material flanking coding regions could theoretically interfere with hybridization during microarray experiments, subsequent empirical results demonstrated that differential expression ratios were not significantly affected by the presence of noncoding sequence. The variation in exon size was similarly found not to affect differential expression ratios significantly; however, variation in exon size was observed to affect the absolute signal intensity (data not shown).

The 350 MB of genomic DNA was, by the above-described process, reduced to 9750 discrete probes, which were spotted in duplicate onto glass slides using commercially available instrumentation (MicroArray GenII Spotter and/or MicroArray GenIII Spotter, Molecular Dynamics, Inc., Sunnyvale, CA). Each slide additionally included either 16 or 32 *E. coli* genes, the average hybridization signal of which was used as a measure of background biological noise.

Each of the probe sequences was BLASTed against the human EST data set, the NR data set, and SwissProt GenBank (May 7, 1999 release 2.0.9).

One third of the probe sequences (as amplified) produced an exact match (BLAST Expect ("E") values less than 1×10^{-100}) to either an EST (20% of sequences) or a known mRNA (13% of sequences). A further 22% of the probe sequences showed some homology to a known EST or mRNA (BLAST E values from 1×10^{-5} to 1×10^{-99}). The remaining 45% of

the probe sequences showed no significant sequence homology to any expressed, or potentially expressed, sequences present in public databases.

All of the probe sequences (as amplified) were then analyzed for protein similarities with the SwissProt database using BLASTX, Gish et al., *Nature Genet.* 3:266 (1993). The predicted functional breakdowns of the 2/3 of probes identical or homologous to known sequences are presented in Table 1.

10

Table 1

Function of Predicted ORFs As Deduced From Comparative Sequence Analysis			
Total	V6 chip	V7 chip	Function Predicted from Comparative Sequence Analysis
211	96	115	Receptor
120	43	77	Zinc Finger
30	11	19	Homeobox
25	9	16	Transcription Factor
17	11	7	Transcription
118	57	61	Structural
95	39	56	Kinase
36	18	18	Phosphatase
83	31	52	Ribosomal
45	19	26	Transport
21	17	14	Growth Factor
17	12	5	Cytochrome
50	33	17	Channel

As can be seen, the two most common types of genes were transcription factors and receptors, making up 2.2% and 1.8% of the arrayed elements, respectively.

15

EXAMPLE 2

Gene Expression Measurements From Genome-Derived Single

5 Exon Microarrays

The two genome-derived single exon microarrays prepared according to Example 1 were hybridized in a series of simultaneous two-color fluorescence experiments to (1) 10 Cy3-labeled cDNA synthesized from message drawn individually from each of brain, heart, liver, fetal liver, placenta, lung, bone marrow, HeLa, BT 474, or HBL 100 cells, and (2) Cy5-labeled cDNA prepared from message 15 pooled from all ten tissues and cell types, as a control in each of the measurements. Hybridization and scanning were carried out using standard protocols and Molecular Dynamics equipment.

Briefly, mRNA samples were bought from commercial 20 sources (Clontech, Palo Alto, CA and Amersham Pharmacia Biotech (APB)). Cy3-dCTP and Cy5-dCTP (both from APB) were incorporated during separate reverse transcriptions of 1 µg of polyA⁺ mRNA performed using 1 µg oligo(dT)12-18 primer and 2 µg random 9mer primers as follows. After heating to 25 70°C, the RNA:primer mixture was snap cooled on ice. After snap cooling on ice, added to the RNA to the stated final concentration was: 1X Superscript II buffer, 0.01 M DTT, 100µM dATP, 100 µM dGTP, 100 µM dTTP, 50 µM dCTP, 50 µM Cy3-dCTP or Cy5-dCTP 50 µM, and 200 U Superscript II 30 enzyme. The reaction was incubated for 2 hours at 42°C. After 2 hours, the first strand cDNA was isolated by adding 1 U Ribonuclease H, and incubating for 30 minutes at 37°C. The reaction was then purified using a Qiagen PCR cleanup column, increasing the number of ethanol washes to 5. 35 Probe was eluted using 10 mM Tris pH 8.5.

Using a spectrophotometer, probes were measured for dye incorporation. Volumes of both Cy3 and Cy5 cDNA corresponding to 50 pmoles of each dye were then dried in a Speedvac, resuspended in 30 μ l hybridization solution containing 50% formamide, 5X SSC, 0.2 μ g/ μ l poly(dA), 0.2 μ g/ μ l human c₀t1 DNA, and 0.5 % SDS.

Hybridizations were carried out under a coverslip, with the array placed in a humid oven at 42°C overnight. Before scanning, slides were washed in 1X SSC, 0.2% SDS at 55°C for 5 minutes, followed by 0.1X SSC, 0.2% SDS, at 55°C for 20 minutes. Slides were briefly dipped in water and dried thoroughly under a gentle stream of nitrogen.

Slides were scanned using a Molecular Dynamics Gen3 scanner, as described. Schena (ed.), Microarray Biochip: Tools and Technology, Eaton Publishing Company/BioTechniques Books Division (2000) (ISBN: 1881299376).

Although the use of pooled cDNA as a reference permitted the survey of a large number of tissues, it attenuates the measurement of relative gene expression, since every highly expressed gene in the tissue/cell type-specific fluorescence channel will be present to a level of at least 10% in the control channel. Because of this fact, both signal and expression ratios (the latter hereinafter, "expression" or "relative expression") for each probe were normalized using the average ratio or average signal, respectively, as measured across the whole slide.

Data were accepted for further analysis only when signal was at least three times greater than biological noise, the latter defined by the average signal produced by the *E. coli* control genes.

The relative expression signal for these probes was then plotted as function of tissue or cell type, and is presented in FIG. 6.

FIG. 6 shows the distribution of expression across a panel of ten tissues. The graph shows the number of sequence-verified products that were either not expressed ("0"), expressed in one or more but not all tested tissues ("1" - "9"), and expressed in all tissues tested ("10").

Of 9999 arrayed elements on the two microarrays (including positive and negative controls and "failed" products), 2353 (51%) were expressed in at least one tissue or cell type. Of the gene elements showing significant signal - where expression was scored as "significant" if the normalized Cy3 signal was greater than 1, representing signal 5-fold over biological noise (0.2) - 39% (991) were expressed in all 10 tissues. The next most common class (15%) consisted of gene elements expressed in only a single tissue.

The genes expressed in a single tissue were further analyzed, and the results of the analyses are compiled in FIG. 7.

FIG. 7A is a matrix presenting the expression of all verified sequences that showed expression greater than 3 in at least one tissue. Each clone is represented by a column in the matrix. Each of the 10 tissues assayed is represented by a separate row in the matrix, and relative expression of a clone in that tissue is indicated at the respective node by intensity of green shading, with the intensity legend shown in panel B. The top row of the matrix ("EST Hit") contains "bioinformatic" rather than "physical" expression data - that is, presents the results returned by query of EST, NR and SwissProt databases using the probe sequence. The legend for "bioinformatic expression" (i.e., degree of homology returned) is presented in panel C. Briefly, white is known, black is novel, with gray depicting nonidentical with significant homology (white: E values < 1e-100; gray: E values from 1e-

05 to $1e-99$; black: E values $> 1e-05$).

As FIG. 7 readily shows, heart and brain were demonstrated to have the greatest numbers of genes that were shown to be uniquely expressed in the respective
5 tissue. In brain, 200 uniquely expressed genes were identified; in heart, 150. The remaining tissues gave the following figures for uniquely expressed genes: liver, 100; lung, 70; fetal liver, 150; bone marrow, 75; placenta, 100; HeLa, 50; HBL, 100; and BT474, 50.

10 It was further observed that there were many more "novel" genes among those that were up-regulated in only one tissue, as compared with those that were down-regulated in only one tissue. In fact, it was found that ORFs whose expression was measurable in only a single of the tested
15 tissues were represented in sequencing databases at a rate of only 11%, whereas 36% of the ORFs whose expression was measurable in 9 of the tissues were present in public databases. As for those ORFs expressed in all ten tissues, fully 45% were present in existing expressed sequence
20 databases. These results are not unexpected, since genes expressed in a greater number of tissues have a higher likelihood of being, and thus of having been, discovered by EST approaches.

25 Comparison of Signal from Known and Unknown Genes

The normalized signal of the genes found to have high homology to genes present in the GenBank human EST database were compared to the normalized signal of those genes not found in the GenBank human EST database. The
30 data are shown in FIG. 8.

FIG. 8 shows the normalized Cy3 signal intensity for all sequence-verified products with a BLAST Expect ("E") value of greater than $1e-30$ (designated "unknown") upon query of existing EST, NR and SwissProt databases, and
35 shows in blue the normalized Cy3 signal intensity for all

sequence-verified products with a BLAST Expect value of less than $1e-30$ ("known"). Note that biological background noise has an averaged normalized Cy3 signal intensity of 0.2.

5 As expected, the most highly expressed of the ORFs were "known" genes. This is not surprising, since very high signal intensity correlates with very commonly-expressed genes, which have a higher likelihood of being found by EST sequence.

10 However, a significant point is that a large number of even the high expressers were "unknown". Since the genomic approach used to identify genes and to confirm their expression does not bias exons toward either the 3' or 5' end of a gene, many of these high expression genes
15 will not have been detected in an end-sequenced cDNA library.

The significant point is that presence of the gene in an EST database is not a prerequisite for incorporation into a genome-derived microarray, and
20 further, that arraying such "unknown" exons can help to assign function to as-yet undiscovered genes.

Verification of Gene Expression

To ascertain the validity of the approach
25 described above to identify genes from raw genomic sequence, expression of two of the probes was assayed using reverse transcriptase polymerase chain reaction (RT PCR) and northern blot analysis.

Two microarray probes were selected on the basis
30 of exon size, prior sequencing success, and tissue-specific gene expression patterns as measured by the microarray experiments. The primers originally used to amplify the two respective ORFs from genomic DNA were used in RT PCR against a panel of tissue-specific cDNAs (Rapid-Scan gene
35 expression panel 24 human cDNAs) (OriGene Technologies,

Inc., Rockville, MD).

Sequence AL079300_1 was shown by microarray hybridization to be present in cardiac tissue, and sequence AL031734_1 was shown by microarray experiment to be present
5 in placental tissue (data not shown). RT-PCR on these two sequences confirmed the tissue-specific gene expression as measured by microarrays, as ascertained by the presence of a correctly sized PCR product from the respective tissue type cDNAs.

10 Clearly, all microarray results cannot, and indeed should not, be confirmed by independent assay methods, or the high throughput, highly parallel advantages of microarray hybridization assays will be lost. However, in addition to the two RT-PCR results presented above, the
15 observation that 1/3 of the arrayed genes exist in expression databases provides powerful confirmation of the power of our methodology - which combines bioinformatic prediction with expression confirmation using genome-derived single exon microarrays - to identify novel genes
20 from raw genomic data.

To verify that the approach further provides correct characterization of the expression patterns of the identified genes, a detailed analysis was performed of the microarrayed sequences that showed high signal in brain.

25 For this latter analysis, sequences that showed high (normalized) signal in brain, but which showed very low (normalized) signal (less than 0.5, determined to be biological noise) in all other tissues, were further studied. There were 82 sequences that fit these criteria,
30 approximately 2% of the arrayed elements. The 10 sequences showing the highest signal in brain in microarray hybridizations are detailed in Table 2, along with assigned function, if known or reasonably predicted.

35 Table 2

Function of the Most Highly Expressed Genes Expressed Only in Brain				
Microarray Sequence Name	Normal ized Signal	Expressi on Ratio	Homology to EST present in GenBank	Gene Function as described by GenBank
AP000217-1	5.2	+7.7	High	S-100 protein, b-chain, Ca ²⁺ binding protein expressed in central nervous system
AP000047-1	2.3		High	Unknown Function
AC006548-9	1.7		High	Similar to mouse membrane glyco-protein M6, expressed in central nervous system
AC007245-5	1.5		High	Similar to amphiphysin, a synaptic vesicle-associated protein. Ref 21
L44140-4	1.2	+2.0	High	Endothelial actin-binding protein found in nonmuscle filamin

AC004689-9	1.2	+3.5	High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases
AL031657-1	1.2	+3.0	High	Unknown function/ Contains the anhyrin motif, a common protein sequence motif
AC009266-2	1.1	+3.7	Low	Low homology to the Synaptotagmin I protein in rat/present at low levels throughout rat brain
AP000086-1	1.0	+2.7	Low	Unknown, very poor homology to collagen
AC004689-3	1.0		High	Protein Phosphatase PP2A, neuronal/ downregulates activated protein kinases

Of the ten sequences studied by these latter confirmatory approaches, eight were previously known. Of these eight, six had previously been reported to be
5 important in the central nervous system or brain. The exon

giving the highest signal (AP00217-1) was found to be the gene encoding an S100B Ca^{2+} binding protein, reported in the literature to be highly and uniquely expressed in the central nervous system. Heizmann, *Neurochem. Res.* 9:1097
5 (1997).

A number of the brain-specific probe sequences (including AC006548-9, AC009266-2) did not have homology to any known human cDNAs in GenBank but did show homology to rat and mouse cDNAs. Sequences AC004689-9 and AC004689-3
10 were both found to be phosphatases present in neurons (Millward et al., *Trends Biochem. Sci.* 24(5):186-191 (1999)). Two microarray sequences, AP000047-1 and AP000086-1 have unknown function, with AP000086-1 being absent from GenBank. Functionality can now be narrowed
15 down to a role in the central nervous system for both of these genes, showing the power of designing microarrays in this fashion.

Next, the function of the chip sequences with the highest (normalized) signal intensity in brain, regardless
20 of expression in other tissues, was assessed. In this latter analysis, we found expression of many more common genes, since the sequences were not limited to those expressed only in brain. For example, looking at the 20 highest signal intensity spots in brain, 4 were similar to
25 tubulin (AC00807905; AF146191-2; AC007664-4; AF14191-2), 2 were similar to actin (AL035701-2; AL034402-1), and 6 were found to be homologous to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (AL035604-1; Z86090-1; AC006064-L, AC006064-K; AC035604-3; AC006064-L). These genes are often
30 used as controls or housekeeping genes in microarray experiments of all types.

Other interesting genes highly expressed in brain were a ferritin heavy chain protein, which is reported in the literature to be found in brain and liver (Joshi et
35 al., *J. Neurol. Sci.* 134(Suppl):52-56 (1995)), a result

duplicated with the array. Other highly expressed chip
 sequences included a translation elongation factor 1 α
 (AC007564-4), a DEAD-box homolog (AL023804-4), and a Y-
 chromosome RNA-binding motif (Chai et al., *Genomics*
 5 49(2):283-89 (1998)) (AC007320-3). A low homology analog
 (AP00123-1/2) to a gene, DSCR1, thought to be involved in
 trisomy 21 (Down's syndrome), showed high expression in
 both brain and heart, in agreement with the literature
 (Fuentes et al., *Mol. Genet.* 4(10):1935-44 (1995)).

10 As a further validation of the approach, we
 selected the BAC AC006064 to be included on the array.
 This BAC was known to contain the GAPDH gene, and thus
 could be used as a control for the ORF selection process.
 The gene finding and exon selection algorithms resulted in
 15 choosing 25 exons from BAC AC006064 for spotting onto the
 array, of which four were drawn from the GAPDH gene. Table
 3 shows the comparison of the average expression ratio for
 the 4 exons from BAC006064 compared with the average
 expression ratio for 5 different dilutions of a
 20 commercially available GAPDH cDNA (Clontech).

Table 3

Comparison of Expression Ratio, for each tissue, of GAPDH		
	AC006064 (n = 4)	Control (n = 5)
Bone Marrow	-1.81 \pm 0.11	-1.85 \pm 0.08
Brain	-1.41 \pm 0.11	-1.17 \pm 0.05
BT474	1.85 \pm 0.09	1.66 \pm 0.12
Fetal Liver	-1.62 \pm 0.07	-1.41 \pm 0.05
HBL100	1.32 \pm 0.05	2.64 \pm 0.12
Heart	1.16 \pm 0.09	1.56 \pm 0.10
HeLa	1.11 \pm 0.06	1.30 \pm 0.15
Liver	-1.62 \pm 0.22	-2.07 \pm

Lung	-4.95 ± 0.93	-3.75 ± 0.21
Placenta	-3.56 ± 0.25	-3.52 ± 0.43

Each tissue shows excellent agreement between the experimentally chosen exons and the control, again demonstrating the validity of the present exon mining approach. In addition, the data also show the variability of expression of GAPDH within tissues, calling into question its classification as a housekeeping gene and utility as a housekeeping control in microarray experiments.

EXAMPLE 3

Representation of Sequence and Expression Data as a "Mondrian"

15

For each genomic clone processed for microarray as above-described, a plethora of information was accumulated, including full clone sequence, probe sequence within the clone, results of each of the three gene finding programs, EST information associated with the probe sequences, and microarray signal and expression for multiple tissues, challenging our ability to display the information.

Accordingly, we devised a new tool for visual display of the sequence with its attendant annotation which, in deference to its visual similarity to the paintings of Piet Mondrian, is hereinafter termed a "Mondrian". FIGS. 3 and 4 present the key to the information presented on a Mondrian.

FIG. 9 presents a Mondrian of BAC AC008172 (bases 25,000 to 130,000 shown), containing the carbamyl phosphate synthetase gene (AF154830.1). Purple background within the region shown as field 81 in FIG. 3 indicates all 37 known

exons for this gene.

As can be seen, GRAIL II successfully identified 27 of the known exons (73%), GENEFINDER successfully identified 37 of the known exons (100%), while DICTION
5 identified 7 of the known exons (19%).

Seven of the predicted exons were selected for physical assay, of which 5 successfully amplified by PCR and were sequenced. These five exons were all found to be from the same gene, the carbamyl phosphate synthetase gene
10 (AF154830.1).

The five exons were arrayed, and gene expression measured across 10 tissues. As is readily seen in the Mondrian, the five chip sequences on the array show identical expression patterns, elegantly demonstrating the
15 reproducibility of the system.

FIG. 10 is a Mondrian of BAC AL049839. We selected 12 exons from this BAC, of which 10 successfully sequenced, which were found to form between 5 and 6 genes. Interestingly, 4 of the genes on this BAC are protease
20 inhibitors. Again, these data elegantly show that exons selected from the same gene show the same expression patterns, depicted below the red line. From this figure, it is clear that our ability to find known genes is very good. A novel gene is also found from 86.6 kb to 88.6 kb,
25 upon which all the exon finding programs agree. We are confident we have two exons from a single gene since they show the same expression patterns and the exons are proximal to each other. Backgrounds in the following colors indicate a known gene (top to bottom):
30 red = kallistatin protease inhibitor (P29622);
purple = plasma serine protease inhibitor (P05154);
turquoise = α 1 anti-chymotrypsin (P01011); mauve = 40S ribosomal protein (P08865). Note that chip sequence 8 and 12 did not sequence verify.

35

EXAMPLE 4Genome-Derived Single Exon Probes Useful For Measuring
Human Gene Expression

5

The protocols set forth in Examples 1 and 2, *supra*, were applied to additional human genomic sequence as it became newly available in GenBank to identify unique exons in the human genome that could be shown to be expressed at significant levels in Fetal liver tissue.

These unique exons are within longer probe sequences. Each probe was completely sequenced on both strands prior to its use on a genome-derived single exon microarray; sequencing confirms the exact chemical structure of each probe. An added benefit of sequencing is that it placed us in possession of a set of single base-incremented fragments of the sequenced nucleic acid, starting from the sequencing primer 3' OH. (Since the single exon probes were first obtained by PCR amplification from genomic DNA, we were of course additionally in possession of an even larger set of single base incremented fragments of each of the 12,673 single exon probes, each fragment corresponding to an extension product from one of the two amplification primers.)

The structures of the 12,673 unique single exon probes are clearly presented in the Sequence Listing as SEQ ID Nos.: 1 - 12,673. The 16 nt 5' primer sequence and 16 nt 3' primer sequence present on the amplicon are not included in the sequence listing. The sequences of the exons present within each of these probes is presented in the Sequence Listing as SEQ ID Nos.: 12,674 - 25,129, respectively. It will be noted that some amplicons have more than one exon, some exons are contained in more than one amplicon.

35

As detailed in Example 2, expression was

demonstrated by disposing the amplicons as single exon probes on nucleic acid microarrays and then performing two-color fluorescent hybridization analysis; significant expression is based on a statistical confidence that the signal is significantly greater than negative biological control spots. The negative biological control is formed from spotted DNA sequences from a different species. Here, 32 sequences from E.Coli were spotted in duplicate to give a total of 64 spots.

For each hybridisation (each slide, each colour) the median value of the signal from all of the spots is determined. The normalised signal value is the arithmetic mean of the signal from duplicate spots divided by the population median.

Control spots are eliminated if there is more than a five-fold difference between each one of the duplicate spots raw signals.

The median of the signal from the remaining control spots is calculated and all subsequent calculations are done with normalised signals.

Control spots having a signal of greater than median + 2.4 (the value 2.4 is roughly 12 times the observed standard deviation of control spot populations) are eliminated. Spots with such high signals are considered to be "outliers".

The mean and standard deviation of the modified control spot populations are calculated.

The mean + 3x the standard deviation (mean + (3*SD)) is used as the signal threshold qualifier for that particular hybridisation. Thus, individual thresholds are determined for each channel and each hybridisation.

This means that, assuming that the data is distributed normally, there is a 99% confidence that any signal exceeding the threshold is significant.

The probes and their expression data are

presented in Table 4, set forth respectively in Example 5. Example 5 presents the subset of probes that is significantly expressed in the human Fetal liver and thus presents the subset of probes that was recognized to be useful for measuring expression of their cognate genes in human Fetal liver tissue.

The sequence of each of the exon probes identified by SEQ ID NOS.: 12,674 to 25,129 was individually used as a BLAST (or, for SWISSPROT, BLASTX) query to identify the most similar sequence in each of dbEST, SwissProt (BLASTX), and NR divisions of GenBank. Because the query sequences are themselves derived from genomic sequence in GenBank, only nongenic hits from NR were scored.

The smallest in value of the BLAST (or BLASTX) expect ("E") scores for each query sequence across the three database divisions was used as a measure of the "expression novelty" of the probe's ORF. Table 4 is sorted in descending order based on this measure, reported as "Most Similar (top) Hit BLAST E Value". Those sequences for which no "Hit E Value" is listed are those exons which were found to have no similar sequences.

As sorted, Table 4 thus lists its respective probes (by "AMPLICON SEQ ID NO.:" and additionally by the SEQ ID NO.: of the exon contained within the probe:"EXON SEQ ID NO.:" from least similar to sequences known to be expressed (i.e., highest BLAST E value), at the beginning of the table, to most similar to sequences known to be expressed (i.e., lowest BLAST E value), at the bottom of the table.

Table 4 further provides, for each listed probe, the accession number of the database sequence that yielded the "Most Similar (top) Hit BLAST E Value", along with the name of the database in which the database sequence is found ("Top Hit Database Source").

Table 4 further provides SEQ ID NOS.

corresponding to the predicted amino acid sequences where they have been determined for the probe and exon nucleotide sequences. These are set out as PEPTIDE SEQ ID NOS.:. The
5 peptide sequences for a given exon are predicted as follows: Since each chip exon is a consensus sequence drawn from predictions from various exon finding programs (i.e. Grail, GeneFinder and GenScan), the multiple initial ORFs are first determined in a uniform way according to each
10 prediction. In particular, the reading frame for predicting the first amino acid in the peptide sequence always starts with the first base of any codon and ends with the last base of non-termination codon. Next, for each strand of the exon, initial ORFs are merged into one or more final ORFs
15 in an exhaustive process based on the following criteria: 1) the merging ORFs must be overlapping, and 2) the merging ORFs must be in the same frame.

The Sequence Listing, which is a superset of all of the data presented in Table 4, further includes, for
20 each probe, the most similar hit, with accession number and BLAST E value, from the each of the three queried databases.

Table 4 further lists, for each probe, a portion of the descriptor for the top hit ("Top Hit Descriptor") as
25 provided in the sequence database. For those ORFs that are similar in sequence, but nonidentical to known sequences (e.g., those with BLAST E values between about $1e-05$ and $1e-100$), the descriptor reveals the likely function of the protein encoded by the probe's ORF.

30 Using BLAST E value cutoffs of $1e-05$ (i.e., 1×10^{-5}) and $1e-100$ (i.e., 1×10^{-100}) as evidence of similarity to sequences known to be expressed is of course arbitrary: in Example 2, *supra*, a BLAST E value of $1e-30$ was used as the boundary when only two classes were to be defined for
35 analysis (unknown, $>1e-30$; known $<1e-30$) (see also FIG. 8).

Furthermore, even when the "Most Similar (Top) Hit BLAST E Value" is low, e.g., less than about $1e-100$ - which is probative evidence that the query sequence has previously been shown to be expressed - the top hit is highly unlikely
5 exactly to match the probe sequence.

First, such expression entries typically will not have the intronic and/or intergenic sequence present within the single exon probes listed in the Table. Second, even the ORF itself is unlikely in such cases to be present
10 identically in the databases, since most of the EST and mRNA clones in existing databases include multiple exons, without any indication of the location of exon boundaries.

As noted, the data presented in Table 4 represent a proper subset of the data present within the attached
15 sequence listing. For each amplicon probe (SEQ ID NOs.: 1 - 12,673) and probe exon (SEQ ID NOs.: 12,674 - 25,129, respectively), the sequence listing further provides, through iterated annotation fields <220> and <223>:

(a) the accession number of the BAC from which
20 the sequence was derived ("MAP TO"), thus providing a link to the chromosomal map location and other information about the genomic milieu of the probe sequence;

(b) the most similar sequence provided by BLAST query of the EST database, with accession number and BLAST
25 E value for the "hit";

(c) the most similar sequence provided by BLAST query of the GenBank NR database, with accession number and BLAST E value for the "hit"; and

(d) the most similar sequence provided by BLASTX
30 query of the SWISSPROT database, with accession number and BLAST E value for the "hit".

EXAMPLE 5

35 Genome-Derived Single Exon Probes Useful For Measuring

Expression of Genes in Human Fetal liver

Table 4 (526 pages) presents expression, homology, and functional information for the genome-derived single exon
5 probes that are expressed significantly in human Fetal liver.

CLAIMS

1. A spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived
5 from human Fetal liver comprising a plurality single exon nucleic probes, said probes comprising any one of the nucleotide sequences set out in SEQ ID NOs: 1 - 12,673 or a complementary sequence, or a portion of such a sequence.
- 10 2. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably amplifiable.
3. A spatially-addressable set of single exon nucleic acid
15 probes as claimed in claim 1 wherein each of said plurality of probes is separately and addressably isolatable from said plurality.
4. A spatially-addressable set of single exon nucleic acid
20 probes as claimed in any of claims 1 to 3 wherein said probes comprise any one of the nucleotide sequences set out in SEQ ID NOS.: 12,674 - 25,129.
5. A spatially-addressable set of single exon nucleic acid
25 probes as claimed in any of claims 1 to 4, wherein each of said plurality of probes is amplifiable using at least one common primer.
6. A spatially-addressable set of single exon nucleic acid
30 probes as claimed in any of claims 1 to 5 wherein the set comprises between 50 - 20,000 single exon nucleic acid probes.
7. A spatially-addressable set of single exon nucleic acid
35 probes as claimed in any of claims 1 to 6, wherein the

average length of the single exon nucleic acid probes is between 200 and 500 bp.

8. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 7, wherein at least 50% of said single exon nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 to 8, wherein at least 50% of said single-exon nucleic acid probes lack homopolymeric stretches of A or T.

10. A spatially-addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 9 characterised in that said set of probes is addressably disposed upon a substrate.

11. A spatially-addressable set of single exon nucleic acid probes as claimed in claim 10 wherein said substrate is selected from glass, amorphous silicon, crystalline silicon and plastic.

12. A microarray comprising a spatially addressable set of single exon nucleic acid probes as claimed in any of claims 1 - 11.

13. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 1 - 12,673 or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid molecule expressed in the human Fetal liver.

14. A single exon nucleic acid probe as claimed in claim 13 comprising a nucleotide sequence as set out in any of SEQ ID NOs.: 12,674 - 25,129 or a complementary sequence or a fragment thereof.

5

15. A single exon nucleic acid probe for measuring human gene expression in a sample derived from human Fetal liver which is a nucleic acid molecule having a sequence encoding a peptide comprising a peptide sequence as set out in any
10 of SEQ ID NOs.: 25,130 - 37,156, or a complementary sequence or a fragment thereof wherein said probe hybridizes at high stringency to a nucleic acid expressed in the human Fetal liver.

15 16. A single exon nucleic acid probe as claimed in any one of claims 13 to 15 wherein said single exon nucleic acid probe comprises between 15 and 25 contiguous nucleotides of said SEQ ID NO.

20 17. A single exon nucleic acid probe as claimed in any one of claims 13 to 15, wherein said probe is between 3 - 25 kb in length.

18. A single exon nucleic acid probe as claimed in any one
25 of claims 13 - 17, wherein said probe is DNA, RNA or PNA.

19. A single exon nucleic acid probe as claimed in any one of claims 13 - 18, wherein said probe is detectably labeled.

30

20. A single exon nucleic acid probe as claimed in any one of claims 13 - 19, wherein said probe lacks prokaryotic and bacteriophage vector sequence.

35 21. A single exon nucleic acid probe as claimed in any one

of claims 13 - 20, wherein said probe lacks homopolymeric stretches of A or T.

22. A method of measuring gene expression in a sample
5 derived from human Fetal liver, comprising:
 contacting the microarray of claim 12, with a first
 collection of detectably labeled nucleic acids,
 said first collection of nucleic acids derived
 from mRNA of human Fetal liver; and then
10 measuring the label detectably bound to each probe of
 said microarray.

23. A method of identifying exons in a eukaryotic genome,
comprising:
15 algorithmically predicting at least one exon from
 genomic sequence of said eukaryote; and then
 detecting specific hybridization of detectably labeled
 nucleic acids to a single exon probe,
wherein said detectably labeled nucleic acids are derived
20 from mRNA from the Fetal liver of said eukaryote, said
probe is a single exon probe having a fragment identical in
sequence to, or complementary in sequence to, said
predicted exon, said probe is included within a microarray
according to claim 12, and said fragment is selectively
25 hybridizable at high stringency.

24. A method of assigning exons to a single gene,
comprising:
 identifying a plurality of exons from genomic
30 sequence according to the method of claim 23; and
 then
 measuring the expression of each of said exons in a
 plurality of tissues and/or cell types using
 hybridization to single exon microarrays having a
35 probe with said exon,

wherein a common pattern of expression of said exons in said plurality of tissues and/or cell types indicates that the exons should be assigned to a single gene.

5 25. A nucleic acid sequence as set out in any of SEQ ID Nos: 1 - 25,129 which encodes a peptide.

26. A peptide encoded by a sequence as set out in any of SEQ ID Nos: 1 - 25,129.

10

27. A peptide comprising a sequence as set out in any of SEQ ID Nos: 25,130 - 37,156.

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
475	13108	25600	4.41				
922	13535	26053	9.9				
1083	13688		2.9				
1345	13940	26462	10.32				
1656	14248	26782	2.59				
1678	14270	26803	5.03				
1763	14353	26899	1.73				
1765	14375	26919	0.99				
1782	14382	26927	9.24				
1935	14519	27075	1.21				
2021	14603	27168	3.24				
2210	14766	27360	4.38				
2318	14890	27485	2.04				
2607	15169	27735	0.89				
2607	15169	27736	0.89				
3220	15932	28311	1.65				
3496	16101	28576	1.22				
3566	16170	28652	10.28				
3617	16220		0.8				
3718	16319	28787	0.97				
4020	16618		0.94				
4275	16861	29310	1.53				
4348	16935	29376	8.4				
4368	16955	29396	0.74				
4368	16955	29397	0.74				
4430	17016		1.3				
4862	17537	29979	1.04				
5007	17580		0.59				
5054	17627	30071	0.61				
5197	17762	30187	5.95				
5212	17777	30198	1.32				
5462	18097	30415	2.1				
5462	18097	30416	2.1				
5615	18244		5.64				

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5783	18408		9.03				
5859	18244		4.85				
5910	18532	31257	0.84				
5915	18537	31262	3.16				
6173	24759	31552	1.41				
6200	18810	31578	1.65				
6548	19146		1.26				
6668	19264	32067	1				
6668	19264	32068	1				
7178	19711	32559	1.13				
7179	19711	32560	1.13				
7441	19965	32831	1.4				
7441	19965	32832	1.4				
8005	20547	33451	1.65				
8422	20962	33878	1.45				
8794	21333	34257	0.57				
8794	21333	34258	0.57				
9453	21978	34931	4.84				
9681	22180	35155	0.78				
9796	22284	35277	1.19				
9836	22431	35406	1.03				
10214	22709	35702	0.48				
10214	22709	35703	0.48				
10326	22820	35815	0.65				
10326	22820	35816	0.65				
10563	23099		3.06				
10725	24799	36268	2.46				
10906	23425		2.99				
11238	23769	36827	2.73				
11336	23034	36043	1.87				
11336	23034	36044	1.87				
11374	23826		2.59				
12117	24376		2.19				
12439	24576	30914	1.6				

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6203	18813	31583	14.37	9.0E+00	AJ239028.1	NT	Homo sapiens LSS gene, partial, exons 15, 16, 17 and 18
7948	20490	33400	1.65	9.8E+00	U32716.1	NT	Haemophilus influenzae Rd section 31 of 163 of the complete genome
9658	22157	35128	0.47	9.8E+00	Y18830.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
9658	22157	35128	0.47	9.8E+00	Y18830.1	NT	Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2
7073	19645	32483	0.8	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
7073	19645	32484	0.8	9.6E+00	AF065630.1	NT	Gallus gallus ornithine transcarbamylase (OTC) gene, exon 1
10319	22813	35808	1.22	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor I1H polypeptide 2 (Gt2h2) genes, complete cds
10319	22813	35809	1.22	9.6E+00	AF242432.1	NT	Mus musculus Naip3 gene, exon 1; neuronal apoptosis inhibitory protein 1 (Naip1) and general transcription factor I1H polypeptide 2 (Gt2h2) genes, complete cds
2889	15247	27814	1.14	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2889	15247	27815	1.14	8.4E+00	L11433.1	NT	Dengue virus type 3 membrane protein (prM/M)/envelope glycoprotein (E) polyprotein mRNA, partial cds
2950	15566	28040	3.19	9.4E+00	AB043785.1	NT	Mus musculus AT3 gene for antithrombin, complete cds
8042	20584	33461	0.99	9.3E+00	AF130980.1	NT	Homo sapiens ectodysplasin-A receptor protein (EDAR) gene, exons 2, 3, and 4
8833	21471	34390	3.48	9.3E+00	P11210	SWISSPROT	IMMEDIATE-EARLY PROTEIN 1 (IE1) (IMMEDIATE-EARLY PHOSPHOPROTEIN PP89)
5500	18134	30543	2.82	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
5500	18134	30544	2.82	9.1E+00	AF095609.1	NT	Leuciscus cephalus orientalis cytochrome b (cyt b) gene, partial cds; mitochondrial gene for mitochondrial product
9351	21865		0.9	9.0E+00	P08241	SWISSPROT	RHODOPSIN
6186	18796	31584	5.12	8.9E+00	BE971808.1	EST_HUMAN	601651038R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934592 3'
6517	19117	31907	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
6517	19117	31908	1.9	8.7E+00	AB019788.1	NT	Cynops pyrrhogaster CpTbx3 premature mRNA, partial cds
465	13099	25590	1.66	8.4E+00	5031804	NT	Homo sapiens insulin receptor substrate 1 (IRS1) mRNA
9376	20315	33217	3.8	8.1E+00	AJ131719.1	NT	Zea mays mRNA for legumain-like protease (see2a)
11048	23561		2.47	8.0E+00	P41820	SWISSPROT	BREFELDIN A RESISTANCE PROTEIN
8092	20633		0.76	7.6E+00	Z21489.1	NT	African swine fever virus NP1450L gene encoding RNA polymerase largest subunit
7384	19910		1.95	7.5E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8302	20843	33784	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
8302	20843	33785	1.54	7.5E+00	P35441	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5988	19589	31324	3.35	7.4E+00	BF700517.1	EST_HUMAN	602128876F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285506 5'
8688	21227	34147	2.63	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8698	21227	34148	2.63	7.4E+00	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3006	15622	28098	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
3006	15622	28100	3.19	7.2E+00	L12051.1	NT	Lycopodium esculentum Mill. GTPase (SAR2) mRNA, complete cds
7097	19668	32507	0.7	7.2E+00	BE179080.1	EST_HUMAN	RCO-HT0613-200300-031-a07 HT0613 Homo sapiens cDNA
7203	19734	32585	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
7203	19734	32586	1.22	7.1E+00	P28166	SWISSPROT	ZINC-FINGER PROTEIN 1 (ZINC-FINGER HOMEODOMAIN PROTEIN 1)
9516	22016		7.96	7.1E+00	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
11263	22791	36848	3.2	7.1E+00	P05850	SWISSPROT	HYPOTHETICAL 17.3 KDA PROTEIN IN MRDA-PHPB INTERGENIC REGION
9892	22969	35367	3.35	7.0E+00	P48610	SWISSPROT	ARGININE KINASE (AK)
11129	23637	36679	1.87	7.0E+00	Q22469	SWISSPROT	WD-40 REPEAT PROTEIN MS13
8225	20766	33694	4.06	6.9E+00	P35679	SWISSPROT	60S RIBOSOMAL PROTEIN L4 (L2)
10253	22748	35736	1.2	6.9E+00	P44834	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
7849	20391	33293	1.38	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:291860 5'
7849	20391	33294	1.38	6.8E+00	W03412.1	EST_HUMAN	za07c11.1 Soares melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:291860 5'
9060	21597		1.13	6.8E+00	P36307	SWISSPROT	OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8]
10110	22605	35595	3.85	6.8E+00	Q03570	SWISSPROT	HYPOTHETICAL 157.0 KDA PROTEIN C38C10.5 IN CHROMOSOME III
5488	18122		0.69	6.6E+00	Q98028	SWISSPROT	CATECHOL-O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)
9886	22481	35465	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
9886	22481	35466	1.89	6.6E+00	Q9ZE07	SWISSPROT	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE)
11008	23522		2.13	6.6E+00	Q10309	SWISSPROT	PROBABLE CATION-TRANSPORTING ATPASE C8C3.05C
9108	21644	34584	7.21	6.5E+00	P03374	SWISSPROT	ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
10206	22701	35695	0.49	6.5E+00	BE866001.1	EST_HUMAN	801878435F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3960989 5'
9657	22166	35127	1.11	6.2E+00	A7010901.1	NT	Schizaphyllum commune unknown mRNA
10455	22946	35958	0.53	6.2E+00	6754621	NT	Mus musculus mannosidase 2, alpha B1 (Man2b1), mRNA
7102	19872	32511	1.34	6.0E+00	BE780163.1	EST_HUMAN	601468031F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871303 5'
9730	22228	35205	0.46	6.0E+00	AF000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1169001-1485000 nt. position (617)
10407	22801	35896	0.6	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
10407	22801	35897	0.6	6.0E+00	AE001862.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
6643	19239	32042	6.67	5.8E+00	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mlk3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
3578	16180		1.18	5.8E+00	7681557	NT	Homo sapiens DESCI1 protein (DESCI1), mRNA
7215	19746	32601	0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds
7215	19746	32602	0.67	5.7E+00	AF302046.1	NT	Mus musculus immunoglobulin scavenger receptor IgSR mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7570	20087		1.31	5.6E+00	P75080	SWISSPROT	DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE (POLIII)
11349	23047	36059	2.68	5.6E+00	Q55278	SWISSPROT	LYCOPENE BETA CYCLASE
8399	19002	31780	0.73	5.5E+00	P47447	SWISSPROT	HEAT-INDUCIBLE TRANSCRIPTION REPRESSOR HRCA
10658	23190		1.54	5.5E+00	AF175425.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 30, 31, and 32
11348	23046	36058	3.79	5.5E+00	P11990	SWISSPROT	PNEUMOLYSIN (THIOL-ACTIVATED CYTOLYSIN)
11578	24024		2.08	5.5E+00	AL161571.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 67
7009	19507	32326	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7009	19507	32327	1.2	5.4E+00	X02212.1	NT	Chicken alpha-cardiac actin gene
7369	19895		0.72	5.4E+00	Q69435	SWISSPROT	NEL PROTEIN PRECURSOR (NEL-RELATED PROTEIN 2)
							VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELLIN LV-1N; LIPOVITELLIN LV-1C;
7811	20354		1.58	5.4E+00	Q91082	SWISSPROT	LIPOVITELLIN LV-2]
8734	21273	34193	0.78	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
8734	21273	34194	0.78	5.4E+00	P40379	SWISSPROT	REP1 PROTEIN
9949	22444	35423	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
9949	22444	35424	1.33	5.4E+00	Q17094	SWISSPROT	RHODOPSIN
4899	17474	29930	1.52	5.3E+00	L43126.1	NT	Bovine immunodeficiency-like virus surface envelope gene, 5' end of cds
6614	19211		0.67	5.3E+00	P41779	SWISSPROT	HOMEBOX PROTEIN CEH-20
8024	20566		3.71	5.3E+00	P54098	SWISSPROT	DNA POLYMERASE GAMMA (MITOCHONDRIAL DNA POLYMERASE CATALYTIC SUBUNIT)
8914	21452		0.62	5.3E+00	AB034990.1	NT	Homo sapiens HERPUD1 gene for stress protein Herp, complete cds
5655	18282		1.04	5.2E+00	BE184940.1	EST_HUMAN	QV4-HT0691-270400-195-109 HT0691 Homo sapiens cDNA
10274	22769		0.78	5.2E+00	AF248070.1	NT	Drosophila orientacea R1B retrotransposable element reverse transcriptase gene, partial cds
11074	23596		2.1	5.2E+00	Q10136	SWISSPROT	HYPOPHYSICAL 61.1 KD PROTEIN C23E2.03C IN CHROMOSOME 1
8892	21430	34354	0.88	5.1E+00	O16005	SWISSPROT	RHODOPSIN
9739	22237	35217	0.97	5.1E+00	P09182	SWISSPROT	COLICIN N IMMUNITY PROTEIN (MICROCIN N IMMUNITY PROTEIN)
6430	19033	31817	0.85	5.0E+00	BF310443.1	EST_HUMAN	601894910F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124114 5'
10086	22591		0.69	5.0E+00	BF308561.1	EST_HUMAN	601890420F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131509 5'
10327	22821	35817	3.37	5.0E+00	AF162445.2	NT	Canis familiaris skeletal muscle chloride channel CIC-1 (CLCN1) mRNA, complete cds
11170	23677	36723	13.54	5.0E+00	Z63860.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 103/162
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (-HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP73) gene, complete cds
10131	22626		0.71	4.9E+00	U91328.1	NT	Eunice australis histone H3 (H3) gene, partial cds
4135	18727		12.08	4.8E+00	AF185255.1	NT	RC3-GN0042-100800-011-c10 GN0042 Homo sapiens cDNA
8095	20638	33547	0.65	4.8E+00	BF367909.1	EST_HUMAN	PM0-BT0547-310100-002-b04 BT0547 Homo sapiens cDNA
8478	21017		4.95	4.8E+00	AW750087.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
311	12986	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
312	12986	25454	1.88	4.7E+00	BF240552.1	EST_HUMAN	601875654F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099716 5'
3312	15923	28399	1.08	4.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment H521C080
8124	21659	34601	1.09	4.6E+00	BE646437.1	EST_HUMAN	7e96g10.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
9124	21659	34602	1.09	4.6E+00	BE646437.1	EST_HUMAN	KIAA0845 PROTEIN; contains element PTR5 repetitive element; 7e96g10.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3292098 3' similar to TR:O75140 O75140
10290	22785		0.77	4.6E+00	AF240786.1	NT	KIAA0845 PROTEIN; contains element PTR5 repetitive element; Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11474	23924	36994	1.99	4.5E+00	AE001044.1	NT	Archaeoglobus fulgidus section 63 of 172 of the complete genome
11598	24039	37108	1.67	4.5E+00	BF588841.1	EST_HUMAN	602123238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4280216 5'
3076	15691	28164	1.53	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
3078	15691	28165	1.53	4.4E+00	BF530893.1	EST_HUMAN	602072585F1 NCI CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4215284 5'
6349	18954		1.8	4.4E+00	X13414.1	NT	Murine I gene for MHC class II (la) associated invariant chain
6268	18874		0.82	4.3E+00	AF059679.1	NT	Homo sapiens neutrophil collagenase (CLGNA) gene, promoter region and 5'UTR
7464	19986	32851	2.36	4.3E+00	Y13402.1	NT	Plasmodium falciparum R29R+var1 gene, exon 1
7611	20124	33001	0.84	4.3E+00	AE001222.1	NT	Treponema pallidum section 38 of 87 of the complete genome
10741	23266	36282	8.92	4.3E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
5708	18334		3.21	4.2E+00	P16444	SWISSPROT	MICROSOMAL DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DIPEPTIDASE) (RDP)
5780	18405	31121	1.48	4.2E+00	P51826	SWISSPROT	LAF-4 PROTEIN (LYMPHOID NUCLEAR PROTEIN)
6859	19603	32435	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
6859	19603	32436	1.86	4.2E+00	P13983	SWISSPROT	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)
8890	21428	34353	4.65	4.2E+00	AI06013.1	EST_HUMAN	wf67g03.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2306992 3'
9832	22330	35312	2.07	4.2E+00	P31368	SWISSPROT	NUBBIN PROTEIN (TWIN PROTEIN) (POU DOMAIN PROTEIN 1) (PDM-1) (DPOU-19) (DOCT1)
7166	19698	32545	0.81	4.1E+00	BE253698.1	EST_HUMAN	601110727F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351534 5'
7284	19792	32648	1.7	4.1E+00	BF247839.1	EST_HUMAN	601859030F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4069758 5'
7657	20189	33056	8.1	4.1E+00	O23810	SWISSPROT	YY1 PROTEIN PRECURSOR
7759	20287	33163	4.03	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7759	20287	33164	4.03	4.1E+00	P28964	SWISSPROT	GENE 68 PROTEIN
7857	20399	33306	2.78	4.1E+00	U57503.1	NT	Pan troglodytes novel repetitive solo LTR element in the RNU2 locus
9459	21985	34939	0.63	4.1E+00	P11253	SWISSPROT	50S RIBOSOMAL PROTEIN L4
9590	22090	35054	2.26	4.1E+00	BF692425.1	EST_HUMAN	602247938F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333209 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10208	22703		0.5	4.1E+00	P46414	SWISSPROT	CYCLIN-DEPENDENT KINASE INHIBITOR 1B (CYCLIN-DEPENDENT KINASE INHIBITOR P27) (P27KIP1)
10499	22993	36003	0.62	4.1E+00	Q84242	SWISSPROT	3-OXOACYL-JACYL-CARRIER-PROTEIN SYNTHASE III (BETA-KETOACYL-ACP SYNTHASE III) (KAS III)
10765	23289		2.97	4.1E+00	P09716	SWISSPROT	HYPOTHETICAL PROTEIN HVLF1
10851	23372		13.84	4.1E+00	BE885880.1	EST_HUMAN	601507510F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3808051 5'
3599	16203		0.82	4.0E+00	P38229	SWISSPROT	GLC7-INTERACTING PROTEIN 1
5650	19515	32336	0.74	4.0E+00	Q82653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
5650	19515	32337	0.74	4.0E+00	Q82653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
5650	19515	32338	0.85	4.0E+00	Q82653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7017	19515	32337	0.85	4.0E+00	Q82653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7017	19515	32337	0.85	4.0E+00	Q82653	SWISSPROT	SUCRASE-ISOMALTASE, INTESTINAL [CONTAINS: SUCRASE ; ISOMALTASE]
7240	19769	32625	1.34	4.0E+00	Q33010	SWISSPROT	CELL DIVISION PROTEIN FTSY HOMOLOG
10070	22565	35560	0.6	4.0E+00	AF002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
10158	22653	35647	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
10158	22653	35648	0.49	4.0E+00	Q00511	SWISSPROT	URICASE (URATE OXIDASE)
11423	23874	36937	3.99	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
11423	23874	36938	3.99	4.0E+00	P07564	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5)]
3550	16154	28636	4.79	3.9E+00	X64518.1	NT	N tabacum chitinase gene 50 for class I chitinase C
4413	16998		0.74	3.9E+00	AF055468.1	NT	Mus musculus seminal vesicle secretory protein 99 (MSVSP99) gene, promoter region
5839	18463	31186	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
5839	18463	31187	3.08	3.9E+00	BE814357.1	EST_HUMAN	MRO-BN0070-300500-028-H05 BN0070 Homo sapiens cDNA
6746	19339	32145	0.71	3.9E+00	AF288209.1	NT	Dicystostellum discoideum non-L TR retrotransposon TRE5-B, polyprotein (gag) and group-specific antigen (pol) genes, complete cds
6792	19383	32198	0.72	3.9E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
6855	19532	32357	4.12	3.9E+00	P39299	SWISSPROT	HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN AIDB-RP5F INTERGENIC REGION
7398	19923	32787	6.09	3.9E+00	M23907.1	NT	Human MHC class II lymphocyte antigen (DPw4-beta-1) gene, exon 2

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8259	20800	33718	2.15	3.9E+00	X65865.1	NT	Xlaevis mRNA for M4 muscarinic receptor
11269	23007	36014	3.27	3.9E+00	Y18000.1	NT	Homo sapiens NF2 gene
11291	23743	36800	1.62	3.9E+00	AA681489.1	EST_HUMAN	nr18a12.s1 NCI CGAP Ewt Homo sapiens cDNA clone IMAGE:1168318 similar to gb:A10416
2658	15217		1.1	3.8E+00	AE001562.1	NT	METALLOPROTEINASE INHIBITOR 1 PRECURSOR (HUMAN); Helicobacter pylori strain J99 section 123 of the complete genome
6525	19125	31918	0.78	3.8E+00	Q57830	SWISSPROT	HYPOTHETICAL PROTEIN MJ0385
8371	20911	33831	1.06	3.8E+00	D44725.1	EST_HUMAN	HUMSUPY135 Human brain cDNA Homo sapiens cDNA clone 148
9710	22208		0.55	3.8E+00	AJ300861.1	NT	Streptococcus oralis partial xpt gene for xanthine phosphoribosyltransferase, strain NCTC7864
4092	16687	28144	13.56	3.7E+00	AL181639.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 39
7218	19749		0.79	3.7E+00	AL445065.1	NT	Thermoplasma acidophilum complete genome; segment 3/5
8842	21181		0.53	3.7E+00	4503950	NT	Homo sapiens glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK), nuclear gene encoding mitochondrial protein, mRNA
9105	21041	34581	0.68	3.7E+00	U43541.1	NT	Mus musculus laminin beta 2 gene, exons 17-33, and complete cds
11308	23801	36861	3.11	3.7E+00	BF669278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11308	23801	36862	3.11	3.7E+00	BF669278.1	EST_HUMAN	602120551F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277748 5'
11707	24158		1.28	3.7E+00	AB013746.3	NT	Gallus gallus mRNA for hypoxia-inducible factor-1 alpha, complete cds
619	13246	25719	2.6	3.6E+00	AV781055.1	EST_HUMAN	AV781055 MDS Homo sapiens cDNA clone MDSBUE10 5'
4917	17492		0.99	3.6E+00	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
8487	21026	33942	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000T808 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8487	21026	33943	0.76	3.6E+00	D12367.1	EST_HUMAN	HUM000T808 Liver HepG2 cell line. Homo sapiens cDNA clone tb08
8579	21118	34038	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome
8579	21118	34039	4.02	3.6E+00	AE004447.1	NT	Pseudomonas aeruginosa PAO1, section 8 of 529 of the complete genome
							Escherichia coli glycerophosphate dehydrogenase (glpD) gene, partial cds; and the translation start site has been verified (glpE), the translation start site has been verified (glpG), and repressor protein (glpR) genes, complete cds
10733	23269		4.32	3.6E+00	M96795.1	NT	Cryptosporidium felis heat shock protein 70 (HSP70) gene, partial cds
3284	15895	28373	1.08	3.5E+00	AF221538.1	NT	Borrelia burgdorferi (strain 25015) outer surface protein (ospC) gene, partial cds
6151	18764		1.06	3.5E+00	L42898.1	NT	9940c08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:34940 5'
6360	18984	31742	0.92	3.5E+00	R19745.1	EST_HUMAN	THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)
8421	20961		0.55	3.5E+00	P24657	SWISSPROT	z86b04.s1 Stratagene HeLa cell s3 837218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
8962	21500	34421	0.88	3.5E+00	AA190998.1	EST_HUMAN	z86b04.s1 Stratagene HeLa cell s3 837218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
8962	21500	34422	0.88	3.5E+00	AA190998.1	EST_HUMAN	z86b04.s1 Stratagene HeLa cell s3 837218 Homo sapiens cDNA clone IMAGE:627055 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element ;
9414	21923	34872	1.12	3.5E+00	AL181553.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 53

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1559	14151	26683	4.49	3.4E+00	AF254577.1	NT	Brassica napus RP85d mRNA, complete cds
2612	15174	27742	1.02	3.4E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7397	19922	32786	2.85	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7690	20199	33086	0.86	3.4E+00	P04052	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
8611	21150		0.89	3.4E+00	U05406.1	NT	Human alternatively spliced potassium channels ROM-K1, ROM-K2, ROM-K3, ROM-K4, ROM-K5, and ROM-K6 (KCNJ1) gene, complete cds
9003	21540	34470	0.7	3.4E+00	AJ229042.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 8
9040	21577	34508	0.5	3.4E+00	AJ250567.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 8
10165	22660	35655	3.61	3.4E+00	AF013197.1	NT	Saccharomyces cerevisiae MSS1 gene, complete cds
11406	23657	36922	1.98	3.4E+00	L77670.1	NT	Homo sapiens DiGeorge syndrome critical region, centromeric end
6218	18828	31601	0.9	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
6218	18828	31602	0.9	3.3E+00	Q09669	SWISSPROT	PUTATIVE IRON ALCOHOL DEHYDROGENASE
7634	20376	33281	0.88	3.3E+00	AF111198.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
10361	22855	35847	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
10361	22855	35848	0.87	3.3E+00	AP001511.1	NT	Bacillus halodurans genomic DNA, section 5/14
526	13158	25640	1.72	3.2E+00	X06422.1	NT	D. rerio zp-50 POU gene
4098	13158	25640	0.7	3.2E+00	X06422.1	NT	D. rerio zp-50 POU gene
4835	17413	26866	1.24	3.2E+00	4502404	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) (CEACAM1), mRNA
5757	18383	31095	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5757	18383	31096	1.34	3.2E+00	P54924	SWISSPROT	SQUALENE-HOPENE CYCLASE
5787	18412	31128	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
5787	18412	31129	2.45	3.2E+00	P12783	SWISSPROT	PHOSPHOGLYCERATE KINASE, CYTOSOLIC
6448	19049	31834	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
6448	19049	31835	1.86	3.2E+00	P18931	SWISSPROT	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4
7601	20114	32991	0.84	3.2E+00	P04275	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
7750	20258	33154	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
7750	20258	33155	2.22	3.2E+00	Y13655.1	NT	Chlamydomonas reinhardtii chloroplast DNA for rps9, ycf4, ycf3, rps18 genes
8960	21498	33155	4.84	3.2E+00	P13061	SWISSPROT	PERIPLASMIC (NIFE) HYDROGENASE SMALL SUBUNIT (NIFE HYDROGENLYASE SMALL CHAIN)
9449	21975	34927	1.52	3.2E+00	M06383.1	NT	S. cerevisiae threonine deaminase (ILV1) gene, complete cds
10047	22542	35539	1.91	3.2E+00	A016081.2	NT	Oryzias latipes OIG06 gene for guanylyl cyclase C, complete cds
11727	24133		4.08	3.2E+00	L33836.1	NT	Sus scrofa choline acetyltransferase gene, promoter region
6035	18654	31396	2.24	3.1E+00	Q10135	SWISSPROT	HYPOTHETICAL 142.5 KO PROTEIN C23E2.02 IN CHROMOSOME 1
7421	18945	32810	0.97	3.1E+00	P52178	SWISSPROT	TRIOSE PHOSPHATE/PHOSPHATE TRANSLOCATOR, NON-GREEN PLASTID PRECURSOR (C1PT)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7711	20220		1.09	3.1E+00	AF303225.1	NT	Bacillus alcalophilus peptidase (pepE) gene, complete cds
8538	21077	33995	4.27	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
8538	21077	33996	4.27	3.1E+00	P49894	SWISSPROT	TYPE I IODOTHYRONINE DEIODINASE (TYPE I 5'DEIODINASE) (DIOI) (TYPE 1 DI) (5DI)
9183	21760		3.77	3.1E+00	Q14957	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
9248	21775	34726	0.52	3.1E+00	Q01149	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9810	22308	35292	0.75	3.1E+00	7524759	NT	Chlorella vulgaris chloroplast, complete genome
9899	22396		0.56	3.1E+00	Q10125	SWISSPROT	HYPOTHETICAL 56.3 KD PROTEIN F52C9.5 IN CHROMOSOME III
10239	22734	35726	4.7	3.1E+00	P49365	SWISSPROT	DEOXYHYPOSINE SYNTHASE (DHS)
11338	23036		2.91	3.1E+00	P33515	SWISSPROT	GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA POLYMERASE (NS5))
11355	23809		7.48	3.1E+00	S66860.1	NT	retinoid acid nuclear receptor isoform beta 2 [mice, embryonal carcinoma cell line, PCC7-MZ1, mRNA, 2871 nt]
12490	24619		1.38	3.1E+00	U77686.1	NT	Brassica rapa pollen coat protein homodog (BAN103) gene, complete cds
5541	18173	30588	1.68	3.0E+00	X53098.1	NT	S aureus genes encoding Sau981 DNA methyltransferase and Sau981 restriction endonuclease
6673	18269	32073	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
6673	18269	32074	0.72	3.0E+00	X56037.1	NT	Corynebacterium glutamicum thrC gene for threonine synthase (EC 4.2.99.2)
7208	19740		10.44	3.0E+00	P18406	SWISSPROT	CYR61 PROTEIN PRECURSOR (3CH61)
7247	19776		0.77	3.0E+00	Q13201	SWISSPROT	ENDOTHELIAL CELL MULTIMERIN PRECURSOR
8838	21377		1.33	3.0E+00	X67838.1	NT	B.napus DNA for myrosinase
10195	22690	35683	0.53	3.0E+00	Q58605	SWISSPROT	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYL TRANSFERASE) (ADOMET SYNTHETASE)
10527	23064	36075	1.62	3.0E+00	Q16181	SWISSPROT	GDC10 PROTEIN HOMOLOG
10888	23409	36426	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10888	23409						RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
10888	23409	36427	7.04	3.0E+00	P51842	SWISSPROT	RETINAL GUANYLYL CYCLASE 2 PRECURSOR (GUANYLYL CYCLASE 2F, RETINAL) (RETGC-2) (ROD OUTER SEGMENT MEMBRANE GUANYLYL CYCLASE 2) (ROS-GC2) (GUANYLYL CYCLASE F) (GC-F)
2055	14636	27207	2.32	2.9E+00	AE002225.2	NT	Chlamydomonas reinhardtii AR39, section 53 of 94 of the complete genome
6224	18833		0.68	2.9E+00	AB026033.1	NT	Bonaparitia pedicellata mitochondrial DNA for 16S ribosomal RNA
6989	19487	32309	3.74	2.9E+00	Z36878.1	NT	F.pirnglei gdcA gene for P-protein of the glycine cleavage system
7282	19780	32644	4.37	2.9E+00	Q14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7262	19760	32845	4.37	2.9E+00	O14514	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 1 PRECURSOR
7479	20001	32866	6.04	2.9E+00	P46989	SWISSPROT	ADHERENCE FACTOR (ADHESION AND AGGREGATION MEDIATING SURFACE ANTIGEN)
7809	20352	33280	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
7809	20352	33281	0.67	2.9E+00	P05844	SWISSPROT	STRUCTURAL POLYPEPTIDE [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2; NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3]
8041	20563	33480	0.89	2.9E+00	BF344171.1	EST_HUMAN	602017413F1 NCL CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4153059 5'
1504	14096	26634	4.87	2.8E+00	AF186398.1	NT	Buxus harlandii malic acid decarboxylase K (malic acid decarboxylase); chloroplast gene for chloroplast product
1875	14267		3.45	2.8E+00	AL161552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
7348	19874	32740	4.88	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
9531	22031		0.57	2.8E+00	BE565182.1	EST_HUMAN	601342758F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3684807 5'
10569	19874	32740	1.68	2.8E+00	8393724	NT	Mus musculus endomucin (LOC53423), mRNA
251	12911	25394	9.31	2.7E+00	6876306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
251	12911	25395	9.31	2.7E+00	6876306	NT	Mus musculus per-hexamer repeat gene 3 (Phxr3), mRNA
5740	18366	31073	1.2	2.7E+00	L14005.1	NT	Homo sapiens apoA polymorphism Kingle IV gene, exons 1 and 2
8088	20628		0.8	2.7E+00	U15947.1	NT	Ipomoea purpurea chalcone synthase (CHS) gene including complete 5'UTR and complete cds
8898	21438		1.68	2.7E+00	AL116459.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9353	20262	33181	0.83	2.7E+00	AW088191.1	EST_HUMAN	xc88912.XT NCL CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2891374 3' similar to gb.M17733
10394	22898		1.48	2.7E+00	BE063527.1	EST_HUMAN	THYMOSIN BETA-4 (HUMAN);
4781	17362	29812	4.97	2.6E+00	AF068749.1	NT	CMO-BT0281-031189-087-h04 BT0281 Homo sapiens cDNA
5736	18362	31088	1.94	2.6E+00	6755601	NT	Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds
5736	18362	31089	1.94	2.6E+00	6755601	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
5992	18812		2.42	2.6E+00	Y17062.1	NT	Mus musculus SRY-box containing gene 13 (Sox13), mRNA
7689	20198		5.98	2.6E+00	AF235502.1	NT	Mycobacterium fortuitum furA II gene
8003	20545	33447	1.08	2.6E+00	AJ132180.1	NT	Mus musculus SH2-containing inositol 5-phosphatase (SHIP) gene, exons 18 through 27, and complete cds
8003	20545	33448	1.08	2.6E+00	AJ132180.1	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
9576	22076	35039	3.02	2.6E+00	AL161540.2	NT	faba bean necrotic yellow virus C2-Eg gene, isolate Egyptian EV1-93
10257	22752		1.51	2.6E+00	9055193	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40
10907	23428	36443	1.69	2.6E+00	AF143875.1	NT	Mus musculus cleavage and polyadenylation specificity factor 3 (Cpsf3), mRNA
12390	24986		2.78	2.6E+00	11419220	NT	Hantavirus Z10 segment M G1/G2 glycoprotein (Z10) gene, complete cds
1513	14105	26840	2.29	2.5E+00	AJ271844.1	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), mRNA
1513	14105	26841	2.29	2.5E+00	AJ271844.1	NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4
						NT	Aspergillus nidulans recQ gene for DNA helicase, exons 1-4

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Single Exon Probes Expressed In Fatal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5981	18601	31334	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
5981	18601	31335	1.71	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	18601	31334	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6586	18601	31335	1.39	2.5E+00	P13485	SWISSPROT	TEICHOIC ACID BIOSYNTHESIS PROTEIN F
6828	19418	32234	0.73	2.5E+00	D30052.1	NT	Vibrio cholerae ctaA gene and ctaB gene for cholera toxins, complete cds
7736	20244	33135	1.05	2.5E+00	AW949158.1	EST_HUMAN	QV4-FT0005-110500-203-g07 FT0005 Homo sapiens cDNA
9032	21569	34498	1.75	2.5E+00	D50307.1	NT	Rice DNA for aldolase C-1, complete cds
9766	22264	35247	0.88	2.5E+00	BE297758.1	EST_HUMAN	60117579F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531090 5'
11724	24131		1.86	2.5E+00	AF289685.1	NT	Mus musculus EIF4H gene, partial cds; LIMK1 gene, complete cds; and ELN gene, partial cds
3047	15663	28144	0.9	2.4E+00	M24282.1	NT	Chicken alpha-3 collagen type VI mRNA, 3' end
5033	17607	30052	6.76	2.4E+00	P02843	4503352 NT	Homo sapiens double C2-like domains, alpha (DOC2A) mRNA
6161	18774	31536	4.02	2.4E+00	P26842	SWISSPROT	VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1)
8082	20624	33536	1.99	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8082	20624	33537	1.99	2.4E+00	P26842	SWISSPROT	CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27) (T14)
8153	20694		2.33	2.4E+00	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
8585	21124		1.62	2.4E+00	AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-405 PT0004 Homo sapiens cDNA
8762	21301	34222	8.16	2.4E+00	P24091	SWISSPROT	ENDOCHITINASE B PRECURSOR (CHN-B)
9951	22446	35427	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
9951	22446	35428	2.59	2.4E+00	P13673	SWISSPROT	SKIN GRANULE PROTEIN PRECURSOR
10017	22512	35504	1.62	2.4E+00	X92511.1	NT	H. sapiens CTGF gene and promoter region
10141	22636		7.38	2.4E+00	P09099	SWISSPROT	XYLULOSE KINASE (XYLULOSE KINASE)
10225	22720	35710	1.63	2.4E+00	BE326702.1	EST_HUMAN	h63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10225	22720	35711	1.63	2.4E+00	BE326702.1	EST_HUMAN	h63f06.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133187 3'
10483	22977	35986	1.27	2.4E+00	Q51481	SWISSPROT	DENITRIFICATION REGULATORY PROTEIN NIRQ
10958	23473	36498	1.69	2.4E+00	Y14079.1	NT	Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFDK operon and downstream
11237	23768	36826	2.27	2.4E+00	AF158652.2	NT	Fragaria x ananassa cytosolic ascorbate peroxidase (ApxSC) gene, ApxSC-c allele, complete cds
1296	13800	26413	11.15	2.3E+00	Z46724.1	NT	G domesticus artificial single chain antibody gene (L3)
4199	16768		1.65	2.3E+00	AJ401081.1	NT	Bos taurus partial cyt b gene for cytochrome b
6000	18620		0.91	2.3E+00	NB6245.1	EST_HUMAN	J7340F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7340 5' similar to
7477	18999	32884	2.54	2.3E+00	6978554	NT	PROLYLCARBOXYPEPTIDASE
7593	25120		4.61	2.3E+00	P07199	SWISSPROT	Rattus norvegicus ATPase, Ca++ transporting, ubiquitous (Atp2a3), mRNA
7756	20284	33159	1.06	2.3E+00	X60265.1	NT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
							M.mazai dnaK and dnaJ genes homologues coding for DnaK and DnaJ

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9038	21575	34505	0.53	2.3E+00	5835317	NT	Polydorus ornalipinnis mitochondrion, complete genome
9097	21633	34572	1.79	2.3E+00	Q11127	SWISSPROT	ALPHA(1.3)-FUCOSYLTRANSFERASE (GALACTOSIDE 3-L-FUCOSYLTRANSFERASE)
10681	23213	36224	2	2.3E+00	Q07076	SWISSPROT	(FUCOSYLTRANSFERASE 4) (FUCT-IV)
11612	24055	37119	2.92	2.3E+00	BF541987.1	EST_HUMAN	ANNEXIN VII (SYNEXIN)
11812	24055	37120	2.92	2.3E+00	BF541987.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
11950	24278	31020	7.31	2.3E+00	BE895237.1	EST_HUMAN	602069121F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4088173 5'
4089	16885	29143	91.07	2.2E+00	AF020528.1	NT	601433673F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918643 5'
4403	16988	29432	4.5	2.2E+00	D97071.1	NT	Magnaporthe grisea Class IV chitin synthase (chs4) gene, complete cds
		29433	4.5	2.2E+00	D67071.1	NT	Rat gene for regucalcin, exon1 (non-coding exon)
							Rat gene for regucalcin, exon1 (non-coding exon)
5545	18177	30591	12.27	2.2E+00	O98307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
5545	18177	30592	12.27	2.2E+00	O98307	SWISSPROT	SORTILIN-RELATED RECEPTOR PRECURSOR (SORTING PROTEIN-RELATED RECEPTOR CONTAINING LDLR CLASS A REPEATS) (MSORLA-1) (SORLA-1) (LOW-DENSITY LIPOPROTEIN RECEPTOR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LDLR RELATIVE WITH 11 LIGAND-BINDING REPEATS) (LR11) (>
6016	18635	31373	0.95	2.2E+00	BE927220.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6212	18822	31583	9.1	2.2E+00	BE250383.1	EST_HUMAN	RC3-CT0254-300800-022-e06 CT0254 Homo sapiens cDNA
6495	19096	31880	4.32	2.2E+00	Q00335	SWISSPROT	600943401T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2959777 3'
6709	19303	32107	3.04	2.2E+00	P51459	SWISSPROT	MINOR VIRION STRUCTURAL PROTEIN MU-2
7037	18057		3.58	2.2E+00	AA594574.1	EST_HUMAN	INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A)
7359	19884	32747	0.9	2.2E+00	AA137027.1	EST_HUMAN	nl95b02.s1 NC1_CGAP_Cot0 Homo sapiens cDNA clone IMAGE:1058379 3'
7602	20115	32992	25.23	2.2E+00	AA449012.1	EST_HUMAN	zn97904.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:568143 5'
8046	20588	33494	0.65	2.2E+00	BE301560.1	EST_HUMAN	zn05g10.r1 Soares fetal_Nb2HIF8_9w Homo sapiens cDNA clone IMAGE:785634 5'
8046	20588	33495	0.65	2.2E+00	BE301560.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9265	21781		12.17	2.2E+00	BE741678.1	EST_HUMAN	bb17h12.x1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2963207 3' similar to gb:D45836 Mouse mRNA for nuclear pore-targeting-complex component of (MOUSE);
9488	24793		2.57	2.2E+00	Q04706	SWISSPROT	601564733F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948561 5'
9566	22461	35443	1.86	2.2E+00	A1290373.1	EST_HUMAN	TRANSPOSIN TY1 PROTEIN A
							qm69b03.x1 Soares_placenta_8to9weeks_2NBH1P8c9W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9966	22461	35444	1.96	2.2E+00	AI290373.1	EST_HUMAN	qm69h03.x1 Soares_placenta_8to6weeks_2NbhP8t09W Homo sapiens cDNA clone IMAGE:1893965 3' similar to gb:Y00433 GLUTATHIONE PEROXIDASE (HUMAN);
10008	22503	35494	3.7	2.2E+00	BF246782.1	EST_HUMAN	601855591F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075391 5'
10353	22847	35841	2.99	2.2E+00	AF183416.1	NT	Homo sapiens ovarian granulosa cell 13.0 kDa protein hGR74 homolog mRNA, complete cds
11316	23014	36023	4.01	2.2E+00	P07911	SWISSPROT	UROMODULIN PRECURSOR (TAMMA-HORSFALL URINARY GLYCOPROTEIN) (THP)
11482	23932	37003	4.23	2.2E+00	P10407	SWISSPROT	EARLY ETA 28 KD PROTEIN
595	15419	25699	6.28	2.1E+00	AF132812.2	NT	Mus musculus pre-T cell receptor alpha gene, enhancer region and upstream region
3848	16251		0.65	2.1E+00	AW449366.1	EST_HUMAN	UI-H-B13-aki-e-08-Q-UI.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734550 3'
6281	18889		0.85	2.1E+00	P75357	SWISSPROT	HYPOTHETICAL PROTEIN MG302 HOMOLOG
6899	19633	32471	3.38	2.1E+00	O70159	SWISSPROT	ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN-A)
7110	19450	32266	5.13	2.1E+00	N28575.1	EST_HUMAN	y08a10.s1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270618 3' similar to gb:M55654
8434	20974		2.27	2.1E+00	AU123630.1	EST_HUMAN	TRANSCRIPTION INITIATION FACTOR TF1D (HUMAN);
10454	22948		0.58	2.1E+00	Y10284.1	NT	AIJ23630 NT2RM2 Homo sapiens cDNA clone NT2RM2000671 5'
1238	13836	26352	1.3	2.0E+00	AF180527.1	NT	H. sapiens TRAF1 gene, putative promoter region
1238	13836	26353	1.3	2.0E+00	AF180527.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1380	13973	26501	0.92	2.0E+00	AF204927.1	NT	Homo sapiens p22Dokdel (DOKDEL) mRNA, complete cds
1619	14212		2.89	2.0E+00	P25582	SWISSPROT	Oryctolagus cuniculus Na ⁺ /K ⁺ -ATPase beta 1 subunit mRNA, complete cds
2184	14770	27343	3.69	2.0E+00	Z78279.1	NT	PUTATIVE RRNA METHYLTRANSFERASE SPB1
2194	14770	27344	3.69	2.0E+00	Z78279.1	NT	R. norvegicus mRNA for collagen alpha1 type I
4176	16767	29215	1.9	2.0E+00	AW664496.1	EST_HUMAN	R. norvegicus mRNA for collagen alpha1 type I
4176	16767	29216	1.9	2.0E+00	AW664496.1	EST_HUMAN	hi13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
7552	20071		0.77	2.0E+00	P07568	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7987	20509	33415	3.56	2.0E+00	AB008676.1	NT	hi13c05.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972168 3' similar to gb:X01677
7987	20509	33416	3.56	2.0E+00	AB008676.1	NT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (HUMAN);
7987	20509	33417	3.56	2.0E+00	AB008676.1	NT	STRUCTURAL POLYPEPTIDE [CONTAINS: NUCLEOCAPSID PROTEIN C; MEMBRANE
8853	21392	34314	3.62	2.0E+00	F31500.1	EST_HUMAN	GLYCOPROTEIN E1 AND E2
12295	24946	30622	7.77	2.0E+00	5834843	NT	GLYCOPROTEIN E1 AND E2
5784	18409	31124	6.89	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
5784	18409	31125	6.89	1.9E+00	6754389	NT	Escherichia coli 0157 DNA, map position at 46 min., complete cds
6249	18856	31630	1.2	1.9E+00	BE686995.1	EST_HUMAN	Escherichia coli 0157 DNA, map position at 46 min., complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6760	19353		1.02	1.9E+00	AW845689.1	EST_HUMAN	MR0-CT0083-071099-002-g02 CT0083 Homo sapiens cDNA
6845	19435		2.31	1.0E+00	Q63627	SWISSPROT	CTD-BINDING SR-LIKE PROTEIN RA4
8396	20936	33858	2.16	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8398	20936	33859	2.16	1.9E+00	P02467	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
8593	21132		2.45	1.9E+00	BF360206.1	EST_HUMAN	CM3-MT0114-010900-323-h12 MT0114 Homo sapiens cDNA
8825	21364		1.35	1.9E+00	O51781	SWISSPROT	ARGININE DEIMINASE (ADI) (ARGININE DIHYDROLASE) (AD)
9548	22048	35009	0.6	1.9E+00	AA669125.1	EST_HUMAN	ab94a04.s1 Stratiogene lung (#937210) Homo sapiens cDNA clone IMAGE:854574 3' similar to contains Alu repetitive element; contains element L1.1 repetitive element ;
10456	22950	35959	0.52	1.9E+00	AF248269.1	NT	Homo sapiens gag-pro-pol precursor protein gene, partial cds
3128	15742	28211	1.88	1.8E+00	P21004	SWISSPROT	PROTEIN B8 PRECURSOR
3154	15768	28234	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
3154	15768	28235	2.42	1.8E+00	U04356.1	NT	Synechococcus sp. PCC7942 copper transporting P-ATPase (ctaA) and ATP synthase epsilon subunit (atpE) genes, complete cds
6027	18646		2.02	1.8E+00	P18502	SWISSPROT	HEDGEHOG RECEPTOR (PATCHED PROTEIN)
6253	18802	31634	2.02	1.8E+00	BF311996.1	EST_HUMAN	601897854F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127364 5'
6532	19132		1.53	1.8E+00	BF683327.1	EST_HUMAN	602139470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298272 5'
6838	19428	32244	1.35	1.8E+00	BF305652.1	EST_HUMAN	601893489F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139038 5'
7119	19459	32274	1.08	1.8E+00	P21249	SWISSPROT	MAJOR ANTIGEN
8060	20602	33512	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8060	20602	33513	0.81	1.8E+00	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
8788	21327	34252	2.12	1.8E+00	O43281	SWISSPROT	EMBRYONAL FYN-ASSOCIATED SUBSTRATE (HEFS)
9102	21638	34577	0.63	1.8E+00	R31042.1	EST_HUMAN	Y972a08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135278 5'
9186	21703	34845	0.8	1.8E+00	AW680004.1	EST_HUMAN	QV0-OT0030-070300-148-a03 OT0030 Homo sapiens cDNA
9763	22261	35244	0.87	1.8E+00	P27080	SWISSPROT	GHITINASE D PRECURSOR
10183	22678		3.78	1.8E+00	AF111849.1	NT	Homo sapiens PRO5530 mRNA, complete cds
10447	22941		0.85	1.8E+00	P44325	SWISSPROT	CYTIDINE DEAMINASE (CYTIDINE AMINOHYDROLASE) (CDA)
12075	24915		6.85	1.8E+00	AF314254.1	NT	Chlamydomonas reinhardtii alternative oxidase 1 (AOX1) gene, nuclear gene encoding mitochondrial protein
12163	24403		4.96	1.8E+00	9508404	NT	Rattus norvegicus Actin-related protein complex 1b (Arp1b), mRNA
12476	24815	30790	1.38	1.8E+00	BF212412.1	EST_HUMAN	601813714F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048251 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1147	13750	28258	2.08	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
2311	14883	27458	2.37	1.7E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2411	14978	27554	1.29	1.7E+00	A1141067.1	EST_HUMAN	oz43h05.x1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1678137 3'
4558	17141	29589	0.74	1.7E+00	Q60114	SWISSPROT	LEVANSUCRASE (BETA-D-FRUCTOFURANOSYL TRANSFERASE) (SUCROSE 6-FRUCTOSYL TRANSFERASE)
5787	18422	31137	1.65	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
5787	18422	31138	1.85	1.7E+00	BE063546.1	EST_HUMAN	CM0-BT0282-171299-127-e05 BT0282 Homo sapiens cDNA
6168	18780	31545	3.35	1.7E+00	Q81TR8	SWISSPROT	COUP TRANSCRIPTION FACTOR 1 (COUP-TF1) (COUP-TF 1)
7270	19788	32654	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7270	19788	32655	1.33	1.7E+00	Q03703	SWISSPROT	HYPOTHETICAL 38.0 KD PROTEIN IN CAT2-AMD1 INTERGENIC REGION
7306	19834	32693	1.83	1.7E+00	P20393	SWISSPROT	ORPHAN NUCLEAR RECEPTOR NR1D1 (V-ERBA RELATED PROTEIN EAR-1) (REV-ERBA-ALPHA)
7786	20339	33247	0.96	1.7E+00	AF021335.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 2 and gamma 4 gene clusters
7878	20518	33425	1.34	1.7E+00	6755715	NT	Mus musculus T-cell acute lymphocytic leukemia 1 (Tcl1), mRNA
8006	20548	33452	0.57	1.7E+00	BF530630.1	EST_HUMAN	602071917F1 NCI_CGAP_Bm07 Homo sapiens cDNA clone IMAGE:4214669 5'
8479	21018	33933	0.61	1.7E+00	AF245513.1	NT	Hippoglossus hippoglossus interferon inducible Mx protein (MX) mRNA, complete cds
8562	21101	34097	2.08	1.7E+00	BF308000.1	EST_HUMAN	601894255F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4140084 5'
8638	21177	34096	0.49	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8638	21177	34097	0.49	1.7E+00	X69063.1	NT	M. musculus Ank-1 mRNA for erythroid ankyrin
8078	24762	34545	2.25	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9076	24762	34546	2.25	1.7E+00	Q60479	SWISSPROT	HOMEBOX PROTEIN DLX-3
9524	22024		1.85	1.7E+00	AF161380.1	NT	Homo sapiens HSPC282 mRNA, partial cds
11467	23917	36985	2.16	1.7E+00	W22424.1	EST_HUMAN	67B7 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12030	24320	30993	1.52	1.7E+00	A1678443.1	EST_HUMAN	tu82d07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2257549 3' similar to contains MSR1.11
12598	24659	30873	1.79	1.7E+00	A1168573.1	EST_HUMAN	MSR1 repetitive element
2078	14658	27229	21.82	1.6E+00	AF169339.1	NT	qf50b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1753417 3' similar to contains L1.11 L1
2087	14668	27238	4.3	1.6E+00	AF077374.1	NT	repetitive element
2093	14673	27243	1.04	1.6E+00	Y11344.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
2323	14894		1.13	1.6E+00	X98373.1	NT	Homo sapiens small proline-rich protein (SPRR3) gene, exons 1, 2, and 3 and complete cds
2988	15604	28084	1.5	1.6E+00	W59426.1	EST_HUMAN	Mus musculus ST6GalNAcII gene, exon 2
4104	16898		7.23	1.6E+00	BF570077.1	EST_HUMAN	B. napus gene encoding endo-polygalacturonase
							z25601.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:341689 5' similar to
							gb:D29805 N-ACETYL LACTOSAMINE SYNTHASE (HUMAN);
							602186085T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310591 3'

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4444	17030	29470	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
4444	17030	29471	1.11	1.6E+00	AF155827.1	NT	Homo sapiens proliferation-associated SNF2-like protein (SMARCA6) mRNA, complete cds
5145	17715	30145	0.8	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5145	17715	30146	0.6	1.6E+00	AF075394.1	NT	Uroteuthis chinensis cytochrome c oxidase subunit I (COI) gene, mitochondrial gene encoding mitochondrial protein, partial cds
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5243	17807	30228	2.2	1.6E+00	Y11344.1	NT	Mus musculus ST6GalNAcII gene, exon 2
5993	18613	31347	1.95	1.6E+00	L04808.1	NT	Brachydanio rerio MHC class II DA-beta-2'01 gene, 3' end
6072	18689	31434	0.82	1.6E+00	AF056631.1	NT	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
6596	19193	31998	0.93	1.6E+00	BF380703.1	EST_HUMAN	IL2-UT0073-080900-145-E02 UT0073 Homo sapiens cDNA
6811	19402	32218	1.07	1.6E+00	AW294881.1	EST_HUMAN	UI-H-B12-shr-b-04-0-UI.s1 NCI CGAP Sub4 Homo sapiens cDNA clone IMAGE:2727511 3'
7293	19821	32680	2.32	1.6E+00	BE697287.1	EST_HUMAN	RCO-CT0415-200700-032-c10 CT0415 Homo sapiens cDNA
7873	20515	33786	1.09	1.6E+00	Q46378	SWISSPROT	VIRULENCE FACTOR MVIN HOMOLOG
8320	20861	33786	3.24	1.6E+00	AJ291131.1	NT	Mus musculus SIL, MAP 17, CYP a, SCL & CYP b genes
8831	21370	34294	0.85	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
8831	21370	34295	0.85	1.6E+00	11437222	NT	Homo sapiens hypothetical protein PRO0971 (PRO0971), mRNA
9381	24790	33222	3.16	1.6E+00	X52046.1	NT	Mus musculus COL3A1 gene for collagen alpha-1
9381	24790	33222	3.16	1.6E+00	X52046.1	NT	Mus musculus COL3A1 gene for collagen alpha-1
9649	22148	35119	1.34	1.6E+00	T41280.1	EST_HUMAN	phb68_19/1TV Outward Alu-pri-med hncDNA library Homo sapiens cDNA clone phb68_19/1TV
10052	22547	35541	0.52	1.6E+00	AF121381.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase 1a1 (AL), and zinc finger protein (DNZ1) genes, complete cds
10088	22583	35575	0.82	1.6E+00	AW835844.1	EST_HUMAN	QV4-LT0018-090200-100-d07 LT0016 Homo sapiens cDNA
10088	22583	35576	0.82	1.6E+00	AW835844.1	EST_HUMAN	QV4-LT0018-090200-100-d07 LT0016 Homo sapiens cDNA
10246	22741	35731	0.49	1.6E+00	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
10650	23192	36196	1.59	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10686	23216	36228	1.56	1.6E+00	P54817	SWISSPROT	CAPSID PROTEIN P40 [CONTAINS: ASSEMBLIN (PROTEASE); CAPSID ASSEMBLY PROTEIN]
10723	18689	31434	6.41	1.6E+00	AF005631.1	NT	Homo sapiens transglutaminase type I (Tgase) gene, promoter region
11552	24000	37072	2.92	1.6E+00	AF104313.1	NT	Homo sapiens unknown mRNA
35	12714	25173	4.02	1.5E+00	U53449.1	NT	Rattus norvegicus jun dimerization protein 2 (jdp-2) mRNA, complete cds
252	12912	25396	2.17	1.5E+00	AE002201.2	NT	Chlamydomonas reinhardtii AR39, section 32 of the complete genome
649	13272		1.98	1.5E+00	6752961	NT	Mus musculus a disintegrin and metalloproteinase domain (ADAM) 15 (metagidlin) (Adam15), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1980	14544	27101	2.55	1.5E+00	AF275265.1	NT	Mus musculus receptor protein tyrosine phosphatase- ρ (Ptp ρ) gene, exons 10 and 11 and partial cds
2454	15021	27592	2.13	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
2558	15120	27690	1.83	1.5E+00	6878350	NT	Mus musculus T-cell lymphoma invasion and metastasis 1 (Tiam1), mRNA
3172	15021	27592	1.54	1.5E+00	AJ131402.1	NT	Potato virus A RNA complete genome, isolate U
3421	16029	28510	0.7	1.5E+00	AE001845.1	NT	Deinococcus radiodurans R1 section 82 of 229 of the complete chromosome 1
5903	18525	31250	0.94	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237
5903	18525	31251	0.94	1.5E+00	AI655301.1	EST_HUMAN	tt12f10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2240587 3' similar to TR:O00237 O00237
6538	19137	31930	2.68	1.5E+00	R17879.1	EST_HUMAN	HKF-1.1
7182	19714	32599	1.37	1.5E+00	BE765358.1	EST_HUMAN	y010602.r1 Soares infant brain tNIB Homo sapiens cDNA clone IMAGE:31693 5'
7214	19745	32599	20.84	1.5E+00	P47179	SWISSPROT	601478745F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3881555 5'
7214	19745	32600	20.84	1.5E+00	P47179	SWISSPROT	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
7383	19809	32774	1.02	1.5E+00	AA889259.1	EST_HUMAN	HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR
8065	20607	33519	0.85	1.5E+00	BE887448.1	EST_HUMAN	ak26f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407115 3'
8578	21117	34037	1.1	1.5E+00	K02138.1	NT	601509586F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911181 5'
8946	21484	34528	0.53	1.5E+00	AB038518.1	NT	Mouse germline IgM chain gene, mu-delta region
9061	21598	34528	0.54	1.5E+00	BF217818.1	EST_HUMAN	Homo sapiens hSP1b alpha gene for platelet glycoprotein Ib alpha, complete cds
9404	21913	34862	0.9	1.5E+00	R81928.1	EST_HUMAN	601887692F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095135 5'
9553	22053	35016	1.12	1.5E+00	AW375697.1	EST_HUMAN	y03h01.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147697 5'
9774	22272	35257	5.97	1.5E+00	BF376754.1	EST_HUMAN	QV3-CT0192-261069-008-d09 CT0192 Homo sapiens cDNA
9965	22460	35595	1.47	1.5E+00	BF337844.1	EST_HUMAN	RC0-TN0078-150900-034-g05 TN0078 Homo sapiens cDNA
10098	22593	35595	2.95	1.5E+00	AA017689.1	EST_HUMAN	602035777F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183865 5'
10098	22593	35596	2.95	1.5E+00	AA017689.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381306 5'
11277	23730	36785	4.1	1.5E+00	AL134197.1	EST_HUMAN	ze38g06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381306 5'
11416	23667	30615	9.57	1.5E+00	X07380.1	NT	DKFZp547P243.s1 547 (synonym: hBr1) Homo sapiens cDNA clone DKFZp547P243 3'
12022	25010	30615	1.59	1.5E+00	D63480.1	NT	Mia2a mitochondrial tRNA-Ser gene and tRNA-Phe pseudogene
12255	24465		4.99	1.5E+00	AL445065.1	NT	Human mRNA for KIAA0146 gene, partial cds
32	12711	25169	1.8	1.4E+00	7661885	NT	Thermoplasma acidophilum complete genome, segment 3/5
32	12711	25170	1.8	1.4E+00	7661885	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1774	14364	26609	1.32	1.4E+00	H19859.1	EST_HUMAN	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
2316	14888		0.98	1.4E+00	AF053357.1	NT	yn57603.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:172540 5'
2372	14942		7.8	1.4E+00	U67922.1	NT	Helicobacter pylori glutamine synthetase (glnA) gene, complete cds
							Ovis aries prion protein gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2683	15250	27820	1.45	1.4E+00	XT4463.1	NT	Human papillomavirus type 7 genomic DNA
2802	15354	27922	2.79	1.4E+00	AF084564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
2802	15354	27923	2.79	1.4E+00	AF084564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
3378	15885		0.88	1.4E+00	5453733	NT	Homo sapiens Mad4 homolog (MAD4) mRNA
4342	16929	29369	1.14	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4342	16929	29370	1.14	1.4E+00	AW900455.1	EST_HUMAN	CM0-NN1005-140300-286-h06 NN1005 Homo sapiens cDNA
4685	17267		1.78	1.4E+00	BF681547.1	EST_HUMAN	602156687F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297556 5'
5575	18206	30657	1.78	1.4E+00	AW054978.1	EST_HUMAN	wt45g07.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510460 3'
5718	18345		5.04	1.4E+00	AB032983.1	NT	Homo sapiens mRNA for KIAA1157 protein, partial cds
6425	18028	31811	2.73	1.4E+00	Q13472	SWISSPROT	DNA TOPOISOMERASE III ALPHA
6437	25116		4.4	1.4E+00	AB020712.1	NT	Homo sapiens mRNA for KIAA0905 protein, complete cds
8544	19143	31936	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
8544	19143	31937	2.32	1.4E+00	Q92777	SWISSPROT	SYNAPSIN II
8583	19181	31981	0.67	1.4E+00	11086333	NT	Mus musculus WW domain binding protein 11 (Wbp11-pending), mRNA
6911	19570	32398	0.77	1.4E+00	AW893057.1	EST_HUMAN	CM3-NN0006-300300-132-b12 NN0006 Homo sapiens cDNA
7330	19857	32720	2.31	1.4E+00	AJ133268.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S822, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
7343	19870	32735	1.1	1.4E+00	AW467760.1	EST_HUMAN	he23f05.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918873 3' similar to contains Alu repetitive element;
8277	20818		0.68	1.4E+00	P07883	SWISSPROT	GLUCOAMYLASE PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8729	21268		4.01	1.4E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
9023	21560	34487	2.13	1.4E+00	R20459.1	EST_HUMAN	Y933f12.r1 Soares infant brain 'NIB Homo sapiens cDNA clone IMAGE:34345 5'
9125	21660	34603	3.72	1.4E+00	BE084687.1	EST_HUMAN	RC1-BT0313-301289-012-405 BT0313 Homo sapiens cDNA
9158	21693	34637	0.58	1.4E+00	AF134844.1	NT	Sceloporus undulatus ornithine transcarbamylase (OTC) mRNA, complete cds
10109	22604	35594	0.77	1.4E+00	BF575545.1	EST_HUMAN	602133135F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288137 5'
10150	22845	35637	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10150	22845	35638	0.67	1.4E+00	BE145374.1	EST_HUMAN	IL5-HT0198-291099-008-C04 HT0198 Homo sapiens cDNA
10418	22912	35912	1.11	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10418	22912	35913	1.11	1.4E+00	D63441.1	NT	Pandorina colemaniae chloroplast rbcL gene for ribulose biphosphate carboxylase, partial cds
10948	23463	36485	2.16	1.4E+00	AA195528.1	EST_HUMAN	z36e09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665512 5' similar to contains element MER22 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11104	23814	36654	6.28	1.4E+00	AB006892.1	NT	Homo sapiens APECED mRNA for AIRE-1, complete cds
11283	23736	36791	3.92	1.4E+00	BE062107.2	EST_HUMAN	601655184R1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3845805 3'
11283	23736	36792	3.92	1.4E+00	BE062107.2	EST_HUMAN	601655184R1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3845805 3'
11304	23797	36855	3.19	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (peg1) gene, complete cds
11304	23797	36856	3.19	1.4E+00	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (peg1) gene, complete cds
11865	24935		2.43	1.4E+00	AL161500.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 12
12267	25108		2.38	1.4E+00	11545836	NT	Homo sapiens cutaneous T-cell lymphoma tumor antigen se70-2 (SE70-2), mRNA
596	13225		1.38	1.3E+00	Z73640.1	NT	M. musculo gene encoding 4-Dihydropyrimidin-thiosulfate dehydrogenase
935	13548	26065	2.33	1.3E+00	AJ271192.1	NT	Cantharellus sp. partial 25S rRNA gene, isolate Tibet
1168	13770		22.19	1.3E+00	Y19213.1	NT	Homo sapiens putative psihHbA pseudogene for hair keratin, exons 2 to 7
1340	13935	26456	13.67	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1340	13935	26457	13.67	1.3E+00	4507998	NT	Homo sapiens zinc finger protein 157 (HZF22) (ZNF157) mRNA
1400	13994		1.05	1.3E+00	U61730.2	NT	Cox lacryme-jobi dihydrodipicolinate synthase (dapA) gene, complete cds
1653	14245		2.35	1.3E+00	AE002338.2	NT	Chlamydia muridarum, section 66 of 85 of the complete genome
2285	14859		1.1	1.3E+00	AB030447.1	NT	Cyprinus carpio MRPb and MASPB genes for mannose-binding lectin-associated serine protease (MASP) and MASP-related protein, complete cds
2586	15149		0.97	1.3E+00	BE068735.2	EST_HUMAN	601661233R1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915945 3'
2866	15581	28060	0.68	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
3657	16260	28732	0.91	1.3E+00	AF016494.1	NT	Fugu rubripes gamma-aminobutyric acid receptor beta subunit gene, partial cds; 55kd erythrocyte membrane protein (P55), synaptic vesicle-associated integral membrane protein (VAMP-1), procollagen C-proteinase enhancer protein (PCOLCE) genes, complete c>
4713	15581	28060	1.31	1.3E+00	6755621	NT	Mus musculus alpha-spectrin 1, erythroid (Spn1), mRNA
5184	17749	30178	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5184	17749	30179	0.92	1.3E+00	AJ252087.1	NT	Plasmodium reichenowi partial 83/AMA-1 gene for apical membrane antigen 1
5705	18331	30835	1.06	1.3E+00	P19732	SWISSPROT	PHENOL HYDROXYLASE P3 PROTEIN (PHENOL 2-MONOOXYGENASE P3 COMPONENT)
6169	18781	31546	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0288-291189-004-f08 CT0289 Homo sapiens cDNA
6169	18781	31547	7.47	1.3E+00	AW362834.1	EST_HUMAN	PMO-CT0288-291189-004-f08 CT0289 Homo sapiens cDNA
6549	19147	31943	1.24	1.3E+00	M33406.1	NT	D.melanogaster no-on-transient A gene product, complete cds
6847	19437		0.71	1.3E+00	Q00156	SWISSPROT	HYPOTHETICAL GENE 64 PROTEIN
6928	19585	32415	0.85	1.3E+00	M13918.2	NT	Homo sapiens fibronectin receptor alpha-subunit precursor (ITGA5) mRNA, partial cds
7033	19567	32394	1.01	1.3E+00	BE538819.1	EST_HUMAN	601061420F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447965 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7157	19689	32533	0.79	1.3E+00	BE243571.1	EST_HUMAN	TCBAP1D0959 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0959
7481	20003	32968	3.97	1.3E+00	P24540	SWISSPROT	ACYLPHOSPHATASE, ORGAN-COMMON TYPE ISOZYMES A AND B (ACYLPHOSPHATE PHOSPHOHYDROLASE)
8239	20780	33701	2.08	1.3E+00	AJ009912.1	NT	Sus scrofa plp gene
8384	20924	33944	2.54	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866195 3'
8498	21035	33956	0.89	1.3E+00	BE974280.1	EST_HUMAN	601680250R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950532 3'
8644	21183		1.57	1.3E+00	8910247	NT	Homo sapiens GL004 protein (GL004), mRNA
8725	21264	34184	0.86	1.3E+00	AJ927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9073	21610	34540	0.48	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Soares breast 3NbHbSt Homo sapiens cDNA clone IMAGE:183076 3'
9073	21610	34541	0.48	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Soares breast 3NbHbSt Homo sapiens cDNA clone IMAGE:183076 3'
9434	21960		4.54	1.3E+00	AF042084.1	NT	Homo sapiens heparan glucosaminyl N-deacetylase/N-sulfotransferase-2 gene, complete cds
9443	21969	34917	2.12	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9443	21969	34918	2.12	1.3E+00	X72019.1	NT	S.alba phr-1 mRNA for photolyase
9542	22042	35003	1.1	1.3E+00	AF059250.1	NT	Homo sapiens lipoygenase (ALOX12B) mRNA, complete cds
9588	22088	35052	1.82	1.3E+00	O00754	SWISSPROT	LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE) (LAMAN)
9665	22164	35137	1.21	1.3E+00	AJ927629.1	EST_HUMAN	wo85a07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462100 3'
9740	22238	35218	0.83	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
9740	22238	35219	0.83	1.3E+00	AJ223962.1	NT	Lactococcus lactis cremoris NCDO-inv1 chromosomal inversion junction DNA
9760	22278	35263	3.85	1.3E+00	BE963379.2	EST_HUMAN	601657145R1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866195 3'
10114	22809	35600	1.25	1.3E+00	AE004392.1	NT	Vibrio cholerae chromosome II, section 49 of 93 of the complete chromosome
10130	22825	35615	2.41	1.3E+00	M29953.1	NT	Campylobacter jejuni kanamycin phosphotransferase (aphA-7) gene, complete cds
10476	22970		0.65	1.3E+00	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
10504	22988		0.52	1.3E+00	8923637	NT	Homo sapiens hypothetical protein FLJ20707 (FLJ20707), mRNA
10507	23001	36008	0.48	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Soares breast 3NbHbSt Homo sapiens cDNA clone IMAGE:183076 3'
10507	23001	36009	0.48	1.3E+00	H42881.1	EST_HUMAN	yo88c03.s1 Soares breast 3NbHbSt Homo sapiens cDNA clone IMAGE:183076 3'
10573	23108		4.66	1.3E+00	Q14117	SWISSPROT	DIHYDROPYRIMIDINASE (DHPASE) (HYDANTONASE) (DHP)
10785	23309	36316	2.3	1.3E+00	P25299	SWISSPROT	MRNA 3'-END PROCESSING PROTEIN RNA15
10807	23330	36342	2.17	1.3E+00	Z18892.2	NT	Mus musculus desmin gene
11215	23718		1.87	1.3E+00	AW274791.1	EST_HUMAN	yo88c03.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2738968 3'
11414	23865	36926	3.09	1.3E+00	D42042.1	NT	Human mRNA for KIAA0085 gene, partial cds
11488	23937	37007	3.09	1.3E+00	Z98882.1	NT	Bacillus subtilis genomic DNA 23.8k fragment
12011	24312		3.63	1.3E+00	AF187873.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.2 (KCNJ12) gene, complete cds

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12192	24423	30949	3.47	1.3E+00	BF348043.1	EST_HUMAN	602023185F1 NCI CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4158452 5'
12204	24826		1.76	1.3E+00	P33464	SWISSPROT	E1 GLYCOPROTEIN PRECURSOR (MATRIX GLYCOPROTEIN) (MEMBRANE GLYCOPROTEIN)
12303	24500		2.08	1.3E+00	AF187035.1	NT	Stunira liliun cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
12673	24904		1.25	1.3E+00	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
678	13302	25784	9.75	1.2E+00	AA676246.1	EST_HUMAN	Z22208.81 Soares fetal_liver_spleen_1NLS_S1 Homo sapiens cDNA clone IMAGE:431535 3'
856	13472	25983	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
856	13472	25984	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
856	13472	25985	1.04	1.2E+00	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
911	13524		1.9	1.2E+00	8924234	NT	Homo sapiens hypothetical protein PRO3077 (PRO3077), mRNA
1203	13803	26316	4.87	1.2E+00	AF080245.2	NT	Elicis oleiferis sesquiterpene synthase mRNA, complete cds
1247	13844	26381	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
1247	13844	26382	1.3	1.2E+00	AJ252242.1	NT	pea seed-borne mosaic virus complete genome
2054	14635	27206	53.59	1.2E+00	AF140631.1	NT	Homo sapiens G-protein coupled receptor 14 (GPR14) gene, complete cds
2417	14985	27559	1.53	1.2E+00	AF156495.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
3144	15758	28224	1.16	1.2E+00	AB020681.1	NT	Homo sapiens mRNA for KIAA0874 protein, partial cds
3201	15813	28287	7.17	1.2E+00	AL181563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3325	15935	28288	7.17	1.2E+00	AL181563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
3399	16007	28489	3.43	1.2E+00	P54910	SWISSPROT	CONJUGAL TRANSFER PROTEIN TRBE PRECURSOR
3774	16374	28839	0.57	1.2E+00	AF188740.1	NT	Homo sapiens LHX3 gene, intron 2
4058	16655	29121	8.66	1.2E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
4386	16007	28489	1.12	1.2E+00	AF188740.1	NT	MR0-FT0175-050900-203-g06_1 FT0175 Homo sapiens cDNA
4570	17153		2.09	1.2E+00	M87080.1	NT	Homo sapiens LHX3 gene, intron 2
4621	17204	29853	1.08	1.2E+00	AL181509.2	NT	Rattus retus cardiac AE3 gene, exons 1-23
4659	17241	29695	1.5	1.2E+00	AF156495.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 21
4690	17272		9.41	1.2E+00	Y08200.1	NT	Homo sapiens post-synaptic density 95 (DLG4) gene, complete cds
4791	18008		0.77	1.2E+00	M81779.1	NT	T. pinatum chloroplast rbcL gene, partial
5628	18258	30728	1.08	1.2E+00	U20760.1	NT	G. gallus T-cadherin mRNA, complete cds
5743	18399	31077	2.27	1.2E+00	AW813276.1	EST_HUMAN	Human extracellular calcium-sensing receptor mRNA, complete cds
6034	18653	31395	0.72	1.2E+00	AF016032.1	NT	MR3-ST0191-140200-013-c05 ST0191 Homo sapiens cDNA
6300	18908	31679	2.17	1.2E+00	X74885.1	NT	Homo sapiens zinc finger protein ZNF181 (ZNF181) gene, complete cds
6361	18985	31743	3.98	1.2E+00	BE003113.1	EST_HUMAN	D. hydei ey1 repeat cluster DNA, fragment D
6433	19036	31822	1.43	1.2E+00	X89084.1	NT	QV4-BN0090-270400-190-a03 BN0090 Homo sapiens cDNA
6433	19036	31823	1.43	1.2E+00	X89084.1	NT	C. glutamicum pla gene and ackA gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6475	19078	31859	34.96	1.2E+00	AA759254.1	EST_HUMAN	ah84g12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1322374 3'
6629	19225	32030	2.25	1.2E+00	AW813276.1	EST_HUMAN	MR3-S10191-140200-013-c05 S10191 Homo sapiens cDNA
6995	19493	32314	1.18	1.2E+00	AB028010.1	NT	Homo sapiens mRNA for KIAA1087 protein, partial cds
7007	19505	32324	2.8	1.2E+00	AJ002141.1	NT	Mus musculus DSPP gene
7300	19828		0.8	1.2E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
7417	24782	32808	1.59	1.2E+00	AV734585.1	EST_HUMAN	AV734585 cda Homo sapiens cDNA clone cdaAFH03 5'
7646	20158	33045	2.84	1.2E+00	X74207.1	NT	L.lactis pyD and pyrF genes
8504	21043	33984	3.05	1.2E+00	AB033030.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
8597	21136	34051	0.69	1.2E+00	P38427	SWISSPROT	ALPHA-ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (UDP-FORMING) 123 KD SUBUNIT (TREHALOSE-6-PHOSPHATE SYNTHASE) (UDP-GLUCOSE-GLUCOSEPHOSPHATE GLUCOSYLTRANSFERASE)
8809	21348		0.53	1.2E+00	7706271	NT	Homo sapiens CGI-30 protein (LOC51611), mRNA
8955	21493	34416	2.03	1.2E+00	AW377210.1	EST_HUMAN	MR2-CT0222-201099-001-e07 CT0222 Homo sapiens cDNA
9319	21833	34783	2.92	1.2E+00	Z32850.1	NT	R. communis gene for pyrophosphate-dependent phosphofructokinase beta subunit
9523	22023	34981	1.86	1.2E+00	D11745.1	EST_HUMAN	HUMH01A01 Liver HepG2 cell line. Homo sapiens cDNA clone hm01a01
9844	22342	35324	3.47	1.2E+00	X56832.1	NT	H. sapiens ENO3 gene for muscle specific endase
10229	22724		0.67	1.2E+00	AB009686.1	NT	Homo sapiens klotho gene, exon 1
11224	23755	36813	2.19	1.2E+00	AW817817.1	EST_HUMAN	PMO-ST0284-161199-001-d01 ST0284 Homo sapiens cDNA
11262	23780		6.64	1.2E+00	BE160781.1	EST_HUMAN	PM1-HT0422-160200-007-g10 HT0422 Homo sapiens cDNA
11331	23029	36038	3.76	1.2E+00	U50147.1	NT	Rattus norvegicus synapse-associated protein 102 mRNA, complete cds
11976	24907	30712	32.4	1.2E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11998	24304		2.11	1.2E+00	AF001515.1	NT	Bacillus halodurans genomic DNA, section 9/14
488	13122	25608	1.19	1.1E+00	D88980.1	NT	Human mRNA for KIAA0227 gene, partial cds
1796	14369	26934	1.48	1.1E+00	AW995393.1	EST_HUMAN	QV0-BN0042-170300-163-g12 BN0042 Homo sapiens cDNA
2617	15178	27746	1.09	1.1E+00	AF087124.1	NT	Wheat yellow mosaic virus RNA1 270 kDa precursor protein gene, complete cds
3373	15981	28458	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3373	15981	28459	9.32	1.1E+00	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
3533	16138	28620	0.84	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA
3639	16242	28718	1.06	1.1E+00	AI808360.1	EST_HUMAN	wf54h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359461 3' similar to SW:P631 HUMAN Q12888 P53-BINDING PROTEIN 53BP1;
3781	16381	28845	1.41	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3781	16381	28846	1.41	1.1E+00	AE003886.1	NT	Xyella fastidiosa, section 32 of 229 of the complete genome
3889	16498		0.61	1.1E+00	X85374.1	NT	H. parahemolyticus hphIM(A), hphIM(C), hphIR and menB genes
4016	16614	29087	0.67	1.1E+00	8922641	NT	Homo sapiens hypothetical protein FLJ10749 (FLJ10749), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4033	16688	29145	0.65	1.1E+00	6755205	NT	Mus musculus proteasome (prosome, macropain) subunit, beta type 7 (Pamb7), mRNA
4295	16881		7.81	1.1E+00	5835331	NT	R.unicornis complete mitochondrial genome
5131	17703	30137	3.54	1.1E+00	U18466.1	NT	African swine fever virus, complete genome
5132	17704	30138	0.98	1.1E+00	AJ271740.1	NT	Drosophila melanogaster D-Titin gene, exons 1-37
5201	17766	30190	1	1.1E+00	U34740.1	NT	Emmericella nidulans sterigmatocystin biosynthetic gene cluster: (stcA), (stcB), (stcC), (stcE), (stcF), (stcI), (stcJ), (stcK), (stcL), (stcO), (stcQ), (stcS), (stcT), (stcU), (stcV) and (stcW) genes, complete cds
5230	17794	30213	0.96	1.1E+00	X78425.1	NT	E.faecalis pbp5 gene
5409	17966		1.04	1.1E+00	AE003869.1	NT	Xylella fastidiosa, section 15 of 229 of the complete genome
5510	18143	30555	1.52	1.1E+00	6978530	NT	Rattus norvegicus Aquaporin 4 (Aqp4), mRNA
5798	18423	31139	19.98	1.1E+00	BE960184.1	EST_HUMAN	601652776R1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3825835 3'
5815	18439	31161	3.23	1.1E+00	AI138562.1	EST_HUMAN	q085c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736280 3'
6242	18851	31621	1.25	1.1E+00	11419739	NT	Homo sapiens solute carrier family 8 (neurotransmitter transporter), member 14 (SLC8A14), mRNA
6420	19023	31807	0.71	1.1E+00	AF197861.1	NT	Macgregoria pulchra cytochrome b gene, complete cds; mitochondrial gene for mitochondrial product
6539	19138	31831	0.71	1.1E+00	R06037.1	EST_HUMAN	ye89e03.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:124924 5'
6817	19408	32225	0.7	1.1E+00	AJ404004.1	NT	Mus musculus mRNA for ER protein 58 (EP58 gene)
7338	19865	32729	0.78	1.1E+00	X55981.1	NT	Maize mRNA for endlease (2-phospho-D-glycerate hydrolase)
7501	20023	32886	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7501	20023	32887	2.08	1.1E+00	Z72338.1	NT	Herpes simplex virus type 1 (strain KOS) UL41 gene
7521	20041	32910	9.72	1.1E+00	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7580	24787	32973	0.99	1.1E+00	11967960	NT	Mus musculus silent mating type information regulation 2, (S.cerevisiae, homolog)-like (Sir2l), mRNA
8074	20616	33530	2.8	1.1E+00	BF693996.1	EST_HUMAN	602082582F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246628 5'
8163	20704	33620	0.76	1.1E+00	AJ478339.1	EST_HUMAN	hm38h11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2160349 3'
8672	21211	34130	0.75	1.1E+00	AB003088.1	NT	Acetabularia caliculus mitochondrial COX-like gene
8749	21298	34208	0.78	1.1E+00	S80750.1	NT	VH-anti-cytomegalovirus glycoprotein B antibody 4D4 heavy chain variable region [human, mRNA Partial, 375 nt]
9358	20297		0.68	1.1E+00	BE384876.1	EST_HUMAN	601276278F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3617418 5'
9546	22046	35007	0.68	1.1E+00	AJ245772.1	NT	Mus musculus mRNA for stretch responsive muscle (X-chromosome) protein (Srmx gene)
9599	22099		0.81	1.1E+00	Y12227.1	NT	Arabidopsis thaliana DNA, 24 kb surrounding PFL locus
9687	22186	35160	0.84	1.1E+00	L76301.1	NT	Yersinia pseudotuberculosis psaE, psaF, adhesin (psaA), chaperone (psaB), and usher (psaC) genes, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9747	22245	35226	1.59	1.1E+00	AB023151.1	NT	Homo sapiens mRNA for KIAA0834 protein, partial cds
9850	22348	35330	4.82	1.1E+00	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9909	22406	35381	19.39	1.1E+00	6754021	NT	Mus musculus guanine nucleotide binding protein (G protein), gamma 3 subunit (Gng3), mRNA
10395	22899	35983	1	1.1E+00	P73799	SWISSPROT	DNA MISMATCH REPAIR PROTEIN MUTS
10530	23087	36079	2.93	1.1E+00	11087364	NT	Homo sapiens KIAA0628 gene product (KIAA0628), mRNA
10586	23121		4.06	1.1E+00	AF068942.1	NT	Klebsornidium fluitans cytochrome c oxidase subunit 2 (cox2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
10978	18026		5.28	1.1E+00	8922373	NT	Homo sapiens hypothetical protein FLJ11280 (FLJ11280), mRNA
10983	23497	36526	3.76	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
10983	23497	36527	3.78	1.1E+00	AF012862.1	NT	Petroselinum crispum cytosolic glucose-6-phosphate dehydrogenase 1 (cG6PDH1) mRNA, complete cds
11234	23765	36822	6.02	1.1E+00	AI009699.1	EST_HUMAN	wf79e11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone IMAGE:2381548 3'
11946	24275		1.82	1.1E+00	P07896	SWISSPROT	LOW TEMPERATURE ESSENTIAL PROTEIN
12051	24335	30697	2.25	1.1E+00	AF216696.1	NT	Taeniala solium immunogenic protein Ts76 mRNA, partial cds
12184	24903		1.64	1.1E+00	AF234169.1	NT	Dicystostellum discoideum isopentenyl pyrophosphate isomerase (Dipi) mRNA, complete cds
103	12779		3.22	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
118	12789	25271	3.48	1.0E+00	D88425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
443	13076		2.14	1.0E+00	AB021694.1	NT	Marchantia polymorpha genes for 26S rRNA, 5S rRNA, 18S rRNA, 5.8S rRNA and 26S rRNA
602	13231	25704	1.53	1.0E+00	AJ251660.1	NT	Girardia tigrina mRNA for homeodomain transcription factor (so gene)
705	13326	25813	7.12	1.0E+00	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
707	13328		0.89	1.0E+00	AF125684.1	NT	Aedes aegypti mucin-like protein MUC1 mRNA, complete cds
1429	15441		1.73	1.0E+00	X80416.1	NT	V. carteri Algal-CAM mRNA
1794	14384	26929	0.91	1.0E+00	AB006531.1	NT	Plautia stali Intestine virus RNA for nonstructural polyprotein, capsid protein precursor, complete cds
2528	15080	27682	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2526	15080	27683	1.2	1.0E+00	P48355	SWISSPROT	DNA GYRASE SUBUNIT B
2900	15517	27986	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2900	15517	27987	4.47	1.0E+00	P24008	SWISSPROT	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1 (STEROID 5-ALPHA-REDUCTASE 1) (SR TYPE 1)
2994	15610		0.83	1.0E+00	O14226	SWISSPROT	HYPOTHETICAL 67.9 KD PROTEIN C6F12.08C IN CHROMOSOME 1
3232	15844	28324	0.91	1.0E+00	AA628453.1	EST_HUMAN	af29g08.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1032830 3' similar to WP:CA2D08.3 CE04204 ; contains element MER22 MER22 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3659	12779		0.78	1.0E+00	U23808.1	NT	Xenopus laevis rhodopsin gene, complete cds
3744	16345	28813	1.55	1.0E+00	AJ223816.1	NT	Agaricus bisporus mRNA for tyrosinase
4144	16736	28189	1.5	1.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
4362	16949		0.64	1.0E+00	8922245	NT	Homo sapiens hypothetical protein FLJ10139 (FLJ10139), mRNA
5165	17734		17.2	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
5339	17800		0.6	1.0E+00	AF200817.1	NT	Pilot whale morbillivirus phosphoprotein (P) gene, partial cds
5432	18010	30394	1	1.0E+00	AB039022.1	NT	Oncorhynchus mykiss slt1 mRNA for rhinose binding lectin STL1, complete cds
5486	18120	30527	2.56	1.0E+00	Z97022.1	NT	Hordeum vulgare gene encoding cysteine proteinase
6013	18633	31368	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6013	18633	31369	4.54	1.0E+00	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6111	18727	31480	1.22	1.0E+00	Z97341.2	NT	Arabidopsis thaliana DNA chromosome 4, ESSA I FCA contig fragment No. 8
6263	18871	31641	4.41	1.0E+00	P04501	SWISSPROT	FIBER PROTEIN
6269	18877	31645	1.56	1.0E+00	AW452782.1	EST_HUMAN	U1-H-B13-alk-d-09-0-U1.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068969 3'
6615	19212	32018	1.79	1.0E+00	U75902.1	NT	Mus musculus subtilisin-like serine protease LPC (PC7) gene, exons 1 to 9, partial cds
6662	19258	32062	0.83	1.0E+00	AF104669.1	NT	Homo sapiens cell cycle protein (PA294) gene, exons 2 through 5
6742	19336		1.5	1.0E+00	P46506	SWISSPROT	SRB-11 PROTEIN
6874	19806	32442	1.27	1.0E+00	Y11204.1	NT	V. carteri gene encoding valoxopain
7192	19724	32573	1.22	1.0E+00	S62770.1	NT	insulin-like growth factor-binding protein 4 [cattle, pulmonary artery endothelial cells, mRNA, 2028 nt]
7493	20016		8.58	1.0E+00	P20273	SWISSPROT	B-CELL RECEPTOR CD22 PRECURSOR (LEU-14) (B-LYMPHOCYTE CELL ADHESION MOLECULE)
7697	20206	33093	1.36	1.0E+00	AF192531.1	NT	Homo sapiens endothelin-converting enzyme 2 (ECE2) mRNA, complete cds
7710	20219	33107	7.92	1.0E+00	AA775191.1	EST_HUMAN	ac76b08.s1 Stratagene lung (8937210) Homo sapiens cDNA clone IMAGE:868791 3'
7802	20444	33349	1.49	1.0E+00	BE668267.1	EST_HUMAN	601443950F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848005 5'
7802	20444	33350	1.49	1.0E+00	BE668267.1	EST_HUMAN	601443950F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3848005 5'
8084	17734		1.28	1.0E+00	D10852.1	NT	Rattus norvegicus mRNA for N-acetylglucosaminyltransferase III, complete cds
8281	20832	33753	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA-OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE : D-3-HYDROXYACYL COA DEHYDROGENASE]

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8291	20832	33754	2.1	1.0E+00	Q02207	SWISSPROT	PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE) (MULTIFUNCTIONAL BETA- OXIDATION PROTEIN) (MFP) [INCLUDES: 2-ENOYL-COA HYDRATASE; D-3-HYDROXYACYL COA DEHYDROGENASE]
8413	20953		0.85	1.0E+00	P51784	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 11) (DEUBIQUITINATING ENZYME 11)
8447	20987	33802	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBPM)
8447	20987	33803	0.48	1.0E+00	Q9Y5T5	SWISSPROT	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 16 (UBIQUITIN THIOLESTERASE 16) (UBIQUITIN- SPECIFIC PROCESSING PROTEASE 16) (DEUBIQUITINATING ENZYME 16) (UBIQUITIN PROCESSING PROTEASE UBPM)
8475	24791		2.17	1.0E+00	BE147331.1	EST_HUMAN	RC1-H10228-181099-011-808 HT0228 Homo sapiens cDNA
8513	21052	33974	1.06	1.0E+00	U42720.2	NT	Simian immunodeficiency virus Gag protein (gag) gene, complete cds; Pol protein (pol) gene, partial cds; and Vif protein (vif), Vpr protein (vpr), Tat protein (tat), Rev protein (rev), Vpu protein (vpu), Env protein (env), and Nef protein (nef) genes, >
8859	21198	34116	1.07	1.0E+00	M38427.1	NT	Human immunodeficiency virus type 1 (HIV-1), isolate SF33,
9185	21712	34655	2.05	1.0E+00	BE907592.1	EST_HUMAN	601497591F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899421 5'
9402	21911	34860	1.34	1.0E+00	8753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9402	21911	34861	1.34	1.0E+00	8753429	NT	Mus musculus chloride channel calcium activated 1 (Clca1), mRNA
9528	22028	34987	2.08	1.0E+00	AV889554.1	EST_HUMAN	AV889554 GKC Homo sapiens cDNA clone GKCCYA11 5'
9534	22034	34993	1.33	1.0E+00	U44852.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
9634	22034	34994	1.33	1.0E+00	U44852.1	NT	Xenopus laevis zona pellucida C glycoprotein precursor (xlZPC) mRNA, complete cds
9767	22265	35248	0.5	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
9767	22265	35249	0.5	1.0E+00	X15498.1	NT	Human Coronavirus gene for membrane protein
10021	22516	35510	0.62	1.0E+00	5174562	NT	Human Coronavirus gene for membrane protein
10021	22516	35511	0.62	1.0E+00	5174562	NT	Human Coronavirus gene for membrane protein
10105	22600	35592	0.75	1.0E+00	AI077920.1	EST_HUMAN	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10230	22725	35716	4.17	1.0E+00	AV758825.1	EST_HUMAN	Homo sapiens MHC binding factor, beta (MHCBBF) mRNA
10372	22868	35859	19.78	1.0E+00	AA004982.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW04 5'
10372	22868	35860	19.78	1.0E+00	AA004982.1	EST_HUMAN	AV758825 BM Homo sapiens cDNA clone BMFAW04 5'
10404	22898	35893	0.93	1.0E+00	L11910.1	NT	zfp4602.11 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10404	22898	35893	0.93	1.0E+00	L11910.1	NT	zfp4602.11 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428906 5'
10853	23374	36393	1.87	1.0E+00	S90825.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
11587	18120	30527	1.57	1.0E+00	Z97022.1	NT	PBR1=proline-rich protein (intron 3) [human, Genomic, 898 nt]
11837	24201		4.85	1.0E+00	P15306	SWISSPROT	Hordeum vulgare gene encoding cysteine proteinase
							THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12171	24410		3.08	1.0E+00	AW978184.1	EST_HUMAN	EST388293 IMAGE resequence, MAGN Homo sapiens cDNA
1816	14209	26742	0.97	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
1616	14209	26743	0.97	9.9E-01	AF245455.1	NT	Drosophila melanogaster regulator of G-protein signalling LOCO III mRNA, complete cds
2664	15222	27784	1.17	9.9E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3665	16267		0.94	9.9E-01	AF174585.1	NT	Apple mosaic virus RNA 2 putative polymerase gene, complete cds
5816	18440	31162	14.59	9.9E-01	P49657	SWISSPROT	SERINE/THREONINE PROTEIN KINASE MINIBRAIN
6029	18448	31389	0.83	9.9E-01	Q09832	SWISSPROT	PROBABLE OXIDOREDUCTASE ZK1290.5 IN CHROMOSOME II
9185	21702		1.39	9.9E-01	U65667.1	NT	Lycopodium obscurum putative M1 copy 1 nematode-resistance gene
9474	21873		2.61	9.9E-01	Q28842	SWISSPROT	B2 BRADYKININ RECEPTOR (BK-2 RECEPTOR)
10593	23128	36142	1.68	9.9E-01	AJ005029.1	NT	Danio rerio mRNA for Eph-like receptor tyrosine kinase rtk8
549	13180	25658	1.77	9.8E-01	P22867	SWISSPROT	AMINO-ACID ACETYLTRANSFERASE (N-ACETYL GLUTAMATE SYNTHASE) (AGS) (NAGS)
2336	14907		0.89	9.8E-01	AJ003108.1	NT	Caillitrix jacchus UBE1 gene derived retroposon on the Y chromosome
2827	15379		2.05	9.8E-01	AF174844.1	NT	Xenopus laevis rec GTPase mRNA, complete cds
3869	18467	28930	0.95	9.8E-01	Q67551	SWISSPROT	PROBABLE ENDONUCLEASE IV (ENDONUCLEASE IV)
3872	18470	28933	0.61	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
3872	16470	28934	0.61	9.8E-01	BE957439.2	EST_HUMAN	601653583R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838461 3'
7250	19779	32634	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7250	19779	32635	4.86	9.8E-01	AJ302158.1	NT	Enterobacteriaceae sp. JM983 partial groES gene for GroES-like protein and partial groEL gene for GroEL-like protein, isolate JM983
7841	20153	33038	1.13	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
7841	20153	33039	1.13	9.8E-01	BF034016.1	EST_HUMAN	601456337F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3860049 5'
8653	21192	34110	0.77	9.8E-01	P38652	SWISSPROT	PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE) (PGM)
10334	22828		0.56	9.8E-01	AA825565.1	EST_HUMAN	cd55d04.s1 NCI_CGAP GCBT Homo sapiens cDNA clone IMAGE:1371847 3'
10874	23395	36410	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
10874	23395	36411	4.86	9.8E-01	BE258705.1	EST_HUMAN	601110258F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350750 5'
11597	24040	37109	1.78	9.8E-01	AI680876.1	EST_HUMAN	b42c10.x1 NCI_CGAP Lu24 Homo sapiens cDNA clone IMAGE:2272242 3'
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CTR), CDM protein (CDM), adrenoleukodystrophy protein >
12058	24341		1.39	9.8E-01	U52111.2	NT	Drosophila melanogaster sodium channel protein (para) gene, exons 9, 10, 11, 12 and optional segments b, c, d and e, partial cds
7212	19743	32597	2.51	9.7E-01	U26716.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8440	20980	33895	1.7	9.7E-01	AF149112.1	NT	Triticum aestivum stripe rust resistance protein Yr10 (Yr10) gene, complete cds
8446	20986	33901	1.28	9.7E-01	MF0544.1	NT	Salmonella typhimurium adenine-methyltransferase (mod) and restriction endonuclease (res)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11049	23502		5.23	9.7E-01	BF511209.1	EST_HUMAN	UI-H-B14-adj-e-07-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085140 3'
12658	24729		2.92	9.7E-01	AL114281.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
4531	17115	29559	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4531	17115	29560	0.58	9.6E-01	AF197925.1	NT	Bromus inermis putative cytosolic phosphoglucomutase (pgm1) mRNA, complete cds
4557	17140	29588	1.71	9.6E-01	AW789874.1	EST_HUMAN	PM2-UM0053-240300-005-112 UM0053 Homo sapiens cDNA
5928	18550	31276	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
5928	18550	31277	3.9	9.6E-01	Z70556.1	NT	Parvovirus B19 DNA, patient C, genome position 2448-2894
8331	20872		1.23	9.6E-01	X95275.1	NT	P.falciparum complete genome map of plasmodium-like DNA (IR-A)
8785	21324	34248	0.47	9.6E-01	L81138.1	NT	Rattus norvegicus (strain R21) Rps27 gene, complete cds
9020	21557	34485	0.62	9.6E-01	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
10866	23481	36507	1.81	9.6E-01	AF041427.1	NT	Homo sapiens ribosomal protein s4 Y isoform gene, complete cds
11395	23847	36912	5.18	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11395	23847	36913	5.18	9.6E-01	AV752605.1	EST_HUMAN	AV752605 NPD Homo sapiens cDNA clone NPDBAG06 5'
11733	24138		2.36	9.6E-01	11421722	NT	Homo sapiens centrosomal protein 2 (CEP2), mRNA
12388	24983	30609	2.8	9.6E-01	U91423.1	NT	Sphyrna tiburo NADH dehydrogenase subunit 2 (NADH2) gene, mitochondrial gene encoding mitochondrial protein, partial cds
2515	15078	27851	1.02	9.5E-01	7705591	NT	Homo sapiens CGI-125 protein (LOC51003), mRNA
2681	15248	27817	1.2	9.5E-01	Q02834	SWISSPROT	ENDOGLUCANASE I PRECURSOR (EGI) (ENDO-1,4-BETA-GLUCANASE) (CELLULOSE 1)
3850	16448	28909	1.89	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
3850	16448	28910	1.89	9.5E-01	BE902340.1	EST_HUMAN	601875639F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958473 5'
8931	21469	34387	0.63	9.5E-01	AH80162.1	EST_HUMAN	qd57d07.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1733581 3'
9034	21571	34500	1.07	9.5E-01	AW861102.1	EST_HUMAN	RC1-CT0295-241189-011-402 CT0295 Homo sapiens cDNA
11123	23631	36874	1.71	9.5E-01	BF218771.1	EST_HUMAN	RC1-CT0295-241189-011-402 CT0295 Homo sapiens cDNA clone IMAGE:4103630 5'
11326	23024	36033	1.59	9.5E-01	AW283789.1	EST_HUMAN	UI-H-B12-ehp-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727677 3'
3235	15847		1.8	9.4E-01	AF165990.1	NT	Bartonella clarridgeiae RNA polymerase beta subunit (rpoB) gene, partial cds
3254	15866		2.47	9.4E-01	AF080595.1	NT	Pimpinella brachycarpa zinc finger protein (ZFP1) mRNA, complete cds
8799	21338	34265	0.88	9.4E-01	MB0724.1	NT	Human Fc-gamma-receptorIIA (FCGR2A) gene, exon 4
1768	14358		0.95	9.3E-01	AF242382.1	NT	Homo sapiens phytenoyl-CoA hydroxylase (PHYH) gene, exon 5
2692	15220	27792	1.09	9.3E-01	BE071172.1	EST_HUMAN	RC5-BT0503-271189-011-B01 BT0503 Homo sapiens cDNA
4107	16701	29154	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome
4107	16701	29155	0.92	9.3E-01	M20219.1	NT	Bovine papillomavirus type 2, complete genome

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5778	18403	31119	1.41	9.3E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
5658	18481	31204	3.69	9.3E-01	L36189.1	NT	Spodoptera frugiperda methylenetetrahydrofolate dehydrogenase mRNA, complete cds
8011	20553	33456	1.82	9.3E-01	AA847040.1	EST_HUMAN	oe09b03.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385357
8748	21287		1.13	9.3E-01	AF061981.1	EST	Xenopus laevis CCCC zinc finger protein C3H-2 (C3H-2) mRNA, complete cds
8867	21408	34330	1.01	9.3E-01	AL161534.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 34
12508	24629	30893	1.87	9.3E-01	11440298	NT	Homo sapiens inositol 1,4,5-trisphosphate receptor, type 2 (ITPR2), mRNA
12515	24634		2	9.3E-01	AF271207.1	NT	Aedes triseriatus putative large subunit ribosomal protein rpl34 mRNA, complete cds
3276	15987	28369	3.99	9.2E-01	BE622702.1	EST_HUMAN	601441338T1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916184.3
5004	17577		0.62	9.2E-01	BF128973.1	EST_HUMAN	601817814F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4041363.5
5894	18516		1.41	9.2E-01	7106410	NT	Mus musculus solute carrier family 30 (zinc transporter), member 4 (Slc30a4), mRNA
6140	18784	31512	4.4	9.2E-01	BF037588.1	EST_HUMAN	601461153F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3664661.5
9578	2078	35042	1.31	9.2E-01	AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
9663	22162	35135	1.15	9.2E-01	6871677	NT	Mus musculus carbonic anhydrase 4 (Car4), mRNA
10166	22661	35656	3.47	9.2E-01	11430963	NT	Homo sapiens lysosomal apyrase-like protein 1 (LALP1), mRNA
10314	22808	35800	1.58	9.2E-01	BF593251.1	EST_HUMAN	7c58e08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3578219.3 similar to SW_NUSM_TRYBB
10526	23063	36074	1.75	9.2E-01	BE563811.1	EST_HUMAN	P04540 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5;
11569	24016	37085	2.27	9.2E-01	BF132402.1	EST_HUMAN	601334943F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688714.5
1666	14259	26793	4.89	9.1E-01	T96675.1	EST_HUMAN	601820312F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052018.5
2169	14748		2.38	9.1E-01	8923056	NT	ye5201.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121369.3 similar to contains Alu repetitive element;
3239	15851	28331	0.93	9.1E-01	T26418.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20048 (FLJ20048), mRNA
3239	15851	28332	0.93	9.1E-01	T26418.1	EST_HUMAN	AB200G8R infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8.5'
6315	18922	31699	1.42	9.1E-01	L36033.1	NT	AB200G8R infant brain, LLNL array of Dr. M. Soares 1NIB Homo sapiens cDNA clone LLAB200G8.5'
6830	19226	32031	2.82	9.1E-01	Q81704	SWISSPROT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
7577	20093	32970	15.95	9.1E-01	AA806623.1	EST_HUMAN	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3 PRECURSOR (ITI HEAVY CHAIN H3)
7719	20227	33115	3.12	9.1E-01	U72995.1	NT	os71g08.s1 NCL_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1336862.3
12093	24976		33.14	9.1E-01	AF050113.1	NT	Rattus norvegicus Rab3 GDP/GTP exchange protein mRNA, complete cds
3241	15853	28335	0.81	9.0E-01	7681625	NT	Homo sapiens uncoupling protein-3 (UCP3) gene, complete cds
3401	16010		0.64	9.0E-01	AL161515.2	NT	Homo sapiens DKFZP564M2423 protein (DKFZP564M2423), mRNA
4468	17054	29498	1.44	9.0E-01	AF099810.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
							Homo sapiens neuroxin III-alpha gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7424	19948	32814	0.78	8.0E-01	L42547.1	NT	Danio rerio LIM class homeodomain protein (lim5) mRNA, complete cds
7450	19974		1.84	8.0E-01	D38621.1	NT	Xenopus laevis gene for aldolase, complete cds
8271	21797	34746	0.54	8.0E-01	AF086761.1	NT	Danio rerio semaphorin 71a mRNA, complete cds
9744	22242	35223	0.47	8.0E-01	U39702.1	NT	Mycoplasma genitalium section 24 of 51 of the complete genome
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 h ₁ analog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit
5875	18497	31222	2.49	8.9E-01	AF028198.1	NT	Rabbit MHC fragment RLA-DF DNA
6398	18988		1.27	8.9E-01	X60986.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
8152	20693		0.47	8.9E-01	AF260225.1	NT	Oithona nana cytochrome-c oxidase subunit I (coxI) gene, partial cds; mitochondrial gene for mitochondrial product
8365	20905	33824	1.04	8.9E-01	AF259667.1	NT	Xylella fastidiosa, section 90 of 229 of the complete genome
11616	24058	37122	2.59	8.9E-01	AE003944.1	NT	Chlamydia pneumoniae AR39, section 21 of 94 of the complete genome
11927	24262		5.33	8.9E-01	AE002186.2	NT	PUTATIVE F420-DEPENDENT NADP REDUCTASE
4640	17222	29876	2.1	8.8E-01	O26350	SWISSPROT	Pseudorabies virus Ea glycoprotein M gene, complete cds
5576	18207	30658	0.7	8.8E-01	AF310617.1	NT	M. aeruginosa (HUB 5-2-4) DNA from plasmid PMA1
10960	23475	36500	3.82	8.8E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
11749	25067		2.27	8.8E-01	D90911.1	NT	Homo sapiens SOST (SOST) gene, partial cds
490	13123	25609	1.48	8.7E-01	AF106953.2	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
2446	15013	27595	1.13	8.7E-01	5901893	NT	m05f11.s1 NCL CGAP_P14.1 Homo sapiens cDNA clone IMAGE:1076877
2898	15515	27984	5.67	8.7E-01	AA595863.1	EST_HUMAN	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
4845	17423	29875	0.61	8.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
4845	17423	29876	0.61	8.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
							Pseudomonas aeruginosa topoisomerase (top), putative transcriptional regulatory protein OhbR (ohbR), ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA (ohbA), OhbC (ohbC), ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB (ohbB), and put
5151	17721		3.08	8.7E-01	AF121970.1	NT	
7983	20525	33431	0.66	8.7E-01	AW897335.1	EST_HUMAN	RC4-NN0057-120500-013-c07 NN0057 Homo sapiens cDNA
8860	21399	34322	0.75	8.7E-01	AI239456.1	EST_HUMAN	qh36e08.x1 Soares_NFL_I_GBC.S1 Homo sapiens cDNA clone IMAGE:1846786 3'
8860	21399	34323	0.75	8.7E-01	AI239456.1	EST_HUMAN	qh36e08.x1 Soares_NFL_I_GBC.S1 Homo sapiens cDNA clone IMAGE:1846786 3'
9653	22182	35122	1.7	8.7E-01	AE004863.1	NT	Pseudomonas aeruginosa PA01, section 524 of 529 of the complete genome
10205	22700	35693	0.56	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309806 3'
10205	22700	35694	0.56	8.7E-01	BF570169.1	EST_HUMAN	602185541T1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309806 3'
10711	23239	36254	5.79	8.7E-01	BF363970.1	EST_HUMAN	QV0-NN1021-100800-337-c03 NN1021 Homo sapiens cDNA
11582	24028	37097	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'
11582	24028	37098	4.31	8.7E-01	BF107694.1	EST_HUMAN	601823684R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043564 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12146	24861		4.44	8.7E-01	AY661898.1	EST_HUMAN	AV661898 QLC Homo sapiens cDNA clone GLCGY907 3'
500	13132		1.55	8.6E-01	X17012.1	NT	Rat IGFII gene for insulin-like growth factor II
891	13505	26024	8.72	8.6E-01	W69089.1	EST_HUMAN	z444e03.r1 Soares_fetal_Nb-HH9W Homo sapiens cDNA clone IMAGE:343516 5'
2310	14882	27457	1.06	8.6E-01	4503210	NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthinosis), polypeptide 1 (CYP27A1b) mRNA
3681	16282	28750	0.78	8.6E-01	AL161585.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
3870	16468	28931	1.38	8.6E-01	U49724.1	NT	Drosophila melanogaster merlin (Dmerlin) mRNA, complete cds
6057	18674	31415	9.06	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6057	18674	31416	8.06	8.6E-01	X60547.1	NT	Chicken lipoprotein lipase gene
6810	19401	32216	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
6810	19401	32217	1.88	8.6E-01	AF143732.1	NT	Grus canadensis recombination activating protein 1 (RAG-1) gene, partial cds
7868	20410	33434	1.33	8.6E-01	AF001578.1	NT	Bacillus halodurans genomic DNA, section 121/4
7868	20410	33434	0.54	8.6E-01	AF001578.1	NT	Drosophila melanogaster collagen response mediator protein (CRMP) mRNA, complete cds
9603	22103		0.48	8.6E-01	AE000979.1	NT	Archaeoglobus fulgidus section 128 of 172 of the complete genome
12338	24812		1.73	8.6E-01	AL112162.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
6828	19416	32232	1.32	8.5E-01	AF165214.1	NT	Bacteriophage D3, complete genome
7533	20053	32926	2.38	8.5E-01	BE542612.1	EST_HUMAN	601067107F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453505 5'
7932	20474	33383	0.51	8.5E-01	AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
8357	20897	33817	0.84	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8357	20897	33818	0.84	8.5E-01	P06601	SWISSPROT	SEGMENTATION PROTEIN PAIRED
8441	20981	33896	0.51	8.5E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10252	22747	35734	1.38	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
10252	22747	35735	1.38	8.5E-01	AB008799.1	NT	Cyanidium caldarium gene for SigC, complete cds
12077	24978		3.12	8.5E-01	11418543	NT	Homo sapiens human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1), mRNA
12084	24355		7.82	8.5E-01	9507008	NT	Rattus norvegicus protein tyrosine phosphatase, non-receptor type 5 (Ptpn5), mRNA
4862	17440	29890	0.62	8.4E-01	AF083975.2	NT	Fowl adenovirus 8, complete genome
5685	24747	30807	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
5685	24747	30808	3.15	8.4E-01	L78726.1	NT	Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 7
9868	22365		2.68	8.4E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
771	13390	25889	2.48	8.3E-01	M93437.1	NT	Thermus thermophilus cytochrome c-552 (cycA) and CycB (cycB) genes, complete cds
3129	15743	28212	3.26	8.3E-01	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 18
3883	16481	28943	0.66	8.3E-01	AB010879.1	NT	Nicotiana tabacum mRNA for chloroplast ribosomal protein L10, complete cds
4084	16680	29140	3.24	8.3E-01	Y19177.1	NT	Streptomyces antibiotic polyketide biosynthetic gene cluster
5473	18107	30426	2.15	8.3E-01	AL161540.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 40

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9587	22087		3.14	8.3E-01	AF1791952.1	EST_HUMAN	nr01f12.y5 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR repetitive element;
10019	22514	35507	1.11	8.3E-01	AF098070.1	NT	Drosophila melanogaster List1 homolog mRNA, complete cds
10119	22614	35604	3.5	8.3E-01	AF108133.1	NT	Mus musculus neuro-d4 gene, exons 3 through 12 and partial cds
10553	23089	36103	2.92	8.3E-01	AE000903.1	NT	Methanobacterium thermoautotrophicum from bases 1270510 to 1283409 (section 109 of 148) of the complete genome
10571	23106		2.52	8.3E-01	7121472	NT	Phytophthora infestans mitochondrion, complete genome
11183	23688	36735	2.45	8.3E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
2096	14675	27244	3.23	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
2137	14715		1.45	8.2E-01	AF145589.1	NT	Mus musculus trophinin (Tnn) gene, complete cds
3989	16567	29036	1.12	8.2E-01	AB014574.1	NT	Homo sapiens mRNA for KIAA0674 protein, partial cds
4209	16798	29246	0.61	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL082w
4209	16798	29247	0.61	8.2E-01	Z72584.1	NT	S. cerevisiae chromosome VII reading frame ORF YGL082w
5270	17832	30258	1.08	8.2E-01	AB000489.1	NT	Rattus norvegicus mRNA for RPHO-1, complete cds
5420	17977	30385	2.11	8.2E-01	AB028957.1	NT	Homo sapiens mRNA for KIAA1034 protein, partial cds
6871	19605	32439	0.8	8.2E-01	AJ010142.1	NT	Amenita muscaria mRNA for SCII125 protein
6978	19554	32379	3.18	8.2E-01	AW379433.1	EST_HUMAN	CM4-HT0243-081189-037-e01 HT0243 Homo sapiens cDNA
7313	24778	32700	4.21	8.2E-01	Z12126.1	NT	S. cerevisiae MET, LEU4, and POL 1 genes encoding MET14 protein, alpha-isopropylmalate (alpha-IPM) synthetase (partial), and DNA polymerase alpha (partial)
9938	22433	35409	0.63	8.2E-01	AB014530.1	NT	Homo sapiens mRNA for KIAA0630 protein, partial cds
9971	22486	35450	1.67	8.2E-01	AF052659.1	NT	Homo sapiens thioredoxin-related protein mRNA, complete cds
10123	22618	35609	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10123	22618	35610	0.59	8.2E-01	AF223888.1	NT	Oncorhynchus tshawytscha isolate T-20 somatolactin precursor gene, exon 1
10286	22781	35772	3.52	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
10286	22781	35773	3.52	8.2E-01	Q9J170	SWISSPROT	MCKUSICK-KAUFMAN/BARDET-BIEDL SYNDROMES PUTATIVE CHAPERONIN
11498	23947	37017	3.33	8.2E-01	L10127.1	NT	Molluscum contagiosum virus type 1 ORF1 and ORF2 DNA
11576	24022	37091	8.05	8.2E-01	P10383	SWISSPROT	OVARIAN TUMOR LOCUS PROTEIN
11583	24029	37099	5.68	8.2E-01	H97398.1	EST_HUMAN	yw14d02.r1 Soares, placenta, 8tc6weeks, 2Nbp8tc6w Homo sapiens cDNA clone IMAGE:252195 5'
12102	24364	30970	1.86	8.2E-01	AJ001261.1	NT	similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN);
2787	15340		1.79	8.1E-01	AF191839.1	NT	Mus musculus mRNA for NIPSNAP2 protein
3504	16109	28585	2.99	8.1E-01	AF050066.1	NT	Mus musculus TANK binding kinase TBK1 (Tbk1) mRNA, complete cds
3504	16109	28586	2.99	8.1E-01	AF050066.1	NT	Homo sapiens MHC class 1 region

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5046	17619		0.66	8.1E-01	AF202634.1	NT	Drosophila melanogaster Na/K-ATPase beta subunit isoform 4 (JYbeta2) mRNA, complete cds
6457	18058	31843	0.88	8.1E-01	U16790.1	NT	Mus musculus putative collagen alpha-2 (X1) chain (COL11A2) gene, partial cds
6735	19329	32134	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
6735	19329	32135	2.54	8.1E-01	Q13491	SWISSPROT	NEURONAL MEMBRANE GLYCOPROTEIN M8-B
7852	20394	33298	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
7852	20394	33299	0.84	8.1E-01	AF022713.2	NT	Drosophila melanogaster putative inorganic phosphate cotransporter (Picot) gene, partial cds; putative sodium channel (Nach) and putative amylase-related protein (Amyrel) genes, complete cds; and putative serine-enriched protein (gprs) gene, partial cd>
8545	21084	34006	0.82	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8545	21084	34007	0.82	8.1E-01	AP001517.1	NT	Bacillus halodurans genomic DNA, section 11/14
8705	21244	34187	1.08	8.1E-01	AW242847.1	EST_HUMAN	xn01h03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2692469 3' similar to SW.LYAR_MOUSE Q08288 CELL GROWTH REGULATING NUCLEAR PROTEIN, contains MER22.b1 PTRS repetitive element;
10032	22527	35522	0.54	8.1E-01	P06425	SWISSPROT	PROBABLE E4 PROTEIN
11356	23810	36969	2.97	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11356	23810	36870	2.97	8.1E-01	BE938558.1	EST_HUMAN	RCO-TN0080-220800-025-d10 TN0080 Homo sapiens cDNA
11811	24183	31031	3.32	8.1E-01	AE001711.1	NT	Thermotoga maritima section 23 of 136 of the complete genome
186	12849		4.89	8.0E-01	AJ271510.1	NT	Staphylococcus aureus partial pla gene for phosphate acyltransferase allele 15
310	12885	25453	7.85	8.0E-01	AJ132772.1	NT	Bos taurus tub and rtf genes
2080	14661		1.47	8.0E-01	BF530982.1	EST_HUMAN	602072473F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4215091 5'
3113	15728	28189	1.24	8.0E-01	AF127897.1	NT	Salimiri boliviensis olfactory receptor (SBO27) gene, partial cds
3354	15882	28439	1.13	8.0E-01	AB006193.1	NT	Mus musculus gene for oviductal glycoprotein, complete cds
3765	16366		1.05	8.0E-01	AL162758.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 7/7
4630	17213	28684	5.65	8.0E-01	X63739.2	NT	G.gallus mRNA for nicotinic acetylcholine receptor (nAChR) beta 3 subunit
5117	17689	30127	1.09	8.0E-01	7657352	NT	Mus musculus myosin IXb (Myo9b), mRNA
7931	20473		2.32	8.0E-01	AW901489.1	EST_HUMAN	RCO-NN1012-270300-021-h08 NN1012 Homo sapiens cDNA
8482	21002	33919	1.17	8.0E-01	Y11095.1	NT	Rice stripe virus RNA 3
479	13112	25602	1.37	7.9E-01	D11476.1	NT	Lymnaea dispar nuclear polyhedrosis virus gene for DNA polymerase, complete cds
744	13364		1.05	7.9E-01	AE002130.1	NT	Ureaplasma urealyticum section 31 of 59 of the complete genome
1648	14240		28.8	7.9E-01	AB040885.1	NT	Homo sapiens mRNA for KIAA1452 protein, partial cds
1695	14288		1.11	7.9E-01	U32739.1	NT	Haemophilus influenzae Rd section 54 of 163 of the complete genome
2303	14876	27452	6.76	7.9E-01	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2304	14877	27453	5.48	7.9E-01	AF130459.1	NT	Danio rerio Trp4-associated protein Tap1A (tap1A) mRNA, complete cds
3587	16171	28653	2.33	7.9E-01	AF228684.1	NT	Gallus gallus SOX8 transcription factor (SOX8) mRNA, complete cds
4389	16975		0.76	7.9E-01	BE263612.1	EST_HUMAN	601192033F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535785 5'
4717	17288	28743	1.04	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
4717	17288	28744	1.04	7.9E-01	6753745	NT	Mus musculus embigin (Emb), mRNA
5315	17877		5.8	7.9E-01	M28930.1	NT	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17
6485	19086	31868	0.69	7.9E-01	D38145.1	NT	Human mRNA for prostacyclin synthase, complete cds
8053	20596	33502	2.52	7.9E-01	X00988.1	NT	P. sativum GR gene
9468	21891	34948	4.57	7.9E-01	U01912.1	NT	Giardia lamblia variant-specific surface protein G3M-B (vspG3M-B) mRNA, partial cds
9962	22457	35440	4.27	7.9E-01	P19719	SWISSPROT	SMALL HYDROPHOBIC PROTEIN
10003	22498	35487	0.75	7.9E-01	AV700860.1	EST_HUMAN	AV700860 GKC Homo sapiens cDNA clone GKCDRE12 3'
10405	22899	35894	0.71	7.9E-01	AB000631.1	NT	Streptococcus mutans DNA for sigma 42 protein, dTDP-4-keto-L-rhamnose reductase, complete cds
10886	23407		2.28	7.9E-01	7682471	NT	Homo sapiens KIAA1072 protein (KIAA1072), mRNA
11089	23801	36839	2.72	7.9E-01	P16022	SWISSPROT	NEURAL-CADHERIN PRECURSOR (N-CADHERIN)
909	13522		1.4	7.9E-01	Z43785.1	EST_HUMAN	HSC1KH041 normalized infant brain cDNA Homo sapiens cDNA clone c-1kh04
2314	14886	27461	1.4	7.9E-01	AW959567.1	EST_HUMAN	EST371637 MAGC resequences, MAGF Homo sapiens cDNA
4811	17389	28840	0.81	7.9E-01	U87305.1	NT	Rattus norvegicus transmembrane receptor Unc5H1 mRNA, complete cds
5189	17754		0.81	7.9E-01	AW753353.1	EST_HUMAN	RC3-CT0254-130100-023-c02 CT0254 Homo sapiens cDNA
6219	18829	31603	2.33	7.9E-01	AF115856.1	NT	Sphenodon punctatus alpha enolase mRNA, partial cds
6387	18971	31750	1.05	7.9E-01	P05231	SWISSPROT	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2) (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR)
6589	19186	31888	0.75	7.9E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome; segment 4/5
8428	20988	33881	1.04	7.9E-01	BF108927.1	EST_HUMAN	7B4d05.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525176 3'
9160	21695	34639	1.02	7.9E-01	Y10159.1	NT	D. discoideum recGAP gene
9255	21781	34733	0.53	7.9E-01	4826873	NT	Homo sapiens nucleoporin 214kd (CAN) (NUP214), mRNA
10031	22526		0.78	7.9E-01	Q25452	SWISSPROT	MUSCLE CALCIUM CHANNEL ALPHA-1 SUBUNIT (MDL-ALPHA1)
12071	24957		2.33	7.9E-01	L28260.1	NT	Arabidopsis thaliana 1-aminocyclopropanecarboxylate synthase (ACS5) gene, complete cds
150	12813	25300	4.65	7.7E-01	AF184345.1	NT	Lycopodium obscurum ADP-glucose pyrophosphorylase large subunit (AGP-L1) mRNA, complete cds
755	13374		1.44	7.7E-01	AF050157.1	NT	Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (Iaalpha) and major histocompatibility protein class II beta chain (Ib beta) genes, complete cds;
2737	15292	27660	2.33	7.7E-01	O33915	SWISSPROT	butyrophilin-like (NG8), butyrophilin-like CITRATE SYNTHASE

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3400	16009		0.62	7.7E-01	8393408	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GALNAC-T7) (GALNAC-T7), mRNA
3660	16262	28734	4.78	7.7E-01	AF118085.1	NT	Homo sapiens PRO1975 mRNA, complete cds
4486	17071	29521	3.17	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
4486	17071	29522	3.17	7.7E-01	AF199488.1	NT	Coturnix coturnix japonica sub-species japonica beta-actin mRNA, partial cds
5749	18375	31084	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
5749	18375	31085	1.33	7.7E-01	P16553	SWISSPROT	RAFFINOSE INVERTASE (INVERTASE)
6110	18726	31479	0.8	7.7E-01	R08900.1	EST_HUMAN	y724b02 s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127755 3'
9758	22266	35239	0.82	7.7E-01	AB021134.1	NT	Daphnia magna hemoglobin gene cluster (dhb3, dhb1 and dhb2 genes), complete cds
11957	24280		15.01	7.7E-01	11497621	NT	Archaeoglobus fulgidus, complete genome
4790	17370	29822	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
4790	17370	29823	19.73	7.6E-01	L27316.1	NT	Oryctolagus cuniculus immunoglobulin VDJ region gene
6248	18857	31628	4.81	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6248	18857	31629	4.81	7.6E-01	AF059510.1	NT	Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit (MCCB) mRNA, complete cds
6641	19237	32039	0.7	7.6E-01	P37938	SWISSPROT	MATING-TYPE PROTEIN A-ALPHA Z4
6935	18043	30465	0.95	7.6E-01	AI253399.1	EST_HUMAN	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
6935	18043	30468	0.95	7.6E-01	AI253399.1	EST_HUMAN	aq14b12.x1 Stanley Frontal NS pool 2 Homo sapiens cDNA clone IMAGE:2030879
7113	19453	32269	0.98	7.6E-01	U72487.1	NT	Rattus norvegicus calcium-independent alpha-latrotoxin receptor mRNA, complete cds
8009	20551	33455	1.34	7.6E-01	AF146793.2	NT	Mus musculus neuromedin U precursor (Nmu) gene, partial cds; PhLP (Tphlp) gene, partial cds; CLOCK (Clock) gene, complete cds; PFT27 (PFT27) gene, complete cds; and H5AR (H5ar) gene, complete cds
8098	20810	33522	1.76	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8098	20810	33523	1.76	7.6E-01	6857752	NT	Mus musculus advillin (Advil-pending), mRNA
8267	20808	33727	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8267	20808	33728	0.55	7.6E-01	Q01098	SWISSPROT	GLUTAMATE (NMDA) RECEPTOR SUBUNIT EPSILON 3 PRECURSOR (N-METHYL D-ASPARTATE RECEPTOR SUBTYPE 2C) (NR2C) (NMDAR2C)
8897	21435	34359	0.91	7.6E-01	6753577	NT	Mus musculus cytochrome P450, 2b9, phenobarbital inducible, type a (Cyp2b9), mRNA
9203	21720	34664	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
9203	21720	34666	3.33	7.6E-01	P30372	SWISSPROT	MUSCARINIC ACETYLCHOLINE RECEPTOR M2
11236	23767	36824	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70
11236	23767	36825	2.74	7.6E-01	X86347.1	NT	H. aspersa mRNA for neurofilament NF70

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11556	24004		5.74	7.6E-01	AL161592.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 88
11711	24121		6.31	7.6E-01	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
539	13170		1.32	7.5E-01	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
610	13238	25712	1.13	7.5E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
7530	20050	32923	0.74	7.5E-01	AF052730.1	NT	Drosophila melanogaster tyrosine kinase receptor protein (eph) mRNA, complete cds
12027	24318		5.28	7.5E-01	AF163151.2	NT	Homo sapiens dentin sialophosphoprotein precursor (DSPP) gene, complete cds
12522	24638	30897	1.91	7.5E-01	D89007.1	NT	Synochocystis sp. PCC6803 complete genome, 9/27, 1058467-1188885
1168	13771	26279	1.36	7.4E-01	AI598146.1	EST_HUMAN	h14b09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2167577 3' similar to contains Alu repetitive element; contains element MIR repetitive element;
3789	16389	28854	0.93	7.4E-01	AF112538.1	NT	Malva pusilla actin (Act1) mRNA, complete cds
4400	16985	29430	7.7	7.4E-01	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
7785	20328	33234	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
7785	20328	33235	1.03	7.4E-01	AL161551.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 51
8588	21107	34026	0.93	7.4E-01	BF340266.1	EST_HUMAN	602018456F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4154340 5'
8647	21186		0.64	7.4E-01	U87960.1	NT	Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon
9026	21563	34492	7.17	7.4E-01	BE747503.1	EST_HUMAN	601573029F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834174 5'
9083	21619	34554	1.19	7.4E-01	AA187896.1	EST_HUMAN	4p67h01.s1 Stratagene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:625297 3' similar to SW:TCPO_MOUSE P42932 T-COMPLEX PROTEIN 1, THETA SUBUNIT;
10301	22795	35786	0.59	7.4E-01	11424833	NT	Homo sapiens NY-REN-45 antigen (LOC51133), mRNA
11516	23984	37034	1.68	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11516	23984	37035	1.88	7.4E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
11677	24096		4.11	7.4E-01	6753217	NT	Mus musculus complement component 1 inhibitor (C1inh), mRNA
11794	24175		1.28	7.4E-01	AI472641.1	EST_HUMAN	1a13M01.x1 NCI_CGAP_Lym5 Homo sapiens cDNA clone IMAGE:2043985 3'
4723	17304	29748	0.72	7.3E-01	AE001166.1	NT	Borrelia burgdorferi (section 52 of 70) of the complete genome
4810	17388	29839	2.93	7.3E-01	AF225421.1	NT	Homo sapiens HT017 mRNA, complete cds
5260	17823	30248	0.99	7.3E-01	O43103	SWISSPROT	FERRICHRONE SIDEROPHORE PEPTIDE SYNTHETASE
6720	19314	32110	5.86	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
6720	19314	32117	5.86	7.3E-01	L35772.1	NT	Mus musculus antigen (CD72) gene
7151	24777	32525	0.82	7.3E-01	AJ011418.1	NT	Lycopodium obscurum mRNA for ubiquitin activating enzyme
7549	20088	32842	7.77	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
7549	20088	32843	7.77	7.3E-01	M26511.1	NT	V.alginolyticus sucrase (scrB) gene, complete cds
11307	23800	36859	3.86	7.3E-01	AA678019.1	EST_HUMAN	z25b08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11307	23800	36860	3.86	7.3E-01	AA878019.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431799 3'
864	13479		1.66	7.2E-01	L29281.1	NT	Reitius norvegicus Initiation factor-2 kinase (eIF-2a) mRNA, complete cds
2000	14582	27141	3.04	7.2E-01	X79140.1	NT	N. tabacum Nelf-4A13 mRNA
2501	15065	27639	1.36	7.2E-01	AB009605.1	NT	Gallus gallus gene for melanocortin 2-receptor, complete cds
3103	15718	28188	1.29	7.2E-01	AF198100.1	NT	Fowlpox virus, complete genome
3500	16105	28580	2.97	7.2E-01	AF056606.1	NT	Giardia intestinalis variant-specific surface protein (vsp417-6) gene, vsp417-6(A-1 allele, complete cds
3940	16538	29005	1.81	7.2E-01	BF338350.1	EST_HUMAN	602035589F1 NCI_CGAP_Brm64 Homo sapiens cDNA clone IMAGE:4183222 5'
4185	16775	29222	0.8	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
4884	17459	29911	2.54	7.2E-01	D90314.1	NT	L. mesenteroides gene for sucrose phosphorylase (EC 2.4.1.7)
5348	17908	30323	0.9	7.2E-01	AF158600.2	NT	Streptococcus thermophilus bacteriophage Sf11, complete genome
5386	17845	30358	0.59	7.2E-01	AL161563.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 63
7265	19793	32849	0.82	7.2E-01	U99833.1	NT	Solanum tuberosum cold-stress inducible protein (C17) gene, complete cds
8391	20931	33851	1.15	7.2E-01	AF238081.1	NT	Oryctolagus cuniculus RING-finger binding protein mRNA, partial cds
8893	21431		0.53	7.2E-01	AV743773.1	EST_HUMAN	AV743773 CB Homo sapiens cDNA clone CBMAFD06 5'
10243	22738	35729	2.14	7.2E-01	BF670081.1	EST_HUMAN	602118381F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275381 5'
10618	23150	36162	5.23	7.2E-01	U82623.1	NT	Reitius norvegicus cytochrome mRNA, complete cds
12037	16775	29222	1.86	7.2E-01	U02568.1	NT	Dictyocaulus viviparus nematode polyprotein antigen precursor (DvA) mRNA, complete cds
12233	24449		4.42	7.2E-01	AF000063.1	NT	Acropyrum pennix genomic DNA, section 8/7
12266	24995		1.67	7.2E-01	Y10168.1	NT	B. thuringiensis PK1 & cap genes, putative
721	13341	25831	10.56	7.1E-01	D21070.1	NT	Rana catesbeiana mRNA for bullfrog skeletal muscle calcium release channel (ryanodine receptor) alpha isoform(RYR1), complete cds
3098	15713	28185	18.71	7.1E-01	AJ270777.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 15-16
4287	16873	29321	4.11	7.1E-01	73053360	NT	Mus musculus otogelin (Otog), mRNA
4287	16873	29322	4.11	7.1E-01	BF681034.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
6103	18719	31471	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
6103	18719	31472	1.81	7.1E-01	BF681034.1	EST_HUMAN	602155438F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4286344 5'
7029	19563	32390	6.04	7.1E-01	U36292.1	NT	Drosophila melanogaster 6-pyruvoylthetrahydropterin synthase (pr) gene, complete cds
8132	20673	33594	0.53	7.1E-01	H54244.1	EST_HUMAN	225508.s1 Soares_fetal_liver_spleen_1NFLS_Homo sapiens cDNA clone IMAGE:202981 3'
8671	21210	34128	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-d09 BT0567 Homo sapiens cDNA
8671	21210	34129	0.78	7.1E-01	BE074185.1	EST_HUMAN	RC1-BT0567-301289-011-d09 BT0567 Homo sapiens cDNA
9769	22267	35252	1.48	7.1E-01	BE904405.1	EST_HUMAN	601496330F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3898495 5'
10309	22803	35795	1.06	7.1E-01	M12981.1	NT	Human T-cell receptor gamma chain J2 gene
12012	24878		2.58	7.1E-01	AA421492.1	EST_HUMAN	zu08h11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731109 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1272	13868	26387	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
1272	13868	26388	1.3	7.0E-01	AB014514.1	NT	Homo sapiens mRNA for KIAA0614 protein, partial cds
2492	15057	27630	1.22	7.0E-01	NC2412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
2492	15057	27631	1.22	7.0E-01	NC2412.1	EST_HUMAN	yz73e07.s1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:288708 3' similar to contains Alu repetitive element
5213	17778		1.98	7.0E-01	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21C101
5362	17922	30336	2.89	7.0E-01	AE003921.1	NT	Xyella fastidiosa, section 67 of 229 of the complete genome
6107	18723		1.03	7.0E-01	AB021316.1	NT	Arabidopsis thaliana mRNA for chlorophyll b synthase, complete cds
8319	20860		11.92	7.0E-01	AE000253.1	NT	Escherichia coli K-12 MG1655 section 143 of 400 of the complete genome
9240	21766	34714	0.61	7.0E-01	U53968.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtdI genes, complete cds
9240	21766	34715	0.61	7.0E-01	U53968.1	NT	Clostridium acetobutylicum mannitol-specific phosphotransferase system (PTS) system, mtdA, mtdR, mtdF, and mtdI genes, complete cds
10998	23513	36546	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
10998	23513	36547	1.99	7.0E-01	AV763842.1	EST_HUMAN	AV763842 MDS Homo sapiens cDNA clone MDSCH04 5'
12594	24918	30715	1.35	7.0E-01	9830464	NT	Bacteriophage N15 virion, complete genome
1005	13616	26130	10.2	6.9E-01	U68674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1005	13616	26131	10.2	6.9E-01	U68674.1	NT	Candida albicans squalene epoxidase (CAERG1) gene, complete cds and translational regulator gene, partial cds
1353	13948	26472	2.8	6.9E-01	AA593530.1	EST_HUMAN	nn28e09.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085176 3'
3256	15868	26348	1.7	6.9E-01	AE002271.2	NT	Chlamydia muridarum, section 3 of 85 of the complete genome
5954	18576	31310	0.8	6.9E-01	AB035692.1	NT	Branchiostoma belcheri BbNA3 mRNA for notochord actin, complete cds
5508	19108	31893	1.31	6.9E-01	BE296188.1	EST_HUMAN	601177333F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532328 5'
7921	20463	33369	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
7921	20463	33370	3.4	6.9E-01	AL161573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
9098	21634		0.83	6.9E-01	AF118046.1	NT	Entamoeba dispar cation transporting ATPase (atpase) gene, partial cds
9611	22111	35073	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
9611	22111	35074	0.62	6.9E-01	AF206319.1	NT	Musa acuminata pectate lyase 1 (PL1) mRNA, complete cds
10307	22801	35793	0.66	6.9E-01	BE242367.1	EST_HUMAN	601880380F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109419 5'
11138	23646	36687	1.94	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds
11138	23646	36688	1.94	6.9E-01	D89013.1	NT	Homo sapiens DAN gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11651	24870		2.36	6.9E-01	Q89958	SWISSPROT	FORKHEAD BOX PROTEIN C2 (FORKHEAD-RELATED PROTEIN FKHL14) (MESENCHYME FORK
12670	25003	30611	1.33	6.9E-01	A188312.1	EST_HUMAN	HEAD PROTEIN 1) (MFH-1 PROTEIN) (TRANSCRIPTION FACTOR FKHL14)
992	13604	26118	1.28	6.8E-01	AF017784.1	NT	wn31f02.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2447067 3'
2698	15255		1.25	6.8E-01	D90917.1	NT	Giardia intestinalis carbamate kinase gene, complete cds
						NT	Synechocystis sp. PCC6803 complete genome, 27/27, 3418852-3573470
2856	14249	26783	1.62	6.8E-01	AA854475.1	EST_HUMAN	aj75a05.s1 Soares_parathyroid_tumor_NHPPA Homo sapiens cDNA clone IMAGE:1402256 3' similar to
4672	17254	29706	1.45	6.8E-01	J00762.1	NT	gb:X56411_ma1 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (HUMAN);
9556	22056	35017	2.11	6.8E-01	AB037766.1	NT	Rat(hooded) prolactin gene : exon III and flanks
						NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
10261	22756		0.48	6.8E-01	AA687936.1	EST_HUMAN	nv13e07.s1 NCI_CGAP_P22 Homo sapiens cDNA clone IMAGE:1220100 3' similar to gb:X13546_ma1
10965	23480	36505	2.96	6.8E-01	AJ276675.1	NT	Human HMG-17 gene for non-histone chromosomal protein (HUMAN);
10965	23480	36506	2.96	6.8E-01	AJ276675.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
10993	23507	36540	2.16	6.8E-01	AF038939.1	NT	Stagonospora avenae bgl1 gene for beta-glucosidase, exons 1-4
10993	23507	36541	2.16	6.8E-01	AF038939.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
11178	23684	36730	2.2	6.8E-01	AF164151.1	NT	Mus musculus zinc finger protein (Peg3) mRNA, complete cds
						NT	Anopheles gambiae strain M2 translation initiation factor 4C (1A) (eIF-4C) mRNA, complete cds
11475	23925	36995	1.77	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1, 3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
11475	23925	36996	1.77	6.8E-01	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1, 3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
320	12974	25463	27.63	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
361	13010	25493	26.51	6.7E-01	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
1955	14539		0.97	6.7E-01	MT12132.1	NT	Quail fast skeletal muscle troponin I gene, complete cds
2192	14768	27340	1.65	6.7E-01	AA451864.1	EST_HUMAN	zx12g12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786310 3' similar to
						EST_HUMAN	contains element TAR1 repetitive element :
2211	15460	27361	2.66	6.7E-01	AF186073.1	NT	Drosophila melanogaster Mts85C gene, complete cds, NMDMC isoform (Nmdmc) gene, complete cds, alternatively spliced; and transcription factor (Relish) gene, complete cds, alternatively spliced
3026	19642	28120	4.28	6.7E-01	6678580	NT	Mus musculus Wiskott-Aldrich syndrome protein (Wasp), mRNA
4550	17133	26581	0.64	6.7E-01	X74421.1	NT	S. tuberosum mRNA for glucose-6-phosphate dehydrogenase

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5100	17672	30111	0.96	6.7E-01	AW079110.1	EST_HUMAN	xa95g12.x1 NCL_CGAP_Cot17 Homo sapiens cDNA clone IMAGE:2574598 3'
5700	18326	30829	0.8	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
5700	18326	30830	0.8	6.7E-01	J04836.1	NT	M.barkeri ATPase alpha and beta subunit (atpA and atpB) genes, complete cds
6116	18732	31485	0.83	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
6465	19066	31851	1.55	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
6465	19066	31852	1.55	6.7E-01	9635035	NT	Galid herpesvirus 2, complete genome
7356	19882		4.12	6.7E-01	AE004606.1	NT	Pseudomonas aeruginosa PA01, section 167 of 529 of the complete genome
7378	19904	32768	0.9	6.7E-01	AE001486.1	NT	Helicobacter pylori, strain J99 section 47 of 132 of the complete genome
10049	22544		0.87	6.7E-01	M34046.1	NT	Human placental protein 14 (PP14) gene, complete cds
10832	23353	36368	2.52	6.7E-01	BF354648.1	EST_HUMAN	CM3-H10769-010600-197-c03 HT0769 Homo sapiens cDNA
11333	23031	36040	3.45	6.7E-01	O14367	SWISSPROT	N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN GP11
2546	15110	27682	2.66	6.6E-01	AF075240.1	NT	Homo sapiens SLIT1 protein (SLIT2) mRNA, partial cds
2724	15279	27846	1.01	6.6E-01	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds
3536	16141	28623	1.35	6.6E-01	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
3719	16320	28786	3.42	6.6E-01	Y07689.1	NT	C.albicans random DNA marker, 282bp
4187	16777						Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5227	17791	30210	0.97	6.6E-01	U91328.1	NT	q22a10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845488 3' similar to contains
6474	19075	31858	4.22	6.6E-01	9680577	EST_HUMAN	PTR5.b2 MER28 repetitive element
7675	20186	33074	3.61	6.6E-01	AV660506.1	EST_HUMAN	Mus musculus kinesin light chain 2 (Klc2), mRNA
8501	21040	33961	0.64	6.6E-01	AV704700.1	EST_HUMAN	AV660506 GLC Homo sapiens cDNA clone GLCGID04 3'
9582	22082		1.73	6.6E-01	AL163278.2	NT	AV704700 ADB Homo sapiens cDNA clone ADBCAF11 5'
9615	22411		0.68	6.6E-01	AU118199.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
12118	24377	30973	1.27	6.6E-01	AF110001.1	NT	AU118198 HEMBA1 Homo sapiens cDNA clone HEMBA1003079 5'
651	13274	25751	1.12	6.5E-01	M75140.1	NT	Homo sapiens guanylate cyclase activating protein 3 (GCAP3) gene, exon 4 and complete cds
651	13274	25752	1.12	6.5E-01	M75140.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
3480	16086	28560	5.04	6.5E-01	AB041225.1	NT	H. vulgaris Na,K-ATPase alpha subunit mRNA, complete cds
4110	16704	29157	1.1	6.5E-01	4504632	NT	Mus musculus gene for Tob2, complete cds
4369	16956	29398	3.29	6.5E-01	AJ272285.1	NT	Homo sapiens interleukin 10 receptor, alpha (IL10RA) mRNA
4699	17281	29728	1.28	6.5E-01	D00584.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
							Oriza sativa gene for prepro-glutelin, exons 1, 2, 3, 4, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5219	17784	30202	2.38	6.5E-01	U28921.1	NT	Phaeosulfonolysin ATPase gamma subunit mRNA, nuclear gene encoding mitochondrial protein, partial cds
5336	17897	30312	1.02	6.5E-01	Z70628.1	NT	H.sapiens mRNA for immunoglobulin heavy chain variable region (9D4-A6, VH4, 4-59/DP-71)
6825	19415	32231	1.26	6.5E-01	D88348.1	NT	Chicken mRNA for 115-kDa melanosomal matrix protein, complete cds
7663	20175	33062	0.66	6.5E-01	A1799882.1	EST_HUMAN	wc46a02.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2321842 3'
9751	22249		1.25	6.5E-01	T78904.1	EST_HUMAN	Yd21b04.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108847 3'
10238	22733	35725	2.49	6.5E-01	AF118676.1	NT	Mus musculus small GTP-binding protein RAB25 (Rab25) gene, complete cds
10512	23050	36081	3.35	6.5E-01	H87583.1	EST_HUMAN	Yw17f06.r1 Soares_placenta_8to8weeks_2Nbl-IP8to9W Homo sapiens cDNA clone IMAGE:252515 5'
10566	23102	36116	4.35	6.5E-01	AA601287.1	EST_HUMAN	nc15c07.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100748 3'
10659	23201		4.29	6.5E-01	AU138078.1	EST_HUMAN	AU138078 PLACET1 Homo sapiens cDNA clone IMAGE:1007810 5'
11470	23920	36989	2.7	6.5E-01	AF014115.1	NT	Plasmodium berghei cytochrome c oxidase subunit III, cytochrome c oxidase subunit I, and cytochrome b genes, mitochondrial genes encoding mitochondrial proteins, complete cds
12067	24348		8.24	6.5E-01	BE465050.1	EST_HUMAN	hw74a10.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3179130 3'
12321	24817		3.04	6.5E-01	Z74145.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL097c
273	12630	25417	9.34	6.4E-01	U48948.1	NT	Drosophila melanogaster 8kd dynein light chain mRNA, complete cds
3502	16107	28583	3.78	6.4E-01	U48854.2	NT	Mus musculus dystroglycan 1 (DAG1) gene, exons 1 and 2 and complete cda
3928	16526	28963	1.33	6.4E-01	AB046827.1	NT	Homo sapiens mRNA for KIAA1607 protein, partial cds
4591	17174	29619	0.86	6.4E-01	Y12488.1	NT	M.musculus whn gene
4591	17174	29620	0.66	6.4E-01	Y12488.1	NT	M.musculus whn gene
5402	17980	30371	0.97	6.4E-01	AE002551.2	NT	Neisseria meningitidis serogroup B strain MC58 section 193 of 208 of the complete genome
8549	21088	34010	1.76	6.4E-01	AE001247.1	NT	Treponema pallidum section 63 of 87 of the complete genome
10001	22496	35486	8.26	6.4E-01	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
10015	22510	35501	1.16	6.4E-01	BF670405.1	EST_HUMAN	602150289F1 NIH_MGC.81 Homo sapiens cDNA clone IMAGE:4291126 5'
12188	24420		29.97	6.4E-01	AV759212.1	EST_HUMAN	AV759212 MDS Homo sapiens cDNA clone MDSCG09 5'
459	13093	25587	3.75	6.3E-01	P05228	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-III)
580	13191	25689	56.3	6.3E-01	U32889.1	NT	Haemophilus influenzae Rd section 4 of 163 of the complete genome
2207	14763	27356	3.24	6.3E-01	U81136.1	NT	Shigella flexneri multi-antigen resistance locus
2614	15176	27744	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
2614	15176	27745	2.78	6.3E-01	U75331.1	NT	Gallus gallus bone morphogenetic protein 1 (BMP1) mRNA, partial cds
3050	15688		0.75	6.3E-01	Y17275.1	NT	Lycopodium obscurum p89a gene, complete CDS
6214	18924	31595	0.78	6.3E-01	BE063906.1	EST_HUMAN	PMO-BT0757-010500-002-a05 BT0757 Homo sapiens cDNA
6712	19308	32110	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds
6712	19308	32111	1	6.3E-01	L27798.1	NT	Streptococcus dysgalactiae (mag) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8458	20988		3.32	6.3E-01	BE902044.1	EST_HUMAN	601870889F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3959351 5'
8819	21358	34284	0.91	6.3E-01	SC2927.1	NT	glycoprotein illa (Alu 1 and 3 fusion junction) [human, Genomic Mutant, 300 nt]
9147	21682	34627	1.15	6.3E-01	BF216984.1	EST_HUMAN	601884050F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4102586 5'
9341	21855	34804	2.9	6.3E-01	9827521	NT	Varicella virus, complete genome
9341	21855	34805	2.9	6.3E-01	9827521	NT	Varicella virus, complete genome
9851	22349		0.87	6.3E-01	AE002329.2	NT	Chlamydia muridarum, section 59 of 85 of the complete genome
10324	22818	35814	1.52	6.3E-01	273003.1	NT	S. cerevisiae chromosome VII reading frame ORF YGR218w
10421	22815	35915	0.87	6.3E-01	AE000313.1	NT	Escherichia coli K-12 MG1685 section 203 of 400 of the complete genome
10939	23456	36479	2.45	6.3E-01	AA877715.1	EST_HUMAN	nr091006.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1161371 3' similar to TR:002916 002916
11216	23719	36773	15.21	6.3E-01	AI904160.1	EST_HUMAN	HLAK. ;
11302	23795	36853	1.94	6.3E-01	P47003	SWISSPROT	GM-BT043-090299-046 BT043 Homo sapiens cDNA
11458	23908	36975	2.02	6.3E-01	P36073	SWISSPROT	HYPOTHETICAL 13.7 KD PROTEIN IN INO1-IDS2 INTERGENIC REGION
11769	25042	30505	30.63	6.3E-01	9910293	NT	HYPOTHETICAL 15.3 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION
11864	24219		1.85	6.3E-01	AF105227.1	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
12082	24953		3.2	6.3E-01	X83528.1	NT	Homo sapiens 3'-phosphoadenosine 5'-phosphosulfate synthetase (PAPSS) mRNA, complete cds
5175	17742	30171	0.71	6.2E-01	AF157898.1	NT	Climicola pscD gene
6030	18649	31390	2.03	6.2E-01	Q10135	SWISSPROT	Spermophilus suslicus isolate S47 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
7506	20028		3.14	6.2E-01	AF022253.1	NT	HYPOTHETICAL 142.5 KD PROTEIN C23E2.02 IN CHROMOSOME 1
7548	24786	32941	1.08	6.2E-01	AL021127.2	NT	Mus musculus calcium-sensing receptor related protein 4 (Casr-rs4) mRNA, partial cds
8243	20784	33703	5.65	6.2E-01	H72285.1	EST_HUMAN	Mus musculus chromosome X contigA; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
8790	21329	34254	0.54	6.2E-01	AF034411.1	NT	ys07e08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213542 3'
9370	20309	33212	1.75	6.2E-01	BE562687.1	EST_HUMAN	Lycopodium esculentum cytosolic Cu,Zn superoxide dismutase (Sod) gene, partial cds; and dehydroquinase dehydratase/shikimate:NADP oxidoreductase gene, complete cds
9429	21638		2.35	6.2E-01	M24461.1	NT	601336146F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690010 5'
9890	22495	35472	5.85	6.2E-01	AL161511.2	NT	Human pulmonary surfactant-associated protein SP-B (SFTPB) mRNA, complete cds
10429	22923	35927	3.76	6.2E-01	P27410	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 23
10429	22923	35928	3.76	6.2E-01	P27410	SWISSPROT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
2438	15005		4.95	6.1E-01	6678076	NT	NON-STRUCTURAL POLYPEPTIDE [CONTAINS: RNA-DIRECTED RNA POLYMERASE ; THIOL PROTEASE P3C ; HELICASE (2C LIKE PROTEIN); COAT PROTEIN]
4632	17215	26668	1.05	6.1E-01	4557538	NT	Mus musculus secreted acidic cysteine rich glycoprotein (Sparc), mRNA
							Homo sapiens solute carrier family 28 (sulfate transporter), member 2 (SLC28A2) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5141	17712	30142	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
5141	17712	30143	1.09	6.1E-01	L20427.1	NT	Rattus norvegicus dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds
5727	18353	31057	1.54	6.1E-01	M59940.1	NT	Caenorhabditis elegans N2 CcMyoD (h1-1) alternatively spliced genes, complete cds
6951	19528	32351	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
6951	19528	32352	3.55	6.1E-01	M64733.1	NT	Rat TRPM-2 gene, complete cds
8175	20716	33632	3.57	6.1E-01	AF093535.1	NT	Arabidopsis thaliana putative zinc transporter (ZIP1) mRNA, complete cds
8730	21269	34187	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
8730	21269	34188	1.23	6.1E-01	11431065	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP4K4), mRNA
9336	21850	34798	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9336	21850	34799	19.4	6.1E-01	AF236117.1	NT	Homo sapiens G-protein coupled receptor EDG-7 mRNA, complete cds
9750	22254	35236	1.15	6.1E-01	AE004482.1	NT	Pseudomonas aeruginosa PA01, section 13 of 529 of the complete genome
9959	22454	35436	1.8	6.1E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
10837	23358		8.53	6.1E-01	X74507.1	NT	P. sativum mdh mRNA for chloroplast malate dehydrogenase (NADP+)
11581	24027	37095	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
11581	24027	37096	2.19	6.1E-01	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
12530	24643		1.91	6.1E-01	X95287.1	NT	M.mazei orfA, orfB, and orfC of archaeal ABC-transporter system
520	13152	25635	1.46	6.0E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
587	13217		3.41	6.0E-01	5802969	NT	Homo sapiens adaptor-related protein complex 3, mu 2 subunit (CLA20), mRNA
1406	13999	26528	1.83	6.0E-01	AF065253.1	NT	Human respiratory syncytial virus strain CH93-53b attachment protein (G) gene, complete cds
3887	19485	28946	0.88	6.0E-01	AJ233396.1	NT	Viral hemorrhagic septicemia virus N, P, M, G, Nv, L genes, French strain 07-71
4287	18853		1.16	6.0E-01	AF058895.1	NT	Homo sapiens Notch3 (NOTCH3) gene, exons 26, 27, and 28
5485	18119	30526	1.93	6.0E-01	P20288	SWISSPROT	D(2) DOPAMINE RECEPTOR
5631	18260	30732	2.28	6.0E-01	AW139713.1	EST_HUMAN	UIH-BH1-aeb-a-10-O-UJ.st1NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718619.3
6660	19256	32059	3.73	6.0E-01	U39813.1	NT	Musca domestica insecticide-susceptible strain voltage-sensitive sodium channel mRNA, complete cds
6767	19360	32169	0.79	6.0E-01	O04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
7391	19916	32780	5.29	6.0E-01	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
8066	20608	33520	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
8066	20608	33521	4.72	6.0E-01	P02835	SWISSPROT	SEGMENTATION PROTEIN FUSHI TARAZU
9737	22235	35214	2.22	6.0E-01	AB008193.1	NT	Homo sapiens genes for leukotriene B4 receptor BLT2, leukotriene B4 receptor BLT1, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10174	22668		1.61	6.0E-01	Q01497	SWISSPROT	PEROXISOMAL MEMBRANE PROTEIN PER8 (PEROXIN-3)
10936	23453	36476	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
10936	23453	36477	2.14	6.0E-01	AJ131892.1	NT	Gallus gallus mRNA for Hyperion protein, 419 kD isoform
11426	23877	36942	2.84	6.0E-01	AI420623.1	EST_HUMAN	t0807.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2095621 3'
12158	24398	30978	1.82	6.0E-01	11421663	NT	Homo sapiens nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA
12265	24475		1.99	6.0E-01	AA708087.1	EST_HUMAN	z98q05.s1 Soares_fetal_liver_spleen_1NFS_S1 Homo sapiens cDNA clone IMAGE:462776 3'
12426	24879		1.29	6.0E-01	5903136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
12469	24885	30709	2.49	6.0E-01	9055303	NT	Mus musculus cGMP-inhibited phosphodiesterase (Pde3a), mRNA
12499	24810		6.92	6.0E-01	BE157617.1	EST_HUMAN	RC1-HT0375-030500-015-c03 HT0375 Homo sapiens cDNA
1038	13648	26160	1.09	5.9E-01	U32701.1	NT	Haemophilus influenzae Rd section 16 of 163 of the complete genome
1447	14039	26568	1.06	5.9E-01	6680232	NT	Mus musculus 3-hydroxy-3-methylglutaryl-Coenzyme A lyase (Hmgcl), mRNA
3308	15919	28395	5.12	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
3308	15919	28396	5.12	5.9E-01	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4304	16860		4.32	5.9E-01	AF162756.1	NT	Rattus norvegicus ceneixin 2 mRNA, partial cds
6591	19188	31991	1.48	5.9E-01	AF065440.2	NT	Homo sapiens low density lipoprotein receptor-related protein II (LRP2) gene, exon 1 and partial cds
7310	19838	32696	5.58	5.9E-01	AB023486.1	NT	Homo sapiens gene for histamine H2 receptor, promoter region and complete cds
7941	20483	33395	0.57	5.9E-01	D90911.1	NT	Synechocystis sp. PCC6803 complete genome, 13/27, 1576593-1719843
9462	21967	34943	0.93	5.9E-01	AF063204.2	NT	Chlamydia trachomatis strain KUW31/Cx major outer membrane protein (omp1) gene, complete cds
9827	22325		0.68	5.9E-01	P08463	SWISSPROT	E6 PROTEIN
10091	22586	35579	1.15	5.9E-01	P55284	SWISSPROT	VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5)
10551	23087	36102	3.24	5.9E-01	Q9X0I3	SWISSPROT	THYMIDYLATE KINASE (DTMP KINASE)
10557	23093	36105	1.75	5.9E-01	AF197944.1	NT	Xenopus laevis receptor protein tyrosine phosphatase delta (XPTP-D) mRNA, complete cds
10840	23361	36376	3	5.9E-01	AV937176.1	EST_HUMAN	PM1-DT0041-190100-002-h03 DT0041 Homo sapiens cDNA
11073	23585	36626	2.25	5.9E-01	AF064628.1	NT	Mus spretus strain SPRETIEI CD48 antigen (Cd48) gene, partial cds
11810	24162	31030	1.92	5.9E-01	L42320.1	NT	Oryctolagus cuniculus alpha 1 anti-trypsin (alpha 1 AT) gene, promoter region
12053	24336		2.88	5.9E-01	AB017705.1	NT	Aspergillus oryzae pyrG gene for orotidine-5'-phosphate decarboxylase, complete cds
12280	24493		7.56	5.9E-01	P34926	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 1A [CONTAINS: MAP1 LIGHT CHAIN LC2]
1652	14536	27092	1.8	5.8E-01	P40472	SWISSPROT	SIM1 PROTEIN
4058	16853	29119	1.22	5.8E-01	BF695738.1	EST_HUMAN	601852474F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076131 5'
4612	17195	29641	3.73	5.8E-01	AB009077.1	NT	Vigna radiata mRNA for proton pyrophosphatase, complete cds
4914	17489		1.18	5.8E-01	AF110846.1	NT	Megascella scalaris sex-lethal homolog (Mgsxl) gene, partial cds, alternatively spliced products
5577	18208		0.75	5.8E-01	AE002152.1	NT	Ureaplasma urealyticum section 53 of 59 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5722	18348	31051	2.52	5.8E-01	Q10689	SWISSPROT	POTENTIAL 5'-3' EXONUCLEASE
6331	18937	31713	2.37	5.8E-01	D78659.1	EST_HUMAN	HUM500E06B Human placenta polyA+ (Tfujiwara) Homo sapiens cDNA clone GEN-500E06 5'
6454	19055	31840	0.71	5.8E-01	D50601.1	NT	Shigella sonnei DNA for 28 ORFs, complete cds
6903	19637		2.47	5.8E-01	S65091.1	NT	cyclic AMP-regulated phosphoprotein [rats, mRNA, 1030 nt]
7828	20370		2.57	5.8E-01	H41571.1	EST_HUMAN	yn91b03.s1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:175757 3' similar to gb:S78187 M-PHASE INDUCER PHOSPHATASE 2 (HUMAN);
8031	20573	33477	0.66	5.8E-01	A1280051.1	EST_HUMAN	qf85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8031	20573	33478	0.66	5.8E-01	A1280051.1	EST_HUMAN	qf85d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1853779 3'
8131	20672	33582	2.34	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8131	20672	33583	2.34	5.8E-01	P14328	SWISSPROT	SPORE COAT PROTEIN SP98
8823	21362	34287	9.48	5.8E-01	AJ270774.1	NT	Homo sapiens partial TCF-4 gene for T-cell transcription factor-4, exons 6-11
8902	21440	34363	0.88	5.8E-01	Q27388	SWISSPROT	TRANSSCRIPTION FACTOR E2F
8903	21441	34364	0.56	5.8E-01	Q20471	SWISSPROT	PUTATIVE CASEIN KINASE I F48F2.2 IN CHROMOSOME X
9514	22014		0.89	5.8E-01	BF031606.1	EST_HUMAN	601557774F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827298 5'
10869	23390	36405	9.44	5.8E-01	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
10915	23434		3.66	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
11021	23535		2.04	5.8E-01	BF700092.1	EST_HUMAN	602127577F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284403 5'
3079	15694		0.66	5.7E-01	6765253	NT	Mus musculus plasmacytoma variant translocation 1 (Pvt1), mRNA
3260	15872	28352	1.58	5.7E-01	Q9WTJ2	SWISSPROT	PUTATIVE TRANSCRIPTION FACTOR OVO-LIKE 1 (MOVO1A)
3552	16156		2.63	5.7E-01	AB033503.1	NT	Populus euramericana peacs-2 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
3973	16571	29041	3.09	5.7E-01	AF011581.1	NT	Homo sapiens T cell receptor beta chain (BV6S772-BJ1S1) mRNA, partial cds
6496	19097	31881	3.87	5.7E-01	BF035413.1	EST_HUMAN	601454962F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3858590 5'
6812	19403	32219	0.72	5.7E-01	AA194201.1	EST_HUMAN	z38c06.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:885674 5'
6945	18053	30476	1.28	5.7E-01	AL111440.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
7741	20249	33142	1.97	5.7E-01	P00373	SWISSPROT	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5OR) (P5C REDUCTASE)
7911	20453		0.57	5.7E-01	AJ251835.1	NT	Mus musculus Kcnq1, Ltrpc5, Mash2, Tapa-1, Tesc4 and Tesc6 genes, alternative transcripts
9715	22213	35186	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
9715	22213	35187	1.17	5.7E-01	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
10468	22662	35973	0.86	5.7E-01	BF540962.1	EST_HUMAN	602067712F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4066810 5'
3410	16019	28498	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3410	16019	28499	1	5.6E-01	AB018283.2	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
4324	16910	29351	0.69	5.6E-01	D83135.1	NT	Chicken TBP gene, exon8, complete cds
8738	21277	34200	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKc Homo sapiens cDNA clone GKCF5F05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8798	21277	34201	4.42	5.6E-01	AV684703.1	EST_HUMAN	AV684703 GKC Homo sapiens cDNA clone GKCF505 5'
9297	21897	34844	1.11	5.6E-01	AB039782.1	NT	Homo sapiens MUC3A gene for intestinal mucin, partial cds
11658	24085		2.5	5.6E-01	BE888280.1	EST_HUMAN	601514007F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915457 5'
11779	24168	36775	1.28	5.6E-01	AA483535.1	EST_HUMAN	ng75g10.s1 NCI_CGAP_P18 Homo sapiens cDNA clone IMAGE:940874 similar to contains element PTR7 repetitive element:
12156	18028	30490	3.31	5.6E-01	AL101501.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
12185	24419		2.56	5.6E-01	P50505	SWISSPROT	HIGH AFFINITY POTASSIUM TRANSPORTER
12619	24698		3.11	5.6E-01	BF573828.1	EST_HUMAN	602132028F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271334 5'
1253	13880	26387	1.13	5.5E-01	8393912	NT	Rattus norvegicus Protonyl Coenzyme A carboxylase, beta polypeptide (Pccb), mRNA
2725	15280	27847	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2725	15280	27848	13.6	5.5E-01	P03341	SWISSPROT	GAG POLYPEPTIDE (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2943	15559	28033	0.69	5.5E-01	5902085	NT	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
3102	15717		1.51	5.5E-01	H46219.1	EST_HUMAN	yo18a10.s1 Soares adult brain N2b9HB55Y Homo sapiens cDNA clone IMAGE:178266 3'
3271	15883	28385	2.88	5.5E-01	AF227240.1	NT	Rabbit oral papillomavirus, complete genome
3755	16356	28825	0.97	5.5E-01	P48755	SWISSPROT	FOS-RELATED ANTIGEN-1
8386	20926	33846	0.86	5.5E-01	A1791768.1	EST_HUMAN	cr62c01.y5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602336 5'
8682	22181		0.74	5.5E-01	U68415.1	NT	Crimson-Congo hemorrhagic fever virus strain SPU 415/85 nucleoprotein gene, complete cds
10279	22774	35763	0.84	5.5E-01	T05047.1	EST_HUMAN	EST02805 Fetal brain, Stragene (cat#836206) Homo sapiens cDNA clone HFBQC35
151	12814	25301	12.97	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
151	12814	25302	12.97	5.4E-01	7657266	NT	Homo sapiens KIAA0929 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
611	13239	25713	1.6	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
611	13239	25714	1.6	5.4E-01	AF232006.1	NT	Pseudomonas syringae pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
1314	13908	29428	2.58	5.4E-01	AW896087.1	EST_HUMAN	QV4-NN0040-070400-160-c04 NN0040 Homo sapiens cDNA
2154	14731		3.6	5.4E-01	AED02247.2	NT	Chlamydomonas reinhardtii AR39, section 74 of 94 of the complete genome
2296	14870	27446	2.18	5.4E-01	AJ276682.1	NT	Drosophila melanogaster mRNA for 15.15' beta carotene dioxygenase (beta-diox gene)
3984	16582	29053	0.62	5.4E-01	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5259	17822		1.04	5.4E-01	AW747972.1	EST_HUMAN	QV0-BT0041-061089-033-e02 BT0041 Homo sapiens cDNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5388	13239	25713	0.59	5.4E-01	AF232006.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
5388	13239	25714	0.59	5.4E-01	AF232006.1	NT	<i>Pseudomonas syringae</i> pv. tomato strain DC3000 AvrE (avrE), HrpW (hrpW), and Gsta (gsta) genes, complete cds; and unknown genes
5838	18462	31185	0.81	5.4E-01	AW842327.1	EST_HUMAN	PM2-CN0030-030200-003-c10 CN0030 Homo sapiens cDNA
6338	18944	31723	1.49	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
7094	19665	32504	1.1	5.4E-01	BE866592.2	EST_HUMAN	801660276R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906090 3'
7374	19900	32762	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7374	19900	32763	0.75	5.4E-01	Z21619.1	NT	<i>S. cerevisiae</i> RIB3 gene encoding DBP synthase
7376	19902	32766	1.47	5.4E-01	Q64428	SWISSPROT	MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) [INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE : LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE]
9901	22398	32766	1.98	5.4E-01	Q64428	SWISSPROT	802079545F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4243690 5'
10957	23472	36497	3.25	5.4E-01	BF572536.1	SWISSPROT	NITRATE REDUCTASE [NADPH] (NR)
11485	23934	37004	5.79	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MIEROSIN HEAVY CHAIN)
11485	23934	37005	5.79	5.4E-01	Q60675	SWISSPROT	LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MIEROSIN HEAVY CHAIN)
11586	18944	31723	2.42	5.4E-01	AB025017.1	NT	<i>Rattus norvegicus</i> gene for TIS11, complete cds
11725	24132		2.52	5.4E-01	AB858998.1	EST_HUMAN	w137g04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2427126 3' similar to gb:M13452 LAMIN A (HUMAN).
542	13173	25653	2.29	5.3E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (BF), and complement component C2 (C2) genes.>
2811	15363	27931	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
2811	15363	27932	6.51	5.3E-01	4506328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
3280	15891	28370	3.13	5.3E-01	AF087658.1	NT	Homo sapiens secreted C-type lectin precursor (LSLCL) gene, complete cds
4290	16876		1.39	5.3E-01	U39697.1	NT	Mycoplasma genitalium section 9 of 51 of the complete genome
5849	18277	30753	1.91	5.3E-01	AB20921.1	EST_HUMAN	z142h12.y6 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5849	18277	30754	1.91	5.3E-01	AB20921.1	EST_HUMAN	z142h12.y6 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740711 5'
5742	18368	31075	0.87	5.3E-01	AA183672.1	EST_HUMAN	z142g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5742	18368	31076	0.87	5.3E-01	AA183672.1	EST_HUMAN	z142g09.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:666112 5'
5827	18451	31174	1.84	5.3E-01	BE845620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5827	18451	31175	1.84	5.3E-01	BE845620.1	EST_HUMAN	7e73c12.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3288118 3' similar to gb:J02783
5827	18451	31175	1.84	5.3E-01	BE845620.1	EST_HUMAN	PROTEIN DISULFIDE ISOMERASE PRECURSOR (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8835	21374		1.83	5.3E-01	L01950.2	NT	Roridula gorgonias ribulose 1,5-bisphosphate carboxylase (rbcl) gene, partial cds; chloroplast gene for chloroplast product
8885	21423	34348	0.63	5.3E-01	BF433986.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MIER29 repetitive element;
8885	21423	34349	0.63	5.3E-01	BF433986.1	EST_HUMAN	7q71c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3' similar to contains element MIER29 repetitive element;
10112	22807	35597	0.48	5.3E-01	A1854210.1	EST_HUMAN	w94b02.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:2551275 3' similar to
11435	23885	36952	6.92	5.3E-01	BE566291.1	EST_HUMAN	SW:COXA_HUMAN P20874 CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR ;
11850	24881		4.22	5.3E-01	AA916053.1	EST_HUMAN	601339867.F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682168 5'
849	13465	25973	19.16	5.2E-01	L20770.1	NT	APOLIPOPROTEIN D PRECURSOR (HUMAN);
1206	13806	26319	10.07	5.2E-01	Q9WV30	SWISSPROT	Drosophila melanogaster helix-loop-helix mRNA, complete cds
1233	13832	26346	2.91	5.2E-01	AF224492.1	NT	NUCLEAR FACTOR OF ACTIVATED T CELLS 5 (T CELL TRANSCRIPTION FACTOR NFAT5) (NF-AT5) (REL DOMAIN-CONTAINING TRANSCRIPTION FACTOR NFAT5)
1930	14514		4.11	5.2E-01	AL163285.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
2191	14767	27339	2.97	5.2E-01	AB018283.2	NT	Homo sapiens chromosome 21 segment HS21C085
3153	15767	28233	1.67	5.2E-01	U65942.1	NT	Homo sapiens mRNA for KIAA0740 protein, partial cds
3274	15886		0.71	5.2E-01	D73443.1	NT	Chlamydomonas abortus strain S203 POMP91A and POMP90A precursor, genes, complete cds
3452	16059		1.74	5.2E-01	AL116780.1	NT	Azotobacter vinelandii fcd gene for isocitrate dehydrogenase, complete cds
3492	16097	28572	2.49	5.2E-01	AA984185.1	EST_HUMAN	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
3694	16295		0.92	5.2E-01	AF020269.1	NT	am77g05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616504 3'
5161	17730		0.87	5.2E-01	7106444	NT	Medicago sativa chloroplast malate dehydrogenase precursor (p1mdh) mRNA, nuclear gene encoding chloroplast protein, complete cds
5314	17876		0.89	5.2E-01	AL163281.2	NT	Mus musculus vanilloid receptor-like protein 1 (Vhl1), mRNA
5834	18498	31179	0.97	5.2E-01	AA284281.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C081
9646	24795	35115	1.19	5.2E-01	X02218.1	NT	zx44d09.T7 Soaree_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:325169 3'
9646	24795	35116	1.19	5.2E-01	X02218.1	NT	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9845	22343	35325	0.64	5.2E-01	AA194518.1	EST_HUMAN	Chicken duplicated genes for histone H2A, H4 and a histone H3 gene
9940	22435	35411	1.65	5.2E-01	AF143952.2	NT	zx05b09.r1 Stralagene muscle 837209 Homo sapiens cDNA clone IMAGE:628793 5'
12590	24682		4.94	5.2E-01	P18516	SWISSPROT	Homo sapiens PELOTA (PELOTA) gene, complete cds
645	13288	25746	2.13	5.1E-01	M58509.1	NT	RETINOIC ACID RECEPTOR GAMMA (RAR-GAMMA) (RETINOIC ACID RECEPTOR DELTA) (RAR-DELTA)
676	13300	25781	3.98	5.1E-01	AJ233944.1	NT	Human adrenodoxin reductase gene, exons 3 to 12
							Polyangium vitellinum (strain PI vt1) 16S rRNA gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
676	13300	25782	3.98	5.1E-01	AJ233944.1	NT	Polyomavirus vitellinum (strain PI VT1) 16S rRNA gene
1692	14284		0.88	5.1E-01	X87885.1	NT	R. norvegicus mRNA for mammalian fusca protein
2069	14849		11.33	5.1E-01	BF683095.1	EST_HUMAN	602139318F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4298117 5'
4151	16743	29197	4.61	5.1E-01	AI859495.1	EST_HUMAN	w39b12.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2427283 3'
4268	16852	29300	3.03	5.1E-01	P06380	SWISSPROT	TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)
5229	17793		0.71	5.1E-01	BE091796.1	EST_HUMAN	IL2-BT0731-250400-077-G08 BT0731 Homo sapiens cDNA
6422	19025		0.79	5.1E-01	AV712326.1	EST_HUMAN	AV712326 DCA Homo sapiens cDNA clone IMAGE:148872 3'
6997	19495	32316	1.42	5.1E-01	RB0873.1	EST_HUMAN	y84409.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148872 3'
8507	21046	33966	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
8507	21046	33987	0.73	5.1E-01	AW806881.1	EST_HUMAN	QV4-ST0023-160400-172-a01 ST0023 Homo sapiens cDNA
9602	22102	35065	4.6	5.1E-01	J05412.1	NT	Human regenerating protein (reg) gene, complete cds
9605	22105	35098	3.4	5.1E-01	W22302.1	EST_HUMAN	65B1 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
10065	22560	35555	0.95	5.1E-01	M84579.1	NT	Human carboxyl ester lipase (CEL) gene, complete cds
11874	24805		2.04	5.1E-01	BF030207.1	EST_HUMAN	60155683F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826787 5'
12129	24385		2.01	5.1E-01	BF439982.1	EST_HUMAN	nac51110.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3408218 3' similar to contains element
2180	14757	27326	1.4	5.0E-01	4885552	NT	TAR1 repetitive element.
2180	14757	27327	1.4	5.0E-01	4885552	NT	Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
							Homo sapiens postmeiotic segregation increased 2-like 9 (PMS2L9), mRNA
2189	14765	27335	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
							Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
2189	14766	27336	5.46	5.0E-01	AF008210.1	NT	Buchnera aphidicola genomic fragment containing (chaperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEF), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene>
3740	16341	28809	5.58	5.0E-01	AE001785.1	NT	Thermotoga maritima section 97 of 136 of the complete genome
3811	16410	28875	0.65	5.0E-01	U55574.1	NT	Mus musculus anti-DNA immunoglobulin light chain IgM mRNA, antibody 363p.138, partial cds
3942	16540	29006	3.11	5.0E-01	AB033010.1	NT	Homo sapiens mRNA for KIAA1184 protein, partial cds
8467	21007		1.78	5.0E-01	M92304.1	NT	Xenopus laevis smooth muscle beta-tropomyosin mRNA, complete cds
8604	21143	34057	0.64	5.0E-01	BF107848.1	EST_HUMAN	601823850R1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4043485 3'
9379	20318	33219	3.1	5.0E-01	BF171212.1	EST_HUMAN	601803871F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4136632 5'
							GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE), AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
9543	22043	35004	1.34	5.0E-01	P35573	SWISSPROT	

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9543	22043	35005	1.34	5.0E-01	P35573	SWISSPROT	GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA-GLUCANOTRANSFERASE (OLIGO-1,4-1,4-GLUCANTRANSFERASE); AMYLO-1,6-GLUCOSIDASE (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)]
10291	22786		1.04	5.0E-01	BE869218.1	EST_HUMAN	601445024F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3849436 5'
11815	24187		3.45	5.0E-01	AF029215.1	NT	Mus musculus MRC OX-2 antigen homolog gene, exons 2-5, and complete cds
12554	24656		2.38	5.0E-01	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
12569	24668		4.27	5.0E-01	O13981	SWISSPROT	NUCLEAR ENVELOPE PROTEIN CUT11
822	13439	25946	2.31	4.9E-01	BF571462.1	EST_HUMAN	602076649F1 NIH_MGC 62 Homo sapiens cDNA clone IMAGE:4243860 5'
1699	14292	28827	1.8	4.9E-01	AJ243955.1	NT	Xenopus laevis mRNA for c-Jun protein, 1978 BP
1949	14533	27089	1.35	4.9E-01	U40869.1	NT	Cavia porcellus pulmonary surfactant protein A (SP-a) mRNA, complete cds
5602	18231	30681	1.32	4.9E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6187	18797	31565	2.35	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
7475	18797	31566	2.35	4.9E-01	AF020931.1	NT	Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 10
8920	21458		1.49	4.9E-01	BF206791.1	EST_HUMAN	Oryza sativa subsp. japonica mEF-G mRNA for mitochondrial elongation factor G, complete cds
9115	21651	34592	0.86	4.9E-01	AW339605.1	EST_HUMAN	601874964F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4102503 5'
9220	25126		2.2	4.9E-01	10948663	NT	hc80c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2907266 3' similar to TR:O95714
10220	22715	35706	0.74	4.9E-01	AF053980.1	NT	O95714 HERC2
11704	24117		2.46	4.9E-01	AF176912.1	NT	Mus musculus unc13 homolog (C. elegans) 1 (Unc13h1), mRNA
12546	25081		5.73	4.9E-01	AA613562.1	EST_HUMAN	Mus musculus adenoviral cyclase 1 (Adcy1) cDNA, partial cds
12555	24657	30872	1.74	4.9E-01	AL163301.2	NT	Homo sapiens neurotrophin-1B-cell stimulating factor-3 gene, complete cds
12630	24708		1.36	4.9E-01	11431438	NT	nq22a11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144652 3'
3591	16195		1.05	4.8E-01	AA912842.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
4782	17011		0.62	4.8E-01	4504850	NT	Homo sapiens eukaryotic translation initiation factor 4 gamma, 1 (EIF4G1), mRNA
5698	18324	30827	8.6	4.8E-01	J02987.1	NT	alpha2a09.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1525144 3'
6790	19381		4.22	4.8E-01	AA659878.1	EST_HUMAN	Homo sapiens potassium channel, subfamily K, member 5 (TASK-2) (KCNK5) mRNA, and translated products
7357	19883		1.85	4.8E-01	5031650	NT	Saccharomyces cerevisiae sporulation protein (SPO11) gene required for meiotic recombination, complete cds
7662	20174	33061	0.87	4.8E-01	AL163209.2	NT	Homo sapiens reproduction 8 (D8S2298E) mRNA
7738	20246	33138	3.72	4.8E-01	AL161492.2	NT	Homo sapiens chromosome 21 segment HS21C009
7738	20246	33139	3.72	4.8E-01	AL161492.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7846	20368	33291	1.36	4.8E-01	AB20744.1	EST_HUMAN	w77f10.y6 Soares breast 2N6HBst Homo sapiens cDNA clone IMAGE:154795 5' similar to contains element
9168	21746		1.13	4.8E-01	BE155148.1	EST_HUMAN	MER6 repetitive element ;
9921	22417		0.58	4.8E-01	BF568633.1	EST_HUMAN	PM1-HT0350-201269-004-604 HT0350 Homo sapiens cDNA
10607	23141		2.02	4.8E-01	X83502.1	NT	602184267F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300048 5'
11788	24170		1.29	4.8E-01	AL163227.2	NT	S.cerevisiae ORFs from chromosome X
12016	24842		3.04	4.8E-01	AF227565.1	NT	Homo sapiens chromosome 21 segment HS21C027
12646	24895		3.36	4.8E-01	AJ132894.1	NT	Trypanosoma cruzi transposon VIP II SIRE repeat region
6638	19234	32036	8.72	4.7E-01	BF217173.1	EST_HUMAN	Chlamydomonas reinhardtii cop gene, exons 1-8
7107	19447	32263	0.78	4.7E-01	AI204374.1	EST_HUMAN	601883880F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095387 5'
7806	20349	33257	0.52	4.7E-01	T11414.1	EST_HUMAN	q172a09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755544 3'
9005	21542	34473	0.5	4.7E-01	T11414.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
10487	22961	35972	0.79	4.7E-01	AW087791.1	EST_HUMAN	hbc811 Human pancreatic islet Homo sapiens cDNA clone hbc811 5'end
10727	23253		4.94	4.7E-01	AF102673.1	NT	Rattus norvegicus Spermine binding protein (Sbp), mRNA
10963	23478	36503	2.19	4.7E-01	U41089.1	EST_HUMAN	xb69e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581560 3'
11163	23670	36715	11.61	4.7E-01	BF528658.1	EST_HUMAN	Influenza A virus isolate hk51687 hemagglutinin (HA) gene, partial cds
11254	23784	36840	2.89	4.7E-01	AW889448.1	EST_HUMAN	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
11904	24243		1.92	4.7E-01	BE887763.1	EST_HUMAN	Human collagen alpha2(XI) (COL11A2) gene, exons 6 through 16, and partial cds
12036	24325		1.33	4.7E-01	AW341561.1	EST_HUMAN	RC6-NT0029-240400-011-E08 NT0029 Homo sapiens cDNA
12666	24736		1.38	4.7E-01	AP000007.1	NT	601511333F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912488 5'
3797	16397	28862	2.23	4.6E-01	AW818638.1	EST_HUMAN	h411c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2809198 3'
3806	16406	28870	1.68	4.6E-01	BF693300.1	EST_HUMAN	Pyrococcus horikoshii OT3 genomic DNA, 1485001-1738505 nt. position (7/7)
3808	16406	28871	1.68	4.6E-01	BF693300.1	EST_HUMAN	RC1-ST0278-040400-018-b06 ST0278 Homo sapiens cDNA
5323	17885		1.03	4.6E-01	M11267.1	NT	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
5429	17886	30390	22.08	4.6E-01	AL163248.2	NT	602081103F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245481 5'
							Bovine steroid 21-hydroxylase gene (P-450-c21) gene, complete cds
							Homo sapiens chromosome 21 segment HS21C048
							AMILORIDE-SENSITIVE SODIUM CHANNEL GAMMA-SUBUNIT (EPITHELIAL NA+ CHANNEL GAMMA SUBUNIT) (GAMMA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 GAMMA SUBUNIT) (SCN3G) (GAMMA NACH)
5440	17895	30400	1.37	4.6E-01	PS11170	SWISSPROT	
5612	18241	30690	1.12	4.6E-01	BF313593.1	EST_HUMAN	601800234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5612	18241	30691	1.12	4.6E-01	BF313593.1	EST_HUMAN	601800234F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129472 5'
5663	18280	30768	3.27	4.6E-01	Q80643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5663	18280	30769	3.27	4.6E-01	Q80643	SWISSPROT	INTERFERON REGULATORY FACTOR 3 (IRF-3)
5735	18361	31067	2.39	4.6E-01	BE734781.1	EST_HUMAN	601568756F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843637 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5748	18374	31082	4.22	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5748	18374	31083	4.22	4.6E-01	A1247679.1	EST_HUMAN	qh59h02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849011 3' similar to TR:O15338 O15338 BUTYROPHILIN.;
5756	18382	31094	1.4	4.6E-01	P20050	SWISSPROT	MEIOSIS SPECIFIC PROTEIN HOP1
5828	18452		1.05	4.6E-01	AF212124.1	NT	Andis schwartz cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product
5907	18529		0.86	4.6E-01	B6917247.1	EST_HUMAN	PMO-BN0260-120600-001-F07 BN0260 Homo sapiens cDNA
6058	18675	31417	0.75	4.6E-01	D26215.1	NT	Unidentified soil bacteria 16S rRNA gene encoding 16S ribosomal RNA
6404	19007	31788	1.05	4.6E-01	AE000894.1	NT	Methanobacterium thermoautotrophicum from bases 1165761 to 1176238 (section 100 of 148) of the complete genome
6865	19599	32429	1.36	4.6E-01	U62332.1	NT	Emertella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
6865	19599	32430	1.36	4.6E-01	U62332.1	NT	Emertella nidulans NEMPA (nempA) gene, mitochondrial gene encoding putative mitochondrial protein, complete cds
7712	20221	33108	0.86	4.6E-01	AA493577.1	EST_HUMAN	nh04h05.s1 NCI_COAP_Thy1 Homo sapiens cDNA clone IMAGE:943353 similar to contains Alu repetitive element; contains element L1 repetitive element;
8282	20803	33721	13.23	4.6E-01	BF697396.1	EST_HUMAN	602130953F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4287628 5'
9225	21741	34684	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B)(ANPRB)(GC-B)(GUANYLATE CYCLASE)
9225	21741	34685	1.04	4.6E-01	P55202	SWISSPROT	ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B)(ANPRB)(GC-B)(GUANYLATE CYCLASE)
9583	22083	35046	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9583	22083	35047	0.55	4.6E-01	AF162283.1	NT	Glycine max acetyl-CoA carboxylase (accB-1) gene, complete cds; nuclear gene for chloroplast product
9886	22383	35358	2.63	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares NSF_F8_9W_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:2370786 3'
9886	22383	35359	2.63	4.6E-01	A1915634.1	EST_HUMAN	wg73e12.x1 Soares NSF_F8_9W_OT_PA_P S1 Homo sapiens cDNA clone IMAGE:2370786 3'
10870	23391		3.09	4.6E-01	P98163	SWISSPROT	PUTATIVE VITELLOGENIN RECEPTOR PRECURSOR (YL)
10879	23400	36416	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
10879	23400	36417	4.13	4.6E-01	BE185449.1	EST_HUMAN	IL5-HT0730-100500-075-g05 HT0730 Homo sapiens cDNA
11346	23044	36054	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
11346	23044	36055	5.52	4.6E-01	AF019369.1	NT	Human thiopurine methyltransferase (TPMT) gene, exon 10 and complete cds
12654	24726		1.26	4.6E-01	M22360.1	NT	Rat plasma proteinase inhibitor alpha-1-inhibitor III group 3 variants 6J, 12J, 13J, and 17J mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1954	14538	27084	1.69	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
1954	14538	27085	1.69	4.5E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2895	15512	27982	4.77	4.5E-01	AA877088.1	EST_HUMAN	Zf55002.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:454179 3'
3346	15956	28431	0.64	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3346	15956	28432	0.64	4.5E-01	AW083761.1	EST_HUMAN	xc25c06.x1 NCI_CGAP_Co19 Homo sapiens cDNA clone IMAGE:2585290 3' similar to gb:L07807 DYNAMIN-1 (HUMAN);
3359	15967	28444	5.18	4.5E-01	Q05783	SWISSPROT	BASEMENT MEMBRANE SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
3424	16032	28512	1.15	4.5E-01	AF126378.1	NT	PRECURSOR (HSPG) (PERLECAN) (PLC)
4100	16694		1.35	4.5E-01	Q28247	SWISSPROT	Mus musculus DNA polymerase epsilon catalytic subunit (Pde) gene, exons 2 through 12
4149	16741	28185	0.73	4.5E-01	AJ708908.1	EST_HUMAN	COLLAGEN ALPHA 5(IV) CHAIN
4255	18015		4.04	4.5E-01	AW873495.1	EST_HUMAN	as96c09.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2353480 3'
5078	17851	30092	1.16	4.5E-01	BE963445.2	EST_HUMAN	h60g02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3041810 3'
5427	17984		26.74	4.5E-01	AF060195.1	NT	601657225R1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866023 3'
5737	18383	31070	1.37	4.5E-01	AW608814.1	EST_HUMAN	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds
6719	19313		1.36	4.5E-01	Q00956	SWISSPROT	QV2-PT0012-140100-031-c09 PT0012 Homo sapiens cDNA
7443	19987	32834	1.69	4.5E-01	M37036.1	NT	COAT PROTEIN
							Rat nuclear proteins B23.1 and B23.2
7604	20117	32993	2.53	4.5E-01	A1858849.1	EST_HUMAN	w32c02.x1 NCI_CGAP_U01 Homo sapiens cDNA clone IMAGE:2426618 3' similar to TR:Q92923 Q92923
8249	20790		0.97	4.5E-01	M32861.1	NT	SWISNF COMPLEX 170 KDA SUBUNIT ;
8342	20883	33804	4.02	4.5E-01	A1648596.1	EST_HUMAN	D.melanogaster Shaw2 protein mRNA, complete cds
							ts58g11.x1 NCI_CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292644 3'
							POLY-BETA-HYDROXYBUTYRATE POLYMERASE (POLY(3-HYDROXYBUTYRATE) POLYMERASE) (PHB POLYMERASE) (PHB SYNTHASE) (POLY(3-HYDROXYALKANOATE) POLYMERASE) (PHA POLYMERASE) (PHA SYNTHASE) (POLYHYDROXYALKANOIC ACID SYNTHASE)
8494	21033	33954	0.69	4.5E-01	Q52728	SWISSPROT	Homo sapiens hypothetical protein DKFZp547G183 (DKFZp547G183), mRNA
8716	21255		1.74	4.5E-01	11444786	NT	Escherichia coli K-12 MG1655 section 108 of 400 of the complete genome
8929	21467	34385	0.69	4.5E-01	AE000218.1	NT	Bombayx mori nuclear polyhedrosis virus, complete genome
9853	22351		1.02	4.5E-01	9630816	NT	EST02831 Fetal brain, Stratagene (cat#36206) Homo sapiens cDNA clone HFBCY17
10389	22883	35877	23.95	4.5E-01	M86008.1	EST_HUMAN	EST02831 Fetal brain, Stratagene (cat#36206) Homo sapiens cDNA clone HFBCY17
10389	22883	35878	23.95	4.5E-01	M86008.1	EST_HUMAN	xo14h01.x1 NCI_CGAP_U03 Homo sapiens cDNA clone IMAGE:2703985 3' similar to SW:INT6_MOUSE
10744	23268	36285	3.01	4.5E-01	AW591271.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 (I) ;
11131	23639		1.9	4.5E-01	AV719382.1	EST_HUMAN	AV719382 GLC Homo sapiens cDNA clone GLCCED12 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11376	23826	36890	1.68	4.5E-01	BE068472.1	EST_HUMAN	RC3-BT0333-160300-016-a03 BT0333 Homo sapiens cDNA
11671	25070		3.3	4.5E-01	BE871461.1	EST_HUMAN	601449201F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852961 5'
12370	24540		2.13	4.5E-01	BF337531.1	EST_HUMAN	602035275F1 NCI_CGAP_Bm84 Homo sapiens cDNA clone IMAGE:4183280 5'
12442	24578		6.25	4.5E-01	11422096	NT	Homo sapiens testis-specific kinase 2 (TESK2), mRNA
2081	14682		1.39	4.4E-01	6880503	NT	Mus musculus integral membrane-associated protein 1 (limap1), mRNA
2432	14999	27572	3.26	4.4E-01	P49765	SWISSPROT	VASCULAR ENDOTHELIAL GROWTH FACTOR B PRECURSOR (VEGF-B) (VEGF RELATED FACTOR)
3357	15965	28442	1.27	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3357	15965	28443	1.27	4.4E-01	AF058790.1	NT	Rattus norvegicus SynGAP-b mRNA, complete cds
3361	15969	28446	2.31	4.4E-01	BF056726.1	EST_HUMAN	7191d02.Y1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3393795 5'
4318	16904		1.28	4.4E-01	BE378707.1	EST_HUMAN	601237139F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609393 5'
5134	17706		2.07	4.4E-01	BE141396.1	EST_HUMAN	MRO-HT0078-131289-007-g05 HT0078 Homo sapiens cDNA
5277	17839	30265	0.94	4.4E-01	U61154.1	NT	Buzura suppressaria nucleopolydnavirus ecdysteroid UDP-glucosyltransferase (egt) gene, complete cds
5417	17974		0.9	4.4E-01	AW814885.1	EST_HUMAN	MR1-ST0208-120400-022-g07 ST0208 Homo sapiens cDNA
5613	18242	30692	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5613	18242	30693	4.06	4.4E-01	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
5867	18489	31215	1.72	4.4E-01	S65019.1	NT	mucin [rats, Sprague-Dawley, sulfur-dioxide-treated tracheal epithelium, mRNA Partial, 390 nt]
5883	18505	31231	1.9	4.4E-01	AV720408.1	EST_HUMAN	AV720408 GLC Homo sapiens cDNA clone GLCSC12 5'
6108	18724	31476	1.53	4.4E-01	A198413.1	EST_HUMAN	UNKNOWN PROTEIN ;
6108	18724	31477	1.53	4.4E-01	A198413.1	EST_HUMAN	UNKNOWN PROTEIN ;
6387	18990	31771	1.69	4.4E-01	AW080795.1	EST_HUMAN	xc27a08.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2585510 3' similar to TR:O95154 O85154
6470	19071		1.02	4.4E-01	AA776132.1	EST_HUMAN	ae85d11.s1 Stratagene echizo brain S11 Homo sapiens cDNA clone IMAGE:970965 3' similar to gb:M18038
7429	19953	32818	0.89	4.4E-01	AE000571.1	NT	Helicobacter pylori 26695 section 49 of 134 of the complete genome
7782	20325		10.05	4.4E-01	Z11679.1	NT	S tuberosum mRNA for induced stolon tip protein (partial)
8698	21237	34160	1.01	4.4E-01	AA056427.1	EST_HUMAN	268a03.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:509836 3'
9078	21614	34549	0.78	4.4E-01	AF112540.1	NT	HIV-1 isolate 08107v6 from USA, envelope glycoprotein (env) gene, partial cds
9111	21647	34587	0.56	4.4E-01	AW612578.1	EST_HUMAN	rh05c08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2854222 3' similar to SW:MSH6_HUMAN_P52701 DNA MISMATCH REPAIR PROTEIN MSH6 ;
9214	21731	34674	1.13	4.4E-01	O62836	SWISSPROT	ZINC FINGER X-CHROMOSOMAL PROTEIN

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9872	22369	35347	1.89	4.4E-01	AI288650.1	EST_HUMAN	qo38f09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910921 3'
9873	22370		2.12	4.4E-01	P28922	SWISSPROT	GLYCOPROTEIN B PRECURSOR (GLYCOPROTEIN 14)
10009	22504	35495	4.51	4.4E-01	P33590	SWISSPROT	TYROSINE-PROTEIN KINASE RECEPTOR TIE-1 PRECURSOR
10276	22771	35759	1.43	4.4E-01	S78404.1	NT	beta-HKA-H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
10278	22771	35760	1.43	4.4E-01	S78404.1	NT	beta-HKA-H-K-ATPase beta-subunit [rats, Genomic, 8983 nt, segment 2 of 2]
11939	24271	31016	4.88	4.4E-01	6877874	NT	Mus musculus sodium channel, type X, alpha polypeptide (Scn10a), mRNA
11952	25000		14.98	4.4E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12517	24635		1.5	4.4E-01	P54725	SWISSPROT	UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG A (HHR23A)
436	13069	25564	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
436	13069	25565	1.77	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
3096	15711	28182	0.81	4.3E-01	AW999477.1	EST_HUMAN	MRO-BN0070-270300-008-g04 BN0070 Homo sapiens cDNA
4231	16819	29268	1.21	4.3E-01	J00306.1	NT	Human somatostatin 1 gene and flanks
4495	13069	25564	3.96	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
4495	13069	25565	3.96	4.3E-01	AF155218.1	NT	Callithrix jacchus MW/LW opsin gene, upstream flanking region
5567	18198	30845	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
5567	18198	30846	0.76	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
6049	18668	31407	1.34	4.3E-01	BE181655.1	EST_HUMAN	QV1-HT0638-070500-191-408 HT0638 Homo sapiens cDNA
6065	18682	31424	2.06	4.3E-01	AF179825.1	NT	Salmir sclereus olfactory receptor (SSC186) gene, partial cds
6909	19400	32215	4.28	4.3E-01	AIJ001878.1	NT	Coturnix coturnix japonica ifnG gene
6949	19526		0.78	4.3E-01	Q33367	SWISSPROT	DNA GYRASE SUBUNIT B
7458	19980		1.78	4.3E-01	BF348001.1	EST_HUMAN	602023134F1 NCI_CGAP_Bn87 Homo sapiens cDNA clone IMAGE:4158296 5'
8368	20906		2.66	4.3E-01	U97040.1	NT	Methanococcus voltae flagellar-related protein C1 (flaC-fla) genes, complete cds
9179	21756	34702	0.7	4.3E-01	Y14604.1	NT	Erwinia amylovora rcsV gene
9842	22142	35109	2.63	4.3E-01	AW630048.1	EST_HUMAN	h174e10.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2868554 5'
9842	22142	35110	2.63	4.3E-01	AW630048.1	EST_HUMAN	h174e10.y1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2868554 5'
10128	22623	35814	0.57	4.3E-01	AW170559.1	EST_HUMAN	xn63005.x1 Soares_NHCoC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698400 3' similar to
10811	19616	32451	2.52	4.3E-01	AF075629.1	NT	TR-000189 O00189 MU-ADAPTIN-RELATED PROTEIN 2
11588	24031	37101	1.54	4.3E-01	AI874332.1	EST_HUMAN	Equus caballus microsatellite LEX027
11632	18198	30845	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
11832	18198	30846	1.55	4.3E-01	P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
12616	24696		2.81	4.3E-01	AIJ003022.1	NT	Streptomyces coelicolor whiH gene
1402	15440	26524	1.39	4.2E-01	Q39102	SWISSPROT	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR
1991	14573		1.04	4.2E-01	AA761653.1	EST_HUMAN	nz24a09.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288696 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2066	14646		1.37	4.2E-01	AF258325.1	NT	Plasmodium falciparum multidrug resistance protein Pgh1 gene, complete cds
3669	16270	28738	4.91	4.2E-01	AE003947.1	NT	Xylella fastidiosa, section 93 of 229 of the complete genome
3699	16300	28768	1	4.2E-01	AI280338.1	EST_HUMAN	q194b01.x1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:1876945 3'
3773	18014		0.6	4.2E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40468
3948	16548	29014	0.73	4.2E-01	AW835527.1	EST_HUMAN	QV0-L T0015-180200-127-h01 LT0015 Homo sapiens cDNA
4054	16651	29118	0.98	4.2E-01	Q04886	SWISSPROT	SOX-8 PROTEIN
4907	17385	29835	4.3	4.2E-01	AA534093.1	EST_HUMAN	np98h01.s1 NCL_CGAP_P110 Homo sapiens cDNA clone IMAGE:997777 similar to gb.M33600 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN (HUMAN);
4895	17470	29926	4.04	4.2E-01	R13467.1	EST_HUMAN	yf77e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28278 5'
5232	17796		3.77	4.2E-01	U50871.1	NT	Human familial Alzheimer's disease (S.TM2) gene, complete cds
5891	18514	31241	1.52	4.2E-01	BF242055.1	EST_HUMAN	601879721F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4108493 5'
5953	18575	31309	2.16	4.2E-01	AW854162.1	EST_HUMAN	RC3-CT0254-060400-028-g04 CT0254 Homo sapiens cDNA
6352	18957	31736	1.06	4.2E-01	AL163247.2	NT	Homo sapiens chromosome 21 segment1:HS21C047
7031	19565	32392	10.28	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7031	19565	32393	10.29	4.2E-01	AU158472.1	EST_HUMAN	AU158472 PLACE2 Homo sapiens cDNA clone PLACE2000470 3'
7082	24776	32492	1.97	4.2E-01	S82504.1	NT	Brcat1=breast cancer gene [rats, WF, spleen, Genomic, 419 nt, segment 2 of 2]
7150	19683	32524	5.81	4.2E-01	AL161547.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 47
7934	20476	33385	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
7934	20476	33386	2.61	4.2E-01	AW957448.1	EST_HUMAN	EST369413 MAGE resequences, MAGE Homo sapiens cDNA
8148	20689	33602	0.55	4.2E-01	4758039	NT	Homo sapiens cytochrome c oxidase subunit VIc (COX6C), nuclear gene encoding mitochondrial protein, mRNA
9235	21761	34706	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9235	21761	34707	0.52	4.2E-01	U57431.1	NT	Human cytomegalovirus early phosphoprotein p50 mRNA, complete cds
9880	22377		0.81	4.2E-01	AA705007.1	EST_HUMAN	z95f01.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:462649 3'
10083	22578	35571	0.5	4.2E-01	AF181854.1	NT	Lassa virus strain 803213 glycoprotein precursor and nucleoprotein genes, complete cds
10390	22884	35879	1.35	4.2E-01	AW863686.1	EST_HUMAN	MR3-SN0010-280300-103-h07 SN0010 Homo sapiens cDNA
10921	23440	36461	3.69	4.2E-01	AB023489.1	NT	Oryzias latipes OIGC7 mRNA for membrane guanylyl cyclase, complete cds
11273	23726	36780	2.65	4.2E-01	BE968485.2	EST_HUMAN	601660352R1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906085 3'
12561	24661		1.49	4.2E-01	AV731815.1	EST_HUMAN	AV731815 HTF Homo sapiens cDNA clone HTFBH105 5'
1133	13736	26245	1.59	4.1E-01	AI905481.1	EST_HUMAN	RC-BT091-210189-142 BT091 Homo sapiens cDNA
1142	13745	26254	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
1142	13745	26255	1.54	4.1E-01	AV705243.1	EST_HUMAN	AV705243 ADB Homo sapiens cDNA clone ADBAHF08 5'
2735	15290	27858	1.58	4.1E-01	7705283	NT	Homo sapiens anaphase-promoting complex subunit 7 (APC7), mRNA
2967	15582	28061	2.11	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36

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Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2867	15582	28062	2.11	4.1E-01	AL161536.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
3342	15552	28428	0.66	4.1E-01	AA06344.1	EST_HUMAN	q94b08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1505943 3'
3839	16438	28599	0.56	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGE Homo sapiens cDNA
3839	16438	28800	0.58	4.1E-01	AW961292.1	EST_HUMAN	EST373364 MAGE resequences, MAGE Homo sapiens cDNA
4361	16948	28390	2.82	4.1E-01	AJ249207.1	NT	Rhodococcus sp. AD45 isoG, isoH, isoI, isoJ, isoK, isoL, isoM, isoN, isoO, isoP, isoQ, isoR, isoS, isoT, isoU, isoV, isoW, isoX, isoY, isoZ, isoAA, isoAB, isoAC, isoAD, isoAE, isoAF, isoAG, isoAH, isoAI, isoAJ, isoAK, isoAL, isoAM, isoAN, isoAO, isoAP, isoAQ, isoAR, isoAS, isoAT, isoAU, isoAV, isoAW, isoAX, isoAY, isoAZ, isoBA, isoBB, isoBC, isoBD, isoBE, isoBF, isoBG, isoBH, isoBI, isoBJ, isoBK, isoBL, isoBM, isoBN, isoBO, isoBP, isoBQ, isoBR, isoBS, isoBT, isoBU, isoBV, isoBW, isoBX, isoBY, isoBZ, isoCA, isoCB, isoCC, isoCD, isoCE, isoCF, isoCG, isoCH, isoCI, isoCJ, isoCK, isoCL, isoCM, isoCN, isoCO, isoCP, isoCQ, isoCR, isoCS, isoCT, isoCU, isoCV, isoCW, isoCX, isoCY, isoCZ, isoDA, isoDB, isoDC, isoDD, isoDE, isoDF, isoDG, isoDH, isoDI, isoDJ, isoDK, isoDL, isoDM, isoDN, isoDO, isoDP, isoDQ, isoDR, isoDS, isoDT, isoDU, isoDV, isoDW, isoDX, isoDY, isoDZ, isoEA, isoEB, isoEC, isoED, isoEE, isoEF, isoEG, isoEH, isoEI, isoEJ, isoEK, isoEL, isoEM, isoEN, isoEO, isoEP, isoEQ, isoER, isoES, isoET, isoEU, isoEV, isoEW, isoEX, isoEY, isoEZ, isoFA, isoFB, isoFC, isoFD, isoFE, isoFF, isoFG, isoFH, isoFI, isoFJ, isoFK, isoFL, isoFM, isoFN, isoFO, isoFP, isoFQ, isoFR, isoFS, isoFT, isoFU, isoFV, isoFW, isoFX, isoFY, isoFZ, isoGA, isoGB, isoGC, isoGD, isoGE, isoGF, isoGG, isoGH, isoGI, isoGJ, isoGK, isoGL, isoGM, isoGN, isoGO, isoGP, isoGQ, isoGR, isoGS, isoGT, isoGU, isoGV, isoGW, isoGX, isoGY, isoGZ, isoHA, isoHB, isoHC, isoHD, isoHE, isoHF, isoHG, isoHH, isoHI, isoHJ, isoHK, isoHL, isoHM, isoHN, isoHO, isoHP, isoHQ, isoHR, isoHS, isoHT, isoHU, isoHV, isoHW, isoHX, isoHY, isoHZ, isoIA, isoIB, isoIC, isoID, isoIE, isoIF, isoIG, isoIH, isoII, isoIJ, isoIK, isoIL, isoIM, isoIN, isoIO, isoIP, isoIQ, isoIR, isoIS, isoIT, isoIU, isoIV, isoIW, isoIX, isoIY, isoIZ, isoJA, isoJB, isoJC, isoJD, isoJE, isoJF, isoJG, isoJH, isoJI, isoJJ, isoJK, isoJL, isoJM, isoJN, isoJO, isoJP, isoJQ, isoJR, isoJS, isoJT, isoJU, isoJV, isoJW, isoJX, isoJY, isoJZ, isoKA, isoKB, isoKC, isoKD, isoKE, isoKF, isoKG, isoKH, isoKI, isoKJ, isoKK, isoKL, isoKM, isoKN, isoKO, isoKP, isoKQ, isoKR, isoKS, isoKT, isoKU, isoKV, isoKW, isoKX, isoKY, isoKZ, isoLA, isoLB, isoLC, isoLD, isoLE, isoLF, isoLG, isoLH, isoLI, isoLJ, isoLK, isoLL, isoLM, isoLN, isoLO, isoLP, isoLQ, isoLR, isoLS, isoLT, isoLU, isoLV, isoLW, isoLX, isoLY, isoLZ, isoMA, isoMB, isoMC, isoMD, isoME, isoMF, isoMG, isoMH, isoMI, isoMJ, isoMK, isoML, isoMN, isoMO, isoMP, isoMQ, isoMR, isoMS, isoMT, isoMU, isoMV, isoMW, isoMX, isoMY, isoMZ, isoNA, isoNB, isoNC, isoND, isoNE, isoNF, isoNG, isoNH, isoNI, isoNJ, isoNK, isoNL, isoNM, isoNO, isoNP, isoNQ, isoNR, isoNS, isoNT, isoNU, isoNV, isoNW, isoNX, isoNY, isoNZ, isoOA, isoOB, isoOC, isoOD, isoOE, isoOF, isoOG, isoOH, isoOI, isoOJ, isoOK, isoOL, isoOM, isoON, isoOO, isoOP, isoOQ, isoOR, isoOS, isoOT, isoOU, isoOV, isoOW, isoOX, isoOY, isoOZ, isoPA, isoPB, isoPC, isoPD, isoPE, isoPF, isoPG, isoPH, isoPI, isoPJ, isoPK, isoPL, isoPM, isoPN, isoPO, isoPP, isoPQ, isoPR, isoPS, isoPT, isoPU, isoPV, isoPW, isoPX, isoPY, isoPZ, isoQA, isoQB, isoQC, isoQD, isoQE, isoQF, isoQG, isoQH, isoQI, isoQJ, isoQK, isoQL, isoQM, isoQN, isoQO, isoQP, isoQQ, isoQR, isoQS, isoQT, isoQU, isoQV, isoQW, isoQX, isoQY, isoQZ, isoRA, isoRB, isoRC, isoRD, isoRE, isoRF, isoRG, isoRH, isoRI, isoRJ, isoRK, isoRL, isoRM, isoRN, isoRO, isoRP, isoRQ, isoRR, isoRS, isoRT, isoRU, isoRV, isoRW, isoRX, isoRY, isoRZ, isoSA, isoSB, isoSC, isoSD, isoSE, isoSF, isoSG, isoSH, isoSI, isoSJ, isoSK, isoSL, isoSM, isoSN, isoSO, isoSP, isoSQ, isoSR, isoSS, isoST, isoSU, isoSV, isoSW, isoSX, isoSY, isoSZ, isoTA, isoTB, isoTC, isoTD, isoTE, isoTF, isoTG, isoTH, isoTI, isoTJ, isoTK, isoTL, isoTM, isoTN, isoTO, isoTP, isoTQ, isoTR, isoTS, isoTT, isoTU, isoTV, isoTW, isoTX, isoTY, isoTZ, isoUA, isoUB, isoUC, isoUD, isoUE, isoUF, isoUG, isoUH, isoUI, isoUJ, isoUK, isoUL, isoUM, isoUN, isoUO, isoUP, isoUQ, isoUR, isoUS, isoUT, isoUU, isoUV, isoUW, isoUX, isoUY, isoUZ, isoVA, isoVB, isoVC, isoVD, isoVE, isoVF, isoVG, isoVH, isoVI, isoVJ, isoVK, isoVL, isoVM, isoVN, isoVO, isoVP, isoVQ, isoVR, isoVS, isoVT, isoVU, isoVV, isoVW, isoVX, isoVY, isoVZ, isoWA, isoWB, isoWC, isoWD, isoWE, isoWF, isoWG, isoWH, isoWI, isoWJ, isoWK, isoWL, isoWM, isoWN, isoWO, isoWP, isoWQ, isoWR, isoWS, isoWT, isoWU, isoWV, isoWW, isoWX, isoWY, isoWZ, isoXA, isoXB, isoXC, isoXD, isoXE, isoXF, isoXG, isoXH, isoXI, isoXJ, isoXK, isoXL, isoXM, isoXN, isoXO, isoXP, isoXQ, isoXR, isoXS, isoXT, isoXU, isoXV, isoXW, isoXX, isoXY, isoXZ, isoYA, isoYB, isoYC, isoYD, isoYE, isoYF, isoYG, isoYH, isoYI, isoYJ, isoYK, isoYL, isoYM, isoYN, isoYO, isoYP, isoYQ, isoYR, isoYS, isoYT, isoYU, isoYV, isoYW, isoYX, isoYY, isoYZ, isoZA, isoZB, isoZC, isoZD, isoZE, isoZF, isoZG, isoZH, isoZI, isoZJ, isoZK, isoZL, isoZM, isoZN, isoZO, isoZP, isoZQ, isoZR, isoZS, isoZT, isoZU, isoZV, isoZW, isoZX, isoZY, isoZZ
9019	21556	34484	1.26	4.1E-01	675552.1	NT	Mus musculus signaling intermediate in Tcd pathway-evolutionarily conserved (Sitpec-pending), mRNA
9484	21941		0.61	4.1E-01	AF160597.1	NT	Voelavo gymnocaudus Vgym560 cytochrome b (cytb) gene, complete cds; mitochondrial gene for mitochondrial product
10164	22659		1.28	4.1E-01	AL139076.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 3/6
10310	22804	35786	0.79	4.1E-01	AV649579.1	EST_HUMAN	AV649579 GLC Homo sapiens cDNA clone GI CBVD12 3'
10401	22895	35890	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10401	22895	35891	0.51	4.1E-01	P18584	SWISSPROT	PROBABLE SERINE PROTEASE DO-LIKE PRECURSOR (59 KDA IMMUNOGENIC PROTEIN) (SK59)
10471	22865		2.29	4.1E-01	BF349382.1	EST_HUMAN	CM2-HT0137-200999-010-608 HT0137 Homo sapiens cDNA
10719	23247	36262	45.22	4.1E-01	X58700.1	NT	Zea mays ZMPMS2 gene for 19 kDa zein protein
11270	23008	36015	3.57	4.1E-01	Q08470	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUK1) (HBK1)
12290	25049		2.6	4.1E-01	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
147	15408		4.55	4.0E-01	AW847123.1	EST_HUMAN	RC2-CT0201-290999-012-d10 CT0201 Homo sapiens cDNA
1077	13681	26191	0.82	4.0E-01	8404656	NT	Laqueus rubellus mitochondrion, complete genome
1384	13978	26505	1.51	4.0E-01	AF203478.1	NT	Drosophila melanogaster Dalmation (dmt) mRNA, complete cds
1532	14124		4.1	4.0E-01	6679258	NT	Mus musculus platelet derived growth factor receptor, beta polypeptide (Pdgfrb), mRNA
2049	15456	27200	1.22	4.0E-01	Z66933.1	NT	Acrobolus immerus masc2 gene
2049	15456	27201	1.22	4.0E-01	Z66933.1	NT	Acrobolus immerus masc2 gene
2204	14780	27352	17.82	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2204	14780	27353	17.82	4.0E-01	AE001931.1	NT	Deinococcus radiodurans R1 section 68 of 229 of the complete chromosome 1
2831	12811	25299	1.45	4.0E-01	6678490	NT	Mus musculus ubiquitin-protein ligase u3 component n-recoglin (Ubr1), mRNA
2895	15611	28090	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
2965	15611	28091	1.23	4.0E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3758	16359	28529	2.17	4.0E-01	AF068803.1	NT	Streptococcus pneumoniae YN1C (y1C), Y1D (y1D), penicillin-binding protein 2x (pbp2x), and undecaprenyl-phosphate-UDP-MurNAc-pentapeptide phospho-MurNAc-pentapeptide transferase (mraY) genes, complete cds
3899	16498	28960	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
3899	16498	28961	3.04	4.0E-01	AJ277511.1	NT	Ovis aries partial JD2 gene for T cell receptor delta chain (TCRDJ2), exon 1
4942	17517		8.41	4.0E-01	Q31849	SWISSPROT	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST
6069	18886	31429	1.16	4.0E-01	AW970610.1	EST_HUMAN	EST382691 MAGE resequences, MAGK Homo sapiens cDNA
6567	19165	31961	0.87	4.0E-01	P27285	SWISSPROT	STRUCTURAL POLYPEPTIDE (P130) [CONTAINS: COAT PROTEIN C; SPIKE GLYCOPROTEINS E3, E2 AND E1; 8 KD PEPTIDE]
7777	20286	33183	0.72	4.0E-01	P27546	SWISSPROT	MICROTUBULE-ASSOCIATED PROTEIN 4
7869	20411	33317	0.46	4.0E-01	BF092634.1	EST_HUMAN	MR4-TN0110-180900-202-g02 TN0110 Homo sapiens cDNA
7954	20496	33406	0.99	4.0E-01	AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
8336	21474	34394	0.98	4.0E-01	AA323289.1	EST_HUMAN	EST26068 Carabellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
11443	23893		1.65	4.0E-01	BF030262.1	EST_HUMAN	EST1558283FT NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3828092 5'
11568	24015		3.52	4.0E-01	L76080.1	NT	Synechocystis sp. PCC 9413 transposase gene, complete cds
11958	24901		2.5	4.0E-01	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
12518	24636		1.42	4.0E-01	P36049	SWISSPROT	HYPOTHETICAL 49.7 KD PROTEIN IN GIN2-STE3 INTERGENIC REGION
1420	14013	26543	1.98	3.9E-01	AF206618.1	NT	Gorilla gorilla carboxyl-ester lipase (CEL) gene, complete cds
2668	15226	27798	3.8	3.9E-01	AB033019.1	NT	Homo sapiens mRNA for KIAA1193 protein, partial cds
2730	15285	27851	3.79	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
2730	15285	27852	3.79	3.9E-01	X82032.1	NT	H. sapiens B-myb gene
3131	15745	28214	3.95	3.9E-01	AJ225896.1	NT	Sinorhizobium meliloti egj, syrB2, cya3 genes and orf3
4153	16745	29199	1.49	3.9E-01	BF592611.1	EST_HUMAN	7161d01.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3339169 3'
5130	17702	30136	1.96	3.9E-01	BE728667.1	EST_HUMAN	601563948FT NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833699 5'
6080	18706	31454	6.44	3.9E-01	BF208036.1	EST_HUMAN	601862362F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082055 5'
6426	19029	31812	0.66	3.9E-01	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7896	20438	33343	0.78	3.9E-01	U76415.1	NT	Homo sapiens prepro dipeptidyl peptidase 1 (DPP-I) gene, complete cds
8795	21334	34259	0.73	3.9E-01	AW177011.1	EST_HUMAN	CM3-CT0105-170899-004-b08 CT0105 Homo sapiens cDNA
8804	21343		0.7	3.9E-01	BF346634.1	EST_HUMAN	602016944F1 NCI_CGAP_Br67 Homo sapiens cDNA clone IMAGE:4155322 5'
9161	21698	34640	1.24	3.9E-01	AW195888.1	EST_HUMAN	xn86404.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2701351 3' similar to TR:O94821 O94821 KIAA0713 PROTEIN;

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9464	21989	34945	1.42	3.9E-01	A1937337.1	EST_HUMAN	wp76a02.x1 NCI CGAP Bm25 Homo sapiens cDNA clone IMAGE:2467658 3' similar to
9792	22290	35274	3.68	3.9E-01	M19879.1	NT	SW:RFX5_HUMAN P46382 BINDING REGULATORY FACTOR. ;
9856	22354		0.5	3.9E-01	11465620	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
10071	22568	35561	0.69	3.9E-01	D86722.1	NT	Porphyra purpurea mitochondrion, complete genome
10492	22986	35993	0.46	3.9E-01	M18440.1	NT	Nicotiana tabacum mRNA for TATA binding protein (TBP), complete cds
10700	23229		1.82	3.9E-01	AV695974.1	EST_HUMAN	Human beta-B2-crystallin (B2-1) gene, exon 4, partial cds
11729	24977		3.42	3.9E-01	AF304354.1	EST_HUMAN	AV695974 GKC Homo sapiens cDNA clone GKBCQC11 5'
11854	24214		1.42	3.9E-01	Q61670	SWISSPROT	Homo sapiens proteoglycan 3 (PRG3) gene, complete cds
11930	24265	31015	1.56	3.9E-01	AE001811.1	NT	HOMEOBOX PROTEIN HLX1
12389	24551		1.37	3.9E-01	11433335	NT	Thermotoga maritima section 123 of 136 of the complete genome
171	12834		19.28	3.8E-01	7019488	NT	Homo sapiens hypothetical protein FLJ10583 (FLJ10583), mRNA
531	13162		3.11	3.8E-01	AB029281.1	NT	Homo sapiens protein kinase PKNbeta (pknbeta), mRNA
1911	14496		0.99	3.8E-01	AE003870.1	NT	Mus musculus pcm-1 mRNA for pericentriolar material-1, complete cds
2605	15167	27734	1.89	3.8E-01	AF214117.1	NT	Xylella fastidiosa, section 16 of 229 of the complete genome
2681	15473	27791	3.94	3.8E-01	6678002	NT	Arabidopsis thaliana putative c-myc-like transcription factor (MYB3R-3) mRNA, complete cds
3034	15650		0.89	3.8E-01	AJ251057.1	NT	Mus musculus solute carrier family 1, member 6 (Slc1a6), mRNA
3084	15699	28173	2.2	3.8E-01	AF043383.1	NT	Human immunodeficiency virus type 1 complete genome (isolate 98SE-MP1213)
3530	16135	28615	9.83	3.8E-01	AL161518.2	NT	Pleurocetes armigerus aminopeptidase N (ampN) gene, partial cds
3592	16166		0.59	3.8E-01	A1807219.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 30
3609	16196		0.75	3.8E-01	A1807219.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3620	16420	28882	0.94	3.8E-01	BE154080.1	EST_HUMAN	wf38b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2357855 3'
3989	16587	29058	0.8	3.8E-01	6754095	NT	PMO-HT0339-200400-010-G01 HT0339 Homo sapiens cDNA
4138	16730	29163	0.69	3.8E-01	AJ271361.2	NT	Mus musculus general transcription factor II I (Gtf2), mRNA
5271	17833	30259	0.99	3.8E-01	BE544653.1	EST_HUMAN	Takifugu rubripes wt12 (partial), frank1, cfr and frank2 (partial) genes
							601074110F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3460154 5'
							Yr68a11.1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:210428 5' similar to
5412	17969	30378	1.07	3.8E-01	H64927.1	EST_HUMAN	gb M87933 HUMAAALU384 Human carcinoma cell-derived Alu RNA transcript, (rRNA); gb:M86956
5794	18419	31135	1.11	3.8E-01	Q04888	SWISSPROT	EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN (HUMAN); contains Alu repetitive
6481	19082		0.68	3.8E-01	S46825.1	NT	element; contains MIER4 repetitive element ;
6737	19331	32137	5.29	3.8E-01	BE072399.1	EST_HUMAN	TRANSCRIPTION FACTOR SOX-10
							prior protein [mink, Genomic, 2446 nt]
							QV3-BT0537-271299-049-a02 BT0537 Homo sapiens cDNA
							ta54f11.x1 Soares, total, fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2047917 3' similar to
6857	19591	32423	3.97	3.8E-01	A1374601.1	EST_HUMAN	contains Alu repetitive element;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7019	19517	32339	1.33	3.8E-01	AL161513.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 25
7525	20045		4.75	3.8E-01	XG1597.1	NT	M.musculus gene for kallikrein-binding protein
8238	20779	33700	0.49	3.8E-01	M81385.1	NT	Mouse liver receptor homologous protein (LRH-1) mRNA, complete cds
8462	21031	33951	2.34	3.8E-01	AB046851.1	NT	Homo sapiens mRNA for KIAA1631 protein, partial cds
8560	21099	34019	1.14	3.8E-01	11441264	NT	Homo sapiens FOS-like antigen-1 (FOSL1), mRNA
8751	21290	34210	1.12	3.8E-01	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9480	21879		4.03	3.8E-01	T95413.1	EST_HUMAN	ye43h06.r1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:120539 5' similar to contains
11408	23859		3.5	3.8E-01	BE719219.1	EST_HUMAN	Alu repetitive element; contains PTR5 repetitive element;
11541	23889	37060	2.95	3.8E-01	R42550.1	EST_HUMAN	RC0-HT0841-040800-032-512 HT0841 Homo sapiens cDNA
11541	23889	37061	2.95	3.8E-01	R42550.1	EST_HUMAN	Yf82h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
11940	24272		2.81	3.8E-01	AE001124.1	NT	Yf82h11.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:30289 3'
12069	24998		1.75	3.8E-01	U94788.1	NT	Borrelia burgdorferi (section 10 of 70) of the complete genome
12189	24421		1.49	3.8E-01	BE829256.1	EST_HUMAN	Human p53 (TP53) gene, complete cds
12565	24864		2.22	3.8E-01	U78031.1	NT	QV3-ET0063-190700-271-a05 ET0063 Homo sapiens cDNA
12638	24713	30866	1.25	3.8E-01	AF194972.1	NT	Mus musculus apoptosis inhibitor bcl-x (bcl-x) gene, exon 3 and complete cds
2521	15085	27657	15.01	3.7E-01	AB037831.1	NT	Mus musculus developmental control protein mRNA, partial cds
3507	16112	28589	10.94	3.7E-01	AF058336.1	NT	Homo sapiens mRNA for KIAA1410 protein, partial cds
3838	16336	29003	0.88	3.7E-01	AA319492.1	EST_HUMAN	Danio rerio bone morphogenetic protein 4 precursor (BMP4) gene, complete cds
4313	16899	29344	9.19	3.7E-01	A1218707.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4412	16997	28440	1.18	3.7E-01	AW878037.1	EST_HUMAN	EST21715 Adrenal gland tumor Homo sapiens cDNA 5' end
4479	17084	28514	3.13	3.7E-01	AE002408.1	NT	MR3-OT007-080300-104-b02 OT0007 Homo sapiens cDNA
5936	18557	31285	1.27	3.7E-01	AF135187.1	NT	Neisseria meningitidis serogroup B strain MC58 section 50 of 208 of the complete genome
6105	18721	31474	0.94	3.7E-01	AL163278.2	NT	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds
6633	19229	32033	1	3.7E-01	M10806.1	NT	Homo sapiens chromosome 21 segment HS21C078
6651	19247		0.81	3.7E-01	L10353.1	NT	Chicken (White leghorn) delta-1 and delta-2 crystallin genes, complete cds
7197	19728	32579	4.44	3.7E-01	11525643	NT	Mus satoda heptoglobin mRNA, complete cds
8271	20812	33733	1.88	3.7E-01	11436739	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
8271	20812	33734	1.88	3.7E-01	11436739	NT	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8306	20847	33770	0.78	3.7E-01	AA902912.1	EST_HUMAN	Homo sapiens chromosome 12 open reading frame 4 (C12ORF4), mRNA
8129	21864		1.54	3.7E-01	AJ271386.1	NT	ak43b11.s1 NCI_CGAP_L22 Homo sapiens cDNA clone IMAGE:1516701 3'
10074	22569		0.48	3.7E-01	K00691.1	NT	Gallus gallus mRNA for beta-carotene 15,15'-dioxygenase (bcdo gene)
10111	22806	35596	4.17	3.7E-01	A1336411.1	EST_HUMAN	mouse Ig germline alpha membrane exons region
10509	23428	36446	3.47	3.7E-01	AJ297357.1	NT	qt46b07.x1 Soares fetal lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950997 3'
							Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10909	23428	36447	3.47	3.7E-01	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene
11341	23039	36048	4.81	3.7E-01	X04122.1	NT	Bovine mRNA for terminal deoxynucleotidyltransferase (TdT) (EC 2.7.7.31)
11549	23097		1.6	3.7E-01	AA073540.1	EST_HUMAN	oo46d03.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1568221 3' similar to gb:M77698
11603	24046		2.76	3.7E-01	6677678	NT	TRANSCRIPTIONAL REPRESSOR PROTEIN YY1 (HUMAN); Mus musculus retinoblastoma 1 (Rb1), mRNA
11640	24601		1.82	3.7E-01	J04982.1	NT	Human heart/skeletal muscle ATP/ADP translocator (ANT1) gene, complete cds
11821	24191		4.15	3.7E-01	AJ243525.1	NT	Chlamydomonas reinhardtii partial omp1 gene for outer membrane protein 1
11913	24251		4.72	3.7E-01	D86976.1	NT	Human mRNA for KIAA0223 gene, partial cds
12302	24499		2.94	3.7E-01	AL121154.1	EST_HUMAN	DKFp762K075.r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFp762K075 5'
12377	24545	30904	7.01	3.7E-01	Y18000.1	NT	Homo sapiens NF2 gene
282	12838	25424	1.07	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
1033	13643		8.45	3.6E-01	U89241.1	NT	Human mlbp gene, partial cds
1357	13951	26477	4.32	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:24443 5'
1357	13951	26478	4.32	3.6E-01	T80255.1	EST_HUMAN	yd03e05.r1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:24443 5'
1959	14543	27099	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847419 3'
1959	14543	27100	6.39	3.6E-01	AW590184.1	EST_HUMAN	hg33f02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2847419 3'
1994	14576	27138	7.23	3.6E-01	AF216207.1	NT	Mus musculus ribosomal protein S19 (Rps19) gene, complete cds
2098	14877		0.88	3.6E-01	AF056927.1	NT	Rattus norvegicus repeat element associated with the Rasgrf1 gene
2309	14881		1.13	3.6E-01	AB002321.1	NT	Human mRNA for KIAA0323 gene, partial cds
2433	15000		2.49	3.6E-01	X76725.1	NT	P. irregularis (P3804) gene for actin
2528	15092	27665	3.34	3.6E-01	AW812033.1	EST_HUMAN	RC5-ST0171-181099-011-g07 ST0171 Homo sapiens cDNA
2659	15218	27789	1.38	3.6E-01	P24206	SWISSPROT	PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE)
2924	18012		10.38	3.6E-01	AF199485.1	NT	Drosophila melanogaster sugar transporter 3 (sug3) mRNA, complete cds
3516	16121	28500	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
3516	16121	28601	2.16	3.6E-01	X76758.1	NT	H. sapiens serotonin transporter gene, exons 9 and 10
4497	17081	28530	1.97	3.6E-01	BE707883.1	EST_HUMAN	RC1-HT0545-150600-014-b12 HT0545 Homo sapiens cDNA
4850	17428	29680	0.94	3.6E-01	AJ009609.1	NT	Brassica napus mRNA for MAP4K alpha2 protein
4867	17443	28894	0.65	3.6E-01	Y11526.1	NT	Z. mays mRNA for casein kinase II alpha subunit
5153	17723	30154	2.28	3.6E-01	AW338393.1	EST_HUMAN	ha02g04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2872566 3'
5261	17824	30249	0.58	3.6E-01	BE067699.1	EST_HUMAN	MR4-BT0358-270300-005-c10 BT0358 Homo sapiens cDNA
6236	18845	31616	1.16	3.6E-01	P16431	SWISSPROT	FORMATE HYDROGENLYASE SUBUNIT 5 PRECURSOR (FHL SUBUNIT 5) (HYDROGENASE-3 COMPONENT E)

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6604	19201	32006	1.68	3.6E-01	Y10106.1	NT	Homo sapiens PHEX gene
7202	19733		4.57	3.6E-01	R94090.1	EST_HUMAN	y174a08.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:275987 5'
7327	19854	32717	1.73	3.6E-01	AW027174.1	EST_HUMAN	w172c10.x1 Soares_thymus_NHFT Homo sapiens cDNA clone IMAGE:2513010 3' similar to TR:O15117
8166	20707	33623	0.98	3.6E-01	P88167	SWISSPROT	O15117 FYN BINDING PROTEIN. [1];
8221	20762	33678	13.59	3.6E-01	AL161583.2	NT	SCO-SPONDIN
							Arabidopsis thaliana DNA chromosome 4, contig fragment No. 79
8932	21470	34388	3.06	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
8932	21470	34389	3.06	3.6E-01	4504956	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), transcript variant LAMP2A, mRNA
9120	21656	34597	1.32	3.6E-01	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9320	21834	34784	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9320	21834	34785	0.92	3.6E-01	X17550.1	NT	D. melanogaster singed gene, exons 3, 4, 5 & 6
9390	21813		0.54	3.6E-01	X82825.1	NT	C.perfringens plc gene for phospholipase C upstream region containing bent DNA fragment
9777	22275	35260	16.15	3.6E-01	Q53184	SWISSPROT	PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TS
9904	22401	35374	0.53	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
9904	22401	35375	0.53	3.6E-01	AW752901.1	EST_HUMAN	MR2-CT0222-211099-002-b10 CT0222 Homo sapiens cDNA
10823	23344	36359	2.51	3.6E-01	BE902390.1	EST_HUMAN	601676418F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958997 5'
10967	23501	36531	4.15	3.6E-01	AB004293.1	NT	Arabidopsis thaliana mRNA for SigB, complete cds
11065	23577	36615	2.02	3.6E-01	L41687.1	NT	Mus musculus T-cell receptor V region delta 1 chain gene, 5' region
							Methanobacterium thermoautotrophicum from bases 702375 to 714311 (section 62 of 148) of the complete genome
11318	23016	36025	4.07	3.6E-01	AE000858.1	NT	Homo sapiens hHb5 gene for hair keratin, exons 1 to 9
11680	25109		2.45	3.6E-01	Y19210.1	NT	Escherichia coli K-12 MG1655 section 225 of 400 of the complete genome
11768	24159		5.79	3.6E-01	AE000335.1	NT	Mus musculus Emr1 mRNA, complete cds
11923	24258		4.7	3.6E-01	U68888.1	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (vithorax (Drosophila) homolog); translocated to, 10 (AF10), mRNA
12308	24502		2.16	3.6E-01	11432598	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36
120	12781	25273	1.35	3.5E-01	AL161536.2	NT	Mus musculus mannose receptor, C type 2 (Mrc2), mRNA
223	12884	25369	2.67	3.5E-01	6678933	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
706	13327	25814	4.48	3.5E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
754	13373	25868	1.39	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
754	13373	25869	1.39	3.5E-01	7706136	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
812	13430	25935	3.83	3.5E-01	BF128766.1	EST_HUMAN	601811060R1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053951 3'

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1882	14274	26807	1.91	3.5E-01	U35776.1	NT	Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds
2322	14953	27469	1.12	3.5E-01	P06798	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3)
2637	15472	27770	1.92	3.5E-01	AA223252.1	EST_HUMAN	zr08a09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650872 3'
2729	15284		11.8	3.5E-01	U05897.1	NT	Fibroblast succinoglycans S85 endoglycanase E (celE) and endoglycanase D (celD) gene, complete cds
3030	15648	28124	0.57	3.5E-01	AA057691.1	EST_HUMAN	294f03.r1 Stratagene corneal stroma (#937722) Homo sapiens cDNA clone IMAGE:512285 5'
3878	16476		1.27	3.5E-01	AA642138.1	EST_HUMAN	m60403.s1 NCI CGAP_Lym3 Homo sapiens cDNA clone IMAGE:1172357 3'
4349	16936	28377	2.3	3.5E-01	AF071253.1	NT	Danio rerio homeobox protein (hoxb5b) gene, complete cds
5014	17588	30031	0.57	3.5E-01	N81203.1	EST_HUMAN	788IE1 fetal brain cDNA Homo sapiens cDNA clone 788IE1-K similar to R07879, Z40498
5066	17639	30082	4.33	3.5E-01	M18349.1	NT	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5
5537	18169	30584	0.74	3.5E-01	Q96687	SWISSPROT	EARLY E2A DNA-BINDING PROTEIN
5738	18364	31071	1.42	3.5E-01	D42045.1	NT	Human mRNA for KIAA0086 gene, complete cds
6384	18988		0.9	3.5E-01	AW863916.1	EST_HUMAN	PM4-SN0012-030400-001-a11 SN0012 Homo sapiens cDNA
6540	19139	31932	0.75	3.5E-01	AA431833.1	EST_HUMAN	zw79f03.r1 Soares, Iestis_NHT Homo sapiens cDNA clone IMAGE:782429 5' similar to TR:G1066935
6578	19176	31976	0.72	3.5E-01	U37150.1	NT	G1066935 F10F2.1;
6770	19363	32172	0.93	3.5E-01	Q24357	SWISSPROT	Bos taurus peptide methionine sulfoxide reductase (msrA) mRNA, complete cds
7116	19458		3.51	3.5E-01	X98505.1	NT	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST PRECURSOR (G6PD)
8016	20558		2.02	3.5E-01	11448042	NT	S. scrofa mRNA for CD31 protein (PECAM-1)
8019	20561	33462	0.65	3.5E-01	BF358871.1	EST_HUMAN	Homo sapiens tumor protein p53-binding protein, 2 (TP53BP2), mRNA
8403	20943		0.61	3.5E-01	AF051561.1	NT	RC4-ET0024-260600-014-407 ET0024 Homo sapiens cDNA
8857	21396	34319	1.12	3.5E-01	4507610	NT	Rattus norvegicus Na-K-Cl cotransporter (Nkcc1) mRNA, complete cds
8951	22150	35120	1.93	3.5E-01	Q02284	SWISSPROT	Homo sapiens tyrosine kinase non-receptor 1 (TNK1), mRNA
9801	22289	35284	4.91	3.5E-01	Z26825.1	NT	VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (CALCIUM CHANNEL, L TYPE, ALPHA-1 POLYPEPTIDE ISOFORM 5) (BRAIN CALCIUM CHANNEL III) (BIII)
9877	22374	35351	1.14	3.5E-01	BE174784.1	EST_HUMAN	X. laevis gene for albumin including HP1 enhancer
10613	23146	36157	4	3.5E-01	X61084.1	NT	QV2-HT0577-090400-128-c07 HT0577 Homo sapiens cDNA
10902	23422	36440	2.09	3.5E-01	AJ243178.1	NT	C. griseus rhodopsin gene for opsin protein
10902	23422	36441	2.09	3.5E-01	AJ243178.1	NT	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11462	23912	36979	1.93	3.5E-01	N77597.1	EST_HUMAN	Gallus gallus SPARC gene for osteonectin, promoter and exon 1
11532	23980	37050	1.71	3.5E-01	L05145.1	NT	y280112.r1 Soares, multiple sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:290375 5'
						NT	Human glucokinase (GCK) gene, repeat polymorphism

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11778	25112		1.51	3.5E-01	AF297468.1	NT	Schistosoma mansoni strain NMRI chromatin assembly factor 1 small subunit-like protein (RBAP48) mRNA, complete cds
11851	24211		7.56	3.5E-01	X64565.1	NT	B.taurus atbA1 gene for F(0)F(1) ATP synthase alpha-subunit
12014	24313		2.03	3.5E-01	AE001774.1	NT	Thermotoga maritima section 86 of 136 of the complete genome
12209	24433		2.21	3.5E-01	AE001891.1	NT	Thermotoga maritima section 3 of 136 of the complete genome
12843	24950	30825	2.84	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
12843	24950	30826	2.84	3.5E-01	H80814.1	EST_HUMAN	ys64f11.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:218597 5'
736	13356		1.5	3.4E-01	AJ242956.1	NT	Homo sapiens partial N-myc (exon 3), HPV45 L2, HPV45 L1, HPV45 E6, HPV45 E7 and HPV45 E1 genes isolated from IC4 cervical carcinoma cell line
1011	13821	26136	7.82	3.4E-01	Y09798.2	NT	Pseudomonas fluorescens colR, colS genes, of222 and partial inaA gene
1013	13823	26138	8.97	3.4E-01	AW380120.1	EST_HUMAN	QV3-HT0261-241198-019-g10 HT0281 Homo sapiens cDNA
1371	13865	28491	1.86	3.4E-01	Y00554.1	NT	Azotobacter vinelandii nifA gene for NifA protein (positive regulatory element)
2445	15012	27584	2.6	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3032	15648	28128	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3032	15648	28127	0.73	3.4E-01	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3183	15796	28268	0.96	3.4E-01	D90909.1	NT	Synechocystis sp. PCC6803 complete genome, 11/27, 1311235-1430418
3197	15809	28282	6.78	3.4E-01	U83905.1	NT	Canis familiaris rod photoreceptor cGMP-gated channel alpha-subunit (CNGC1) mRNA, complete cds
3387	15998	28473	0.84	3.4E-01	AF034862.1	NT	Homo sapiens pulmonary surfactant protein D, promoter region and exon 1
3584	16188	28671	4.84	3.4E-01	AF106835.1	NT	Methylovorus sp. strain SST putative GrpE (grpE), DnaK (dnaK), and putative DnaJ (dnaJ) genes, complete cds
3858	16456		1.32	3.4E-01	BF449010.1	EST_HUMAN	Tn94801.X1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3572232 3' similar to TR:Q9UJ15 Q9UJ15 DJ18C9.1
4108	16702		1.23	3.4E-01	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4128	16718		1.56	3.4E-01	AA584186.1	EST_HUMAN	not1b10.st NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100347 3'
4594	17177	28624	0.7	3.4E-01	AF166341.1	NT	Homo sapiens integrin alpha 6 (ITGA6) gene, exons 12 through 23
4749	17330	28773	2	3.4E-01	BE089912.1	EST_HUMAN	MIR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
4765	17346	28795	1.01	3.4E-01	BF314889.1	EST_HUMAN	MIR4-BT0403-230200-202-c01 BT0403 Homo sapiens cDNA
5087	17660		4.2	3.4E-01	AJ240973.1	EST_HUMAN	q95c05.x1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1867208 3' similar to contains Alu repetitive element
5864	18486	31210	2.9	3.4E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 80
5979	18559		5.68	3.4E-01	AA085313.1	EST_HUMAN	zn12d11.st Sitratogene hNT neuron (8837233) Homo sapiens cDNA clone IMAGE:547221 3'
6158	18771		2.44	3.4E-01	U02971.1	NT	Echovirus 22 1AB, 1C, 1D, 2A, 2B, 2C, 3A, 3B, 3C, 3D proteins RNA, complete mature peptides and cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6181	18791	31560	0.89	3.4E-01	BE748912.1	EST_HUMAN	60157181.1T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838928 3'
6256	18865	31535	2.45	3.4E-01	AW204505.1	EST_HUMAN	U1-H-B11-aet-12-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2719582 3'
6382	18886	31766	1.62	3.4E-01	AL120544.1	EST_HUMAN	DKFZp761A249_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A249 5'
6841	19431		1.32	3.4E-01	N85225.1	EST_HUMAN	z553s12.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:307342 3'
7027	19561	32388	1.09	3.4E-01	AI468082.1	EST_HUMAN	tm83g05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162840 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN)
7847	20389		0.51	3.4E-01	AE000493.1	NT	Escherichia coli K-12 MG1655 section 383 of 400 of the complete genome
8179	20720	33635	0.51	3.4E-01	Y14930.1	NT	Homo sapiens TORAV28 gene, allele A4, partial
8424	20864		1.92	3.4E-01	AA337083.1	EST_HUMAN	EST41765 Endometrial tumor Homo sapiens cDNA 5' and
8498	21037	33958	0.88	3.4E-01	L04690.1	NT	Cricetulus griseus cholesterol 7-alpha-hydroxylase gene, complete cds
8786	21325	34249	1.63	3.4E-01	9633624	NT	Bovine enterovirus strain K2577, complete genome
9139	21674	34616	3.89	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9139	21674	34617	3.89	3.4E-01	P28013	SWISSPROT	INTEGRIN BETA-8 PRECURSOR
9342	21856		0.59	3.4E-01	AB017510.1	NT	Ephydratia fluviatilis mRNA for PLC-gamma5, complete cds
9367	20308	33208	4.77	3.4E-01	U18492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9367	20308	33209	4.77	3.4E-01	U18492.1	NT	Saccharomyces cerevisiae Maf1p (MAF1) gene, complete cds
9812	22112	35075	0.86	3.4E-01	U88763.1	NT	Glycine max putative transcription factor SCOF-1 (scdf-1) mRNA, complete cds
9804	22302	35288	1.99	3.4E-01	AJ225084.1	NT	Homo sapiens FAA gene, exon 16, 17 and 18
10373	22867		0.54	3.4E-01	AE004096.1	NT	Vibrio cholerae chromosome I, section 4 of 251 of the complete chromosome
10895	23416		4.42	3.4E-01	AE000881.1	NT	Methanobacterium thermoautotrophicum from bases 1018444 to 1029212 (section 87 of 148) of the complete genome
10932	23450	38471	2.61	3.4E-01	P06925	SWISSPROT	PROBABLE E4 PROTEIN
10969	23484	36512	2.72	3.4E-01	AF045981.1	NT	Rutillus arcasii cytochrome b (cyb) gene, mitochondrial gene encoding mitochondrial protein, partial cds
11164	23671	36718	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11164	23671	36717	1.89	3.4E-01	M25856.1	NT	Human von Willebrand factor gene, exons 36 and 37
11372	23824	36887	2.27	3.4E-01	AB035607.1	NT	Rattus norvegicus mRNA for s-glycerin/MUC18, complete cds
11401	23852	36917	4.36	3.4E-01	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
11614	24056	37121	1.75	3.4E-01	BF061948.1	EST_HUMAN	7469412.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3480646 3'
11655	24082		2.12	3.4E-01	U93604.1	NT	Citrus variegation virus putative replicase gene, partial cds
11771	24160		1.44	3.4E-01	Z21621.1	NT	S cerevisiae RIB5 gene encoding Riboflavin synthase
11873	24836		1.8	3.4E-01	AF254351.1	NT	Schizosaccharomyces pombe Cwf8p (cwf8) gene, complete cds
11996	24303		14.59	3.4E-01	L26339.1	NT	Human autoantigen mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12023	24865		3.18	3.4E-01	BE218652.1	EST_HUMAN	hV42h08.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176127 3' similar to contains PTR5.13
12079	24974		2.44	3.4E-01	9838361	NT	PTR5 repetitive element 1
12196	24424	30850	2.66	3.4E-01	AJ297131.1	NT	Beta vulgaris mitochondrion, complete genome
12427	25068		1.25	3.4E-01	AJ288948.1	NT	Mus musculus SIL, MAP_17, CYP_a, SCL & CYP_b genes
							Clostridium cellulolyticum partial spoVA gene, strain ATCC 35319
12523	24639		2.55	3.4E-01	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (BF), and complement component C2 (C2) genes, >
12651	24723		2.71	3.4E-01	11466174	NT	Neogleria gruberi mitochondrion, complete genome
16	12695	25151	13.68	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
110	12695	25151	3.75	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
473	13106	25599	1.08	3.3E-01	AL161545.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 45
861	13285	25768	1.87	3.3E-01	7662485	NT	Homo sapiens KIAA1100 protein (KIAA1100), mRNA
1242	13840	26358	2.96	3.3E-01	Q12446	SWISSPROT	PROLINE-RICH PROTEIN LAS17
1350	13945	26468	3.58	3.3E-01	BF598860.1	EST_HUMAN	602184016T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300251 3'
1649	14241	26775	1.43	3.3E-01	6753685	NT	Mus musculus disintegrin 5 (Dign5), mRNA
1773	14363		1.44	3.3E-01	AA332734.1	EST_HUMAN	EST36722 Embryo, 8 week I Homo sapiens cDNA 5' end
2075	14655		1.22	3.3E-01	AF031148.1	NT	Methylococcus capsulatus strain Bath outer membrane protein MopB (mopB) gene, complete cds
							Homo sapiens uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (UMPS) mRNA
2450	15017		5.41	3.3E-01	4507834	NT	Bacteriophage phi-YeO3-12 complete genome
2976	15592	28074	2.14	3.3E-01	AJ251805.1	NT	INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (IL-12A) (CYTOTOXIC LYMPHOCYTE MATURATION FACTOR 35 KD SUBUNIT) (CLMF P35)
3049	15665		0.66	3.3E-01	O02743	SWISSPROT	Streptomyces argillaceus mithramycin biosynthetic genes
3091	15706	28178	0.82	3.3E-01	AJ007932.2	NT	Homo sapiens MTA1-L1 gene, complete cds
3542	16147	28629	0.99	3.3E-01	AB012922.1	NT	EXODEOXYRIBONUCLEASE V BETA CHAIN
3882	16480	28942	2.14	3.3E-01	O84645	SWISSPROT	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE (HC-PRO); PROTEIN P3]
3890	16489	28949	0.85	3.3E-01	P22602	SWISSPROT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4037	16635	29104	1.49	3.3E-01	AL161498.2	NT	Hypoxylon fragiforme chitin synthase gene, partial cds
4073	16669	29130	1.95	3.3E-01	AF200446.1	NT	Rattus norvegicus DNA for regucalcin, partial cds
4457	17043		1.44	3.3E-01	D31082.1	NT	tp78b12.x1 NCI CGAP_U13 Homo sapiens cDNA clone IMAGE:2205407 3' similar to gp:X57522 ANTIGEN
4769	17377		1.57	3.3E-01	AI539114.1	EST_HUMAN	PEPTIDE TRANSPORTER 1 (HUMAN);
4964	17538	28980	1.44	3.3E-01	D64003.1	NT	Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5527	18159	30573	2.75	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
5527	18159	30574	2.75	3.3E-01	X89819.1	NT	R.norvegicus mRNA for 3'UTR of ubiquitin-like protein
6101	18171	31468	1.72	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6101	18171	31469	1.72	3.3E-01	BE619650.1	EST_HUMAN	601472768T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875753 3'
6188	18788	31567	12.71	3.3E-01	P05691	SWISSPROT	CIRCUMSPOROZOITE PROTEIN (CS)
6969	19546	32369	4.8	3.3E-01	A1628131.1	EST_HUMAN	h84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
6969	19546	32370	4.8	3.3E-01	A1628131.1	EST_HUMAN	h84h01.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2285809 3' similar to contains Alu repetitive element; contains element L1 repetitive element;
7758	20286	33162	1.61	3.3E-01	N85148.1	EST_HUMAN	J2498F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2498 5' similar to TEGT
8497	21036	33957	17.55	3.3E-01	BF683954.1	EST_HUMAN	602140372F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301800 5'
8663	21202	34120	0.48	3.3E-01	BF210322.1	EST_HUMAN	601873281F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097180 5'
8698	21235	34157	0.49	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
8698	21235	34158	0.49	3.3E-01	AU126115.1	EST_HUMAN	AU126115 NT2RP1 Homo sapiens cDNA clone NT2RP1000130 5'
9042	21570	34508	0.83	3.3E-01	Q62925	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 (MAPK/ERK KINASE 1) (MEK KINASE 1) (MEKK 1)
9300	21900	34848	0.99	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9300	21900	34849	0.99	3.3E-01	BE828461.1	EST_HUMAN	CM3-ET0041-180500-187-d10 ET0041 Homo sapiens cDNA
9430	21939	34887	3.24	3.3E-01	N69866.1	EST_HUMAN	z667h01.s1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:287649 3'
9471	21870	34819	2.93	3.3E-01	BF376745.1	EST_HUMAN	RC4-TN0077-250800-011-g04 TN0077 Homo sapiens cDNA
9902	22399		2.16	3.3E-01	L41044.1	NT	Homo sapiens high-mobility group phosphoprotein (HMG1-C) gene, exons 1-3, complete cds
10600	23134	36147	2.93	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10600	23134	36148	2.93	3.3E-01	X63953.1	NT	D.mauritiana Adh gene
10905	23424		1.8	3.3E-01	BF620498.1	EST_HUMAN	602070802F1 NCL_CGAP_Bln64 Homo sapiens cDNA clone IMAGE:4213585 5'
11110	23620	36661	17.52	3.3E-01	BE219351.1	EST_HUMAN	hsv51g02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176978 3'
11223	23754	36812	4.97	3.3E-01	P47863	SWISSPROT	L-29 (CBP30)
11565	24012		4.68	3.3E-01	AA806821.1	EST_HUMAN	6071g02.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
11584	12695	25151	2.48	3.3E-01	X07980.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nodX gene
11759	24153	36771	1.96	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
12510	24631		36.28	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (2/7)
482	13115		1.79	3.2E-01	AF018261.1	NT	Rattus norvegicus EF domain binding protein Epsin mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
747	13357		0.76	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1204	13804	26317	27.96	3.2E-01	AF047013.1	NT	Fusarium poae virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1325	13919	26441	1.39	3.2E-01	Z50202.1	NT	P. vulgaris arc5-1 gene
1434	14027	26555	7.37	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1811	14401	26946	0.92	3.2E-01	Z36041.1	NT	S. cerevisiae chromosome II reading frame ORF YBR172c
1819	14409	26954	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1819	14409	26955	6.36	3.2E-01	AW957194.1	EST_HUMAN	EST369264 IMAGE resequences, MAGD Homo sapiens cDNA
1883	14469	27026	1.22	3.2E-01	AL111655.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2205	14751	27334	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2578	15140		2.24	3.2E-01	7710079	NT	Mus musculus Pbx/knotted 1 homeobox (Pbxox1), mRNA
2734	15289	27857	1.09	3.2E-01	AF060588.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3668	16269		0.78	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
4023	16621		0.61	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4483	17068	29518	1.64	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4597	17181	29628	1.56	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4844	17422		6.52	3.2E-01	BF603617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4246505 5'
5009	17582	30025	0.63	3.2E-01	Q57081	SWISSPROT	CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 3 (CYTADHERENCE ACCESSORY PROTEIN 3) (ACCESSORY ADHESIN PROTEIN 3) (P69)
5174	17741	30170	0.58	3.2E-01	BE782748.1	EST_HUMAN	601465591F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3868799 5'
5392	17950	30363	0.83	3.2E-01	AY008947.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5476	18110	30519	2.5	3.2E-01	BE173984.1	EST_HUMAN	CM0-HT0569-060300-269410 HT0569 Homo sapiens cDNA
6112	18728	31481	1.18	3.2E-01	L27221.1	NT	Giardia intestinalis pyruvate:flavodoxin oxidoreductase and flanking genes
6831	19421		1.03	3.2E-01	AB002359.1	NT	Human mRNA for KIAA0361 gene, KIAA0361 protein
8113	20654	33563	1.33	3.2E-01	M60266.1	NT	Rat ISO-alpha natriuretic factor gene, complete cds
8210	20751	33665	0.51	3.2E-01	AJ231001.1	NT	Rattus norvegicus repeat; map NOS-D12W ox1
8308	20849	33772	11.34	3.2E-01	X02508.1	NT	H. sapiens gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
8311	20852	33777	16.78	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'
8398	20938		1.43	3.2E-01	AL181574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 70
8437	20977	33891	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8437	20977	33892	1.22	3.2E-01	BF246771.1	EST_HUMAN	601855580F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075627 5'
8508	21047	33968	2.72	3.2E-01	AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
8605	21144	34058	0.69	3.2E-01	U51028.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds

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8605	21144	34059	0.69	3.2E-01	U51026.1	NT	Oryctolagus cuniculus Ig H-chain pseudogene, V-region (VH6-a2) gene, partial cds
8997	21535	34485	0.58	3.2E-01	AL103204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9007	21544		2.08	3.2E-01	MB6511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
9077	21813	34547	0.48	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9077	21813	34548	0.48	3.2E-01	AF041828.1	NT	Homo sapiens 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) gene, exons 12 and 13
9905	22402	35376	3.22	3.2E-01	U44814.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds, and unknown genes
10100	22595	35588	0.51	3.2E-01	BE326230.1	EST_HUMAN	h99f05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181569 3'
10213	22708		3.03	3.2E-01	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
10548	23084	36098	3.28	3.2E-01	T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#936206) Homo sapiens cDNA clone HFB0Z21
11796	24999		4.31	3.2E-01	L07288.1	NT	Drosophila melanogaster lamtrophin A (Lam-A) mRNA, complete cds
12344	24525		4.65	3.2E-01	O83217	SWISSPROT	ELONGATION FACTOR TU(EF-TU)
12441	24819		3.37	3.2E-01	AF157625.1	NT	Bos taurus inositol 1,4,5-trisphosphate receptor type I mRNA, complete cds
12489	24818		1.94	3.2E-01	L39874.1	NT	Homo sapiens deoxycytidylate deaminase gene, complete cds
12550	25041	30504	1.98	3.2E-01	BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2695	15252	27823	2.39	3.1E-01	R18051.1	EST_HUMAN	ye90h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to
2722	15403	27843	3.67	3.1E-01		NT	gb:M64241 QM PROTEIN (HUMAN);
2722	15403	27844	3.67	3.1E-01	7661971	NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2883	15501		1.35	3.1E-01	AW629036.1	EST_HUMAN	h46h08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875391 3'
3208	15820		3.53	3.1E-01	AB028069.1	NT	Mus musculus gene for Ser/Thr kinase KKIAMRE, exon 6
3978	16576	28046	0.91	3.1E-01	AJ251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5055	17628	30072	0.79	3.1E-01	S68245.1	NT	carbonic anhydrase IV [rats, Sprague-Dawley, lung, mRNA, 1205 nt]
5097	17670	30108	0.82	3.1E-01	AE003984.1	NT	Xylella fastidiosa, section 130 of 229 of the complete genome
5206	17771	30194	0.98	3.1E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
5669	18296	30776	10.9	3.1E-01	AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5786	18411	31127	0.75	3.1E-01	Z74883.1	NT	S.cerevisiae chromosome XV reading frame ORF YOL141w
5786	18421		0.99	3.1E-01	Y13278.1	NT	Mus musculus mRNA for polycystin
5945	18565	31295	2.16	3.1E-01	AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
6992	19189	31992	2.63	3.1E-01	AW983549.1	EST_HUMAN	RC3-HN0001-310300-011-504 HN0001 Homo sapiens cDNA
6654	19250	32052	0.87	3.1E-01	AJ264458.1	EST_HUMAN	q136d01.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1874689 3'
6784	19375	32191	0.81	3.1E-01	X71887.1	NT	H.sapiens gene for immunoglobulin kappa light chain variable region AB and A9
6863	19597		0.9	3.1E-01	AW377354.1	EST_HUMAN	MR2-C10222-281099-005-105 C10222 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7048	24741	30458	2.4	3.1E-01	BE737392.1	EST_HUMAN	601306121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7671	20183	33071	1.18	3.1E-01	4885390	NT	Homo sapiens hyaluronan synthase 2 (HAS2), mRNA
8592	21121	34041	1.22	3.1E-01	R45318.1	EST_HUMAN	yg46f01.s1 Soares infant brain TNIB Homo sapiens cDNA clone IMAGE:35639 3'
9816	22314	35295	0.45	3.1E-01	6676322	NT	Mus musculus phosphatidylinositol-4-phosphate 5-kinase, type 1 gamma (Pip5k1c), mRNA
9979	22474	35456	0.81	3.1E-01	BF686839.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
9979	22474	35457	0.81	3.1E-01	BF686839.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
10035	22530	35525	1.7	3.1E-01	A124400.1	EST_HUMAN	q61611.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700 HYDROXYMETHYLGLUTARYL-COA LYASE PRECURSOR (HUMAN);
10204	22699		0.54	3.1E-01	T55325.1	EST_HUMAN	yg47f08.s1 Strategene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:74367 3' similar to similar to gb:M91036_mae2 HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS (HUMAN)
10717	23245	36281	1.95	3.1E-01	BF216117.1	EST_HUMAN	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
11411	23862	36923	2.03	3.1E-01	7662281	NT	Homo sapiens KIAA0764 gene product (KIAA0764), mRNA
11921	24257		2.13	3.1E-01	AF294308.1	NT	Andis opalinus isolate QS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11960	24282		1.95	3.1E-01	AF304182.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
12108	24370		3.31	3.1E-01	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
12496	24624		3.89	3.1E-01	AF196779.1	NT	Homo sapiens transcription factor ICHM enhancer 3, JM11 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
12535	25035		1.62	3.1E-01	10946623	NT	Mus musculus peptidoglycan recognition protein-like (Pglyrpl-pending), mRNA
76	15392	25234	1.37	3.0E-01	6755083	NT	Mus musculus protein kinase C, epsilon (Pkc ϵ), mRNA
275	12932	25419	11.51	3.0E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1266	13863	26380	2.05	3.0E-01	AW300400.1	EST_HUMAN	xs63f08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1555	14147	26680	6.64	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
3248	15860		1.4	3.0E-01	A5030481.1	NT	Corynebacterium sp. ALY-1 alyPG gene for polygluturonate lyase, complete cds
3932	16530	28997	2.1	3.0E-01	AW817785.1	EST_HUMAN	PM1-ST0262-261199-001-g01 ST0262 Homo sapiens cDNA
4046	16843	29109	1.01	3.0E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4611	17194	29640	1.78	3.0E-01	AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5554	18186	30601	5.34	3.0E-01	BE741629.1	EST_HUMAN	601594960F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5627	18256	30726	0.88	3.0E-01	AF229247.1	NT	Canigalo orthopoxvirus hemagglutinin gene, complete cds
5695	18321	30820	4.03	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5695	18321	30821	4.03	3.0E-01	BE693575.1	EST_HUMAN	RC3-BT0333-180700-111-e03 BT0333 Homo sapiens cDNA
5731	18357	31062	4.57	3.0E-01	U01247.1	NT	Mus musculus 120/1sv Clara cell 10 kd protein (mCC10) gene, complete cds
6919	19578	32407	3.14	3.0E-01	D16313.1	NT	Mouse cyokeratin 15 gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6944	18052	30475	0.7	3.0E-01	U02369.1	NT	Strongylocentrotus purpuratus 34/87 kDa laminin-binding protein mRNA, partial cds
7005	18503	32322	0.96	3.0E-01	AF228247.1	NT	Centigale orthopoxvirus hemagglutinin gene, complete cds
7175	19707	32555	0.76	3.0E-01	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
7367	18953	32756	6	3.0E-01	10947007	NT	Mus musculus midnolin (Midn-pending), mRNA
7512	20033	32889	1.88	3.0E-01	AF071810.1	NT	Streptococcus pneumoniae strain DBL5 PspA (pspA) gene, partial cds
7867	20409	33316	1.07	3.0E-01	AE001755.1	NT	Thermotoga maritima section 67 of 136 of the complete genome
8314	20855		3.82	3.0E-01		NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec3f), mRNA
8411	20951	33870	1.27	3.0E-01	BE568083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
8763	21302	34223	0.82	3.0E-01	AF141678.1	NT	Streptomyces sulfodiazolens isopenicillin N synthase (pcbC) gene, partial cds
8805	21344		0.95	3.0E-01	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
9145	21880	34824	0.98	3.0E-01	AF220507.1	NT	Anabaena PCC7120 cytosine-specific DNA methyltransferase (dimB) gene, complete cds; putative anthranilate phosphoribosyltransferase gene, partial cds, and unknown gene
9493	21993	34949	0.55	3.0E-01	P76389	SWISSPROT	HYPOTHETICAL 59.5 KD PROTEIN IN WZA-ASMA INTERGENIC REGION
9878	22375	35352	0.84	3.0E-01	BF574812.1	EST_HUMAN	602133271F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288338 5'
10294	22788	35778	0.96	3.0E-01	AW118111.1	EST_HUMAN	xe03d10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2606035 3'
10296	22780	35780	1.95	3.0E-01	AB030231.1	NT	Aspergillus oryzae bpaA gene for ER chaperone BiP, complete cds
10315	22809	35801	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
10315	22809	35802	0.73	3.0E-01	BF683841.1	EST_HUMAN	602140133F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301097 5'
11604	24047	37112	2.87	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
11604	24047	37113	2.87	3.0E-01	H51029.1	EST_HUMAN	yp84b10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194107 5'
11975	24287		1.37	3.0E-01	P54660	SWISSPROT	PONTICULIN PRECURSOR
12227	24884		2.83	3.0E-01	AJ287631.1	NT	Rattus norvegicus mRNA for glyceraldehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
12529	25033		2.51	3.0E-01	6977769	NT	Mus musculus ribose 5-phosphate isomerase A (Rpia), mRNA
1924	14509	27064	2.27	2.9E-01	5174502	NT	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1) mRNA
2070	14950	27221	1.38	2.9E-01	AE000736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2524	15088		1.22	2.9E-01	M32360.1	NT	Mouse apolipoprotein A-II (AIIp-2) gene, complete cds
3289	15900	28378	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3289	15900	28380	2.07	2.9E-01	AW754239.1	EST_HUMAN	PM1-CT0326-171299-001-f12 CT0326 Homo sapiens cDNA
3965	16563	29032	0.71	2.9E-01	A1610836.1	EST_HUMAN	tp21a11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2188412 3' similar to gb:D15050 NIL-2-A
4159	16751		0.87	2.9E-01	AW002802.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4583	17168	28609	1.21	2.9E-01	AA284468.1	EST_HUMAN	wr02f10.x1 NCL_CGAP_GCB8 Homo sapiens cDNA clone IMAGE:2480395 3'
							zs57d12.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701591 5' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4793	17372		0.63	2.9E-01	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
5148	17718		1.02	2.9E-01	U90756.1	NT	Lymantria dispar vitalogenin gene, complete cds
5154	17724	30155	1.43	2.9E-01	7662169	NT	Homo sapiens KIA0537 gene product (KIA0537), mRNA
5285	17847		1.7	2.9E-01	A1670899.1	EST_HUMAN	wc06f03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297309 3' similar to contains L1.12 L1 repetitive element;
5463	18098		1.25	2.9E-01	R37485.1	EST_HUMAN	y77612.s1 Soares Infant brain INIB Homo sapiens cDNA clone IMAGE:28261 3'
5592	19522	32344	0.79	2.9E-01	AF321001.1	NT	Suaeda maritima subsp. salisa S-adenosylmethionine synthetase 2 mRNA, complete cds
5937	18558	31286	5.1	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5937	18558	31287	5.1	2.9E-01	X56098.1	NT	B. subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5949	18570	31302	6.06	2.9E-01	6678662	NT	Mus musculus Eph receptor A8 (Epha8), mRNA
6206	18816	31587	1.26	2.9E-01	AA418145.1	EST_HUMAN	z097b12.1 Soares NHMPu_S1 Homo sapiens cDNA clone IMAGE:767711 5'
6427	19030	31813	0.93	2.9E-01	A1797128.1	EST_HUMAN	wc27605.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2342312 3' similar to contains L1.11 L1 repetitive element;
6467	19068	31854	2.3	2.9E-01	U03420.1	NT	Bos taurus myosin I mRNA, complete cds
6585	19183	31983	0.72	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
6585	19183	31984	0.72	2.9E-01	R69194.1	EST_HUMAN	y39d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:141615 5'
7092	18081	30437	1.35	2.9E-01	AF142328.1	NT	Mus musculus Filth protein (Filth) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
7153	19885	32527	2.87	2.9E-01	Q04399	SWISSPROT	PUTATIVE MULTICOPPER OXIDASE YDR506C
7213	19744	32598	1.61	2.9E-01	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RafGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3- galactosyl transferase (beta1.3-galactosyl tr>
7860	20402	33308	1.92	2.9E-01	BE540422.1	EST_HUMAN	601066830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
7860	20402	33309	1.92	2.9E-01	BE540422.1	EST_HUMAN	601066830F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452287 5'
8103	20644	33990	0.89	2.9E-01	BF217743.1	EST_HUMAN	601882570F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095113 5'
8531	21070	34318	0.66	2.9E-01	AU150910.1	EST_HUMAN	AU150910 NT2RP2 Homo sapiens cDNA clone NT2RP2003901 3'
8556	21395	34318	1.07	2.9E-01	AF225908.1	NT	Arabidopsis thaliana sulfonyleurea receptor-like protein mRNA, complete cds
8963	21501	34423	0.71	2.9E-01	M22452.1	NT	Baboon lymphocyte homing/adhesion receptor mRNA, complete cds
9170	21747	34689	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
9170	21747	34690	0.77	2.9E-01	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 5/6
10773	23297	36302	2.24	2.9E-01	AF128843.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
11041	23555	36589	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
11041	23555	36590	2.88	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11453	23903	36970	2.07	2.9E-01	AA835373.1	EST_HUMAN	ny35h02.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1273779 similar to contains LTR8.2 LTR8 repetitive element;
11456	23908	36973	5.52	2.9E-01	AL139078.2	NT	Campylobacter jejuni NCTC11188 complete genome; segment 5/6
12172	24411	30944	1.54	2.9E-01	AW005671.1	EST_HUMAN	wz88f05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2565921 3' similar to contains element
12262	24472	30932	1.47	2.9E-01	AF092453.1	NT	MER29 repetitive element;
12313	24505		1.4	2.9E-01	BE788199.1	EST_HUMAN	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
12586	24679	30877	1.57	2.9E-01	Y08937.1	NT	601482059F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884559 5'
594	13224	30878	1.57	2.9E-01	U08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
599	13228		2.06	2.8E-01	U67138.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
1122	13725	26238	0.75	2.8E-01	L28145.1	NT	Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds
1320	13914	26435	3.51	2.8E-01	BE313442.1	EST_HUMAN	Prune dwarf virus movement protein, complete cds; coat protein, complete cds
1320	13914	26436	3.51	2.8E-01	BE313442.1	EST_HUMAN	Guinea oocyte maturation factor Mos (C-mos) gene, partial cds
1334	13928	26448	1.03	2.8E-01	DB6550.1	NT	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1765	14355	26902	2.01	2.8E-01	AW860020.1	EST_HUMAN	601148733F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
2057	14638	27210	2.12	2.8E-01	ALD47620.1	EST_HUMAN	Human mRNA for serine/threonine protein kinase, complete cds
2175	14752	27322	3.53	2.8E-01	AW511195.1	EST_HUMAN	QV1-CT0364-120200-065-b05 CT0364 Homo sapiens cDNA
2511	15075	27648	2.41	2.8E-01	AE000494.1	NT	DKFZp586I2321_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp586I2321
2511	15075	27649	2.41	2.8E-01	AE000494.1	NT	hd44b03.x1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:2912333 3'
2584	15147		2.75	2.8E-01	AL161565.2	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2688	15246	27813	1.21	2.8E-01	AB020975.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2998	15614		1.7	2.8E-01	AF179480.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2999	15615	28094	2.36	2.8E-01	Z14037.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
3425	16033	28513	1.26	2.8E-01	AF000004.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
4068	16664	29125	2.06	2.8E-01	AE001180.1	NT	B.taurus microsatellite (ETH121)
4202	16791		0.62	2.8E-01	AE004450.1	NT	B.taurus microsatellite (ETH121)
4276	16862		2.75	2.8E-01	AI060868.1	EST_HUMAN	B.taurus microsatellite (ETH121)
4553	17136	29584	1.32	2.8E-01	AL021127.2	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
4559	17142	29590	2.47	2.8E-01	P13615	SWISSPROT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
4897	17472	29828	1.07	2.8E-01	DT5050.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
							Pseudomonas aeruginosa PAO1, section 11 of 529 of the complete genome
							ov44g10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
							Mus musculus chromosome X contig; putative Magea9 gene, Caltractin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
							RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
							Human mRNA for transcription factor AREB6, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4897	17472	29929	1.07	2.8E-01	D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4937	17512	29958	1.02	2.8E-01	AW594539.1	EST_HUMAN	Hg66d05.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2950569 3'
4949	17524	29965	1.17	2.8E-01	AF075238.1	NT	Hepatitis G virus isolate 60 (SZNAE12) polyprotein precursor, gene, partial cds
4955	17530	29972	3.5	2.8E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
4988	17560	30003	1.67	2.8E-01	BF528188.1	EST_HUMAN	602042601F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180129 5'
5013	17587	30030	2.82	2.8E-01	AI272669.1	EST_HUMAN	ql59c11.x1 Soares_NhlMpu_S1 Homo sapiens cDNA clone IMAGE:1878628 3' similar to contains Alu repetitive element/contains element LTR5 repetitive element ;
5514	24744	30558	21.59	2.8E-01	AA348997.1	EST_HUMAN	EST157072 Infant brain Homo sapiens cDNA 5' end
5791	18416	31132	2.78	2.8E-01	AB018825.1	NT	Homo sapiens OCTN2 gene, complete cds
5983	18603		0.97	2.8E-01	AW992583.1	EST_HUMAN	CM1-BN0024-150200-118-g12 BN0024 Homo sapiens cDNA
6078	18695	31442	0.69	2.8E-01	AA765296.1	EST_HUMAN	ca01d08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1303691 3' similar to gb:M34539 FK508-BINDING PROTEIN (HUMAN);
6323	25114		0.75	2.8E-01	M36588.1	NT	Bovine 680 bp repeated unit of 1.723 satellite DNA
6366	18970	31748	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6366	18970	31749	1.55	2.8E-01	AF003124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
6829	19419	32235	8.4	2.8E-01	BF511215.1	EST_HUMAN	UI-H-B14-ekd-f04-Q-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'
7467	19989		1.19	2.8E-01	U05633.1	NT	Marsilea quadrifolia ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (rbcl) gene, chloroplast gene encoding chloroplast protein, partial cds
7768	20276	33174	0.69	2.8E-01	BE537151.1	EST_HUMAN	601063103F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449569 5'
8036	20578	33482	1.12	2.8E-01	AI346128.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8036	20578	33483	1.12	2.8E-01	AI346128.1	EST_HUMAN	MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3 (HUMAN);
8150	20691	33605	2.16	2.8E-01	U51688.1	NT	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
8451	20991	33909	0.47	2.8E-01	AA911628.1	EST_HUMAN	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
8525	21064		6.69	2.8E-01	BF347847.1	EST_HUMAN	g02h05.s1 NCI_CGAP_Co12 Homo sapiens cDNA clone IMAGE:1419993 3' similar to gb:M87789 IG
9387	21810	34781	1.22	2.8E-01	U17251.1	NT	GAMMA-1 CHAIN C REGION (HUMAN);
9627	22127		1.03	2.8E-01	L13654.1	NT	602022987F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4158525 5'
9803	22301	35286	1.04	2.8E-01	AF132728.1	NT	Neurospora crassa negative regulator sulfur controller-2 (scor-2) gene, complete cds
9803	22301	35287	1.04	2.8E-01	AF132728.1	NT	Lycopodium esculentum peroxidase (TPX1) mRNA, complete cds
9861	22358	35338	0.64	2.8E-01	AF294393.1	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
9972	22467	35451	1.91	2.8E-01	7706163	NT	Escherichia coli translocated intimin receptor Tir (tir) gene, complete cds
							Rattus norvegicus glycerol-3-phosphate dehydrogenase gene, promoters A and B and exons 1a and 1b; nuclear gene for mitochondrial product
							Homo sapiens hypothetical protein (LOC51319), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10215	22710		0.81	2.8E-01	9828154	NT	Fujinami sarcoma virus, complete genome
10255	22750	35738	0.47	2.8E-01	BE959727.2	EST_HUMAN	601654822R1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839785 3'
10622	23154	36166	2.26	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10622	23154	36167	2.26	2.8E-01	BF241062.1	EST_HUMAN	601880794F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
10651	23183	36187	2.83	2.8E-01	BF695970.1	EST_HUMAN	601852148F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4076028 5'
10760	23284	36287	3.31	2.8E-01	AF051662.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
11158	23665		4.56	2.8E-01	BF674023.1	EST_HUMAN	602137418F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
12213	24436		15.74	2.8E-01	D83329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
12328	24514	30920	8.89	2.8E-01	BE178699.1	EST_HUMAN	PM4-HT0608-030400-001-a07 HT0608 Homo sapiens cDNA
12356	24533	30927	1.25	2.8E-01	BE900116.1	EST_HUMAN	601673020F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955986 5'
12519	24988		2.21	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BPB), mRNA
502	13134	25622	3.21	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
641	13264	25740	2.53	2.7E-01	AA450081.1	EST_HUMAN	z39b10.s1 Soares, total, fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:768827 3' similar to contains Alu repetitive element;
1304	13888	26418	1.69	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
1682	14255		2.17	2.7E-01	X70815.1	NT	G lamblia SR2 gene
1787	14357	26903	3.34	2.7E-01	W58087.1	EST_HUMAN	z322h10.r1 Soares, fetal, heart_NbHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1813	14403	26948	4.14	2.7E-01	P03341	SWISSPROT	GAG POLYPROTEIN (CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10)
2181	15459		2.77	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monamine transporter type 2, promoter region and exon 1
2405	14973	27545	7.35	2.7E-01	Y13868.1	NT	Feline immunodeficiency virus env gene, isolate ITT0088P1U (M88), partial
2498	15080	27634	3.82	2.7E-01	A1310858.1	EST_HUMAN	ta43c11.x2 NCL_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
3013	15628		0.73	2.7E-01	BF088284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
4082	16678	29138	1.98	2.7E-01	A1928015.1	EST_HUMAN	wo92e11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
4096	16691	29147	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4096	16691	29148	0.79	2.7E-01	AF216214.1	NT	Drosophila buzzatii alpha-esterase 6 (ae6) gene, partial cds
4101	16695	29151	2.31	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5020	17584	30037	0.98	2.7E-01	L27618.1	NT	Triticum aestivum (W cs68) gene, complete cds
5193	17758		3.82	2.7E-01	AW858131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5471	18105	30424	2.07	2.7E-01	PI7277	SWISSPROT	HOMEOBOX PROTEIN HOX-A4 (HOX-1.4)
5681	18308		0.96	2.7E-01	AB033171.1	NT	Astreporea mytilophthalma mitochondrial cyb gene for cytochrome b, partial cds
6724	19318	32122	1.07	2.7E-01	AE001084.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome

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6724	19318	32123	1.07	2.7E-01	AE001094.1	NT	Archaeoglobus fulgidus section 13 of 172 of the complete genome
6875	19609	32443	2.03	2.7E-01	Q81554	SWISSPROT	FIBRILLIN 1 PRECURSOR
7085	19656	32495	0.76	2.7E-01	U15967.1	NT	Drosophila melanogaster rfc40 protein, Rop protein (Rop), and small GTP binding protein (DRas2) genes, complete cds
7393	19818	32782	0.87	2.7E-01	Q11079	SWISSPROT	HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X
7562	20079	32854	0.85	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7562	20079	32855	0.85	2.7E-01	Q01168	SWISSPROT	NITROGEN REGULATORY PROTEIN NUT1
7677	20188	33076	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7677	20188	33077	2.21	2.7E-01	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7720	20228	33116	0.92	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
7720	20228	33117	0.92	2.7E-01	AA351121.1	EST_HUMAN	EST58740 Infant brain Homo sapiens cDNA 5' and similar to similar to myosin-binding protein H
7805	20348	33256	0.95	2.7E-01	AA013147.1	EST_HUMAN	z335b11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360957 3' similar to contains Alu repetitive element;
7969	20511		0.51	2.7E-01	AF048820.1	NT	Carassius auratus pituitary adenylate cyclase activating polypeptide type 1 receptor precursor mRNA, complete cds
8079	20621	33534	0.59	2.7E-01	AW868503.1	EST_HUMAN	MR1-SN0062-100500-002-d08 SN0062 Homo sapiens cDNA
8127	20688	33577	0.48	2.7E-01	R39257.1	EST_HUMAN	yc91h08.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:23511 3'
8232	20773	33694	0.94	2.7E-01	AL181552.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 52
8694	21233	34154	0.83	2.7E-01	Q14784	SWISSPROT	MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN)
8957	21495	34418	0.53	2.7E-01	X03216.1	NT	Staphylococcus aureus transposon Tn554
9256	21782	34734	9.93	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9256	21782	34735	9.93	2.7E-01	O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRS)
9259	21785		2.02	2.7E-01	P37928	SWISSPROT	FIMBRIAE W PROTEIN
9716	22214	35188	0.67	2.7E-01	D98680.1	NT	Rattus norvegicus DNA for peroxisome assembly factor-2, exon 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17 and complete cds
9993	22498	35476	0.91	2.7E-01	AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
10026	22521	35517	2.5	2.7E-01	AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
10148	22843	35634	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10148	22843	35635	0.69	2.7E-01	AF156539.1	NT	Homo sapiens xeroderma pigmentosum complementation group C (XPC) gene, intron 9
10691	23221	36233	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'
10691	23221	36234	2.31	2.7E-01	AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADBCOD05 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10702	23231	38244	3.65	2.7E-01	AJ133289.1	NT	Homo sapiens carvedin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
12296	24893		1.72	2.7E-01	AB008782.1	NT	Arabidopsis thaliana mRNA for sulfate transporter, complete cds
12501	24827		3.98	2.7E-01	AF217491.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exon 6
495	15416	25615	2.06	2.6E-01	P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
506	13139		1.24	2.6E-01	D16439.1	NT	Bos taurus mRNA for mb-1, complete cds
1437	14030	26558	2.19	2.6E-01	BE885087.1	EST_HUMAN	601510839F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1485	14078	26616	1.36	2.6E-01	AB013290.1	NT	Glycine max pseudogene for Bd 30K
1941	14525	27080	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
1941	14525	27081	6.59	2.6E-01	AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 2
							bb04d10 x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:M36072.60S RIBOSOMAL PROTEIN L7A (HUMAN); gb:M14689_cds1 Mouse surfactant protein 3 protein gene (MOUSE);
2140	14718		13.12	2.6E-01	AW733152.1	EST_HUMAN	Human prealbumin gene, complete cds
2197	14773	27347	1.41	2.6E-01	M11844.1	NT	B. maritimus rbcL gene
2512	15076		2.09	2.6E-01	Y12986.1	NT	601126016F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2890043 5'
2583	15148		10.77	2.6E-01	BE272440.1	EST_HUMAN	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds
3640	16243	28719	0.86	2.6E-01	M22342.1	NT	
3705	16306	28775	2.13	2.6E-01	AF228118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
4175	16766	29214	0.7	2.6E-01	AW090510.1	EST_HUMAN	EST371580 IMAGE resequences, MAGF Homo sapiens cDNA
4234	16822	29273	19.98	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0630-040400-132-e03 BT0630 Homo sapiens cDNA
4448	17034	29477	1.57	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds, and unknown gene
4593	17176	29622	0.76	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4593	17176	29623	0.76	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4646	17228	29684	1.35	2.6E-01	AA457617.1	EST_HUMAN	aa89d07.r1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838477 5'
4752	17333	29776	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lhca3*) mRNA, complete cds
4825	17403	29856	1.47	2.6E-01	AF142703.1	NT	Ophrestia radicata matras-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
5107	17679	30118	3.56	2.6E-01	H04858.1	EST_HUMAN	y51e05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:162288 5'
5195	17760		0.58	2.6E-01	AA894623.1	EST_HUMAN	am33b11.st Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1488603 3'
5544	18176		1.29	2.6E-01	AB035972.1	NT	Paramacium caudatum gene for PAP, complete cds
5540	18269	30742	0.68	2.6E-01	M90060.1	NT	Acetobacter xylinum cellulose synthase (bcsA) gene, partial cds, CMCax and CcpA genes, complete cds

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5760	18386		0.81	2.6E-01	AI862388.1	EST_HUMAN	td19a03.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2075788 3' similar to contains element MER35 repetitive element ;
5947	18568	31299	0.69	2.6E-01	AF207550.1	NT	Homo sapiens protein translocase, JM28 protein, UDP-galactose translocator, pim-2 protooncogene homolog pim-2h, and shal-type potassium channel genes, complete cds; JM12 protein and transcription factor (GHM enhancer 3 genes, partial cds; and unknown g>
6221	25113		2.36	2.6E-01	AE001811.1	NT	Thermoplasma maritima section 123 of 136 of the complete genome
6348	18953	31732	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6348	18953	31733	1.89	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q84289 NEUROGENIC DIFFERENTIATION FACTOR 1 ; contains element LTR1 repetitive element ;
6554	19152	31848	1.05	2.6E-01	AL162757.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 6/7
7103	19673	32512	0.97	2.6E-01	AI914380.1	EST_HUMAN	wd48c04.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331368 3' similar to gb:M37721 PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (HUMAN);
7457	24783		0.96	2.6E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
7721	20226	33118	1.6	2.6E-01	R10365.1	EST_HUMAN	yf37a03.s1 Scores fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:129004 3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
7791	20394	33240	1.14	2.6E-01	R02411.1	EST_HUMAN	ye82a07.r1 Scores fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:124212 5'
7845	20387	33280	1.18	2.6E-01	BE144331.1	EST_HUMAN	MRO-HT0166-181199-003-d12 HT0166 Homo sapiens cDNA
8083	20625	33538	0.67	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8083	20625	33539	0.67	2.6E-01	X82641.1	NT	D.melanogaster mRNA for alpha 1,2 mannosidase (Berlin)
8276	20817	33738	2.99	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4190396 5'
8349	20890	33810	1.89	2.6E-01	Q10199	SW/ISSPROT	HYPOPHYSICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
8627	21166	34080	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC6-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
8627	21166	34081	4.49	2.6E-01	BE830339.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
9388	21811	34762	0.96	2.6E-01	X17604.1	NT	S. occidentalis INV gene for invertase (EC 3.2.1.26)
9654	22153		0.5	2.6E-01	AF057121.1	NT	Lontra canadensis cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, complete cds
9782	22280	35265	0.93	2.6E-01	P87366	SW/ISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
9782	22280	35268	0.93	2.6E-01	P87366	SW/ISSPROT	GREEN-SENSITIVE OPSIN (GREEN CONE PHOTORECEPTOR PIGMENT) (KHF-G)
10083	22586		0.5	2.6E-01	Q28295	SW/ISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
10403	22897		0.91	2.6E-01	Y10196.1	NT	Homo sapiens PHEX gene
10500	22894		0.51	2.6E-01	AI978681.1	EST_HUMAN	wf58b09.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491865 3'

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11300	23752	36809	2.18	2.6E-01	P48280	SWISSPROT	CELL DIVISION PROTEIN FTSW HOMOLOG
11400	23851		30.68	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11777	24166		1.72	2.6E-01	10190855	NT	Mus musculus Jerky (Jrk), mRNA
11973	24991		4.06	2.6E-01	BE883491.1	EST_HUMAN	601511052F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612 5'
12042	24328	30996	4.8	2.6E-01	AF316896.1	NT	Homo sapiens Na/K-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced
12396	24556		1.34	2.6E-01	DB8425.1	NT	Cavia cobaya mRNA for serine/threonine kinase, complete cds
12478	24612		1.98	2.6E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
12526	24641		1.37	2.6E-01	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
12567	24666		3.74	2.6E-01	P47285	SWISSPROT	HYPOTHETICAL PROTEIN MG039
262	12921	25407	1.48	2.5E-01	4502298	NT	Homo sapiens ATP synthase H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
263	12921	25407	1.77	2.5E-01	4502296	NT	Homo sapiens ATP synthase H+ transporting, mitochondrial F1 complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
276	12933		4.29	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
865	13480	25994	1.02	2.5E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1098	13703		1.03	2.5E-01	AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1160	13763	26274	11.59	2.5E-01	T69837.1	EST_HUMAN	ye11g07.r1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:117468 5'
1566	14158	26689	0.87	2.5E-01	AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1766	14356		6.09	2.5E-01	4855406	NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1927	15434	27067	1.29	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
1927	15454	27068	1.28	2.5E-01	BE696604.1	EST_HUMAN	PM4-CT0400-310700-005-408 CT0400 Homo sapiens cDNA
2452	15019		12.93	2.5E-01	AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2536	15100	27673	0.93	2.5E-01	6079216	NT	Mus musculus protein-L-isopentate (D-aspartate) O-methyltransferase 1 (Pcm11), mRNA
2540	15104		1.49	2.5E-01	AA251987.1	EST_HUMAN	zs11a12.r1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:684862 5'
3459	16066		3.41	2.5E-01	AW073471.1	EST_HUMAN	EST385464 IMAGE resequences, MAGM Homo sapiens cDNA
3587	16191	26675	0.84	2.5E-01	AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3603	16207	26685	7.87	2.5E-01	AL161517.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
4143	16735		1.38	2.5E-01	P32323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4409	16994		0.9	2.5E-01	Q03314	SWISSPROT	RHB PROTEIN
4722	17303	26747	0.59	2.5E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naiip6) gene, complete cds; and Naiip3 gene, exons 2-9 and 11-16
4860	17438		1.47	2.5E-01	Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MIH)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4869	17445	29896	4.69	2.5E-01	AF007768.1	NT	Choristoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4898	17471	29927	2.82	2.5E-01	AE004418.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4924	17499		3.21	2.5E-01	AJ230113.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5' LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4959	17534	29976	0.81	2.5E-01	BE896785.1	EST_HUMAN	60143748F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922600 5'
5262	12933		0.65	2.5E-01	M26501.1	NT	Starfish (P. ochraceus) cytoplasmic actin gene, complete cds
5529	18161	30576	12.86	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]
6114	18730		0.84	2.5E-01	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6738	19332	32138	0.83	2.5E-01	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
7389	19914	32778	0.82	2.5E-01	U13992.1	NT	Feline calicivirus CFI/68 RNA helicase/cysteine protease/RNA-dependent RNA polymerase polyprotein precursor and capsid protein precursor, genes, complete cds; and unknown gene
7413	19938		1.35	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
7632	20144	33025	4.48	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
7788	20329	33236	2.31	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525389 3'
7797	20340	33248	0.7	2.5E-01	BE960712.1	EST_HUMAN	60165339J12 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3826198 3'
8168	20709	33625	2.2	2.5E-01	BF038595.1	EST_HUMAN	60149238F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3862809 5'
8336	20877	33798	0.72	2.5E-01	P04492	SWISSPROT	E1B PROTEIN, SMALL T-ANTIGEN (E1B 18k)
8571	21110	34029	3.03	2.5E-01	H53238.1	EST_HUMAN	yq84707.1 Soares fetal liver spleen (NFLS) Homo sapiens cDNA clone IMAGE:202501 5'
8808	21347	34271	0.88	2.5E-01	M88626.1	NT	Mouse testis-specific protein (TPX-1) gene, exon 10
9435	21961	34909	15.98	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9435	21961	34910	15.98	2.5E-01	U89651.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
9492	21948	34897	2.09	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
9492	21948	34898	2.09	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, partial cds
10010	22505	35496	1.66	2.5E-01	AW581997.1	EST_HUMAN	RC3-ST0186-130100-015-a07 ST0186 Homo sapiens cDNA
10436	22630	35937	1.53	2.5E-01	AW152246.1	EST_HUMAN	xg40c10.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
10439	22833	35941	1.31	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
10459	22953	35982	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10459	22953	35963	2.03	2.5E-01	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
10955	23470	36495	4.3	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
11712	24122	37153	5.29	2.5E-01	AF200328.1	NT	Zea mays cellulose synthase-4 (Cesa-4) mRNA, complete cds
11740	25075		10.13	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
579	13208	25987	1.67	2.4E-01	AA936316.1	EST_HUMAN	on70d04.a1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
881	13495	26014	2.4	2.4E-01	BF578124.1	EST_HUMAN	60213244F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1347	13942	28464	21.36	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1347	13942	28465	21.38	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1427	14020	28548	0.83	2.4E-01	Y17293.1	NT	Homo sapiens FLI-1 gene, partial
1891	14478		27.27	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mktip mRNA, complete cds
1944	14528	27084	1.17	2.4E-01	AF251708.1	NT	Zaocys dhumnades fucose-1,6-bisphosphatase mRNA, complete cds
2079	14659	27230	1.49	2.4E-01	AF742958.1	EST_HUMAN	wg76d05.x1 Soares NSF F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371017 3' similar to TR:O60267 O60267 KIAA0512 PROTEIN ;
2183	14759	27328	1.04	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2213	14798		1.04	2.4E-01	P45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2302	14875	27451	1.78	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome
2425	14993	27566	1.26	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCL_CGAP_Col16 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XENLA
2575	15138	27708	3.05	2.4E-01	Z36534.1	NT	O42588 28S PROTEASE REGULATORY SUBUNIT 6A ;
2790	15343	27813	1.79	2.4E-01	X71783.1	NT	D discoideum (Ax3-K) penA gene
2812	15364	27833	3.88	2.4E-01	AF030154.1	NT	S.pombe swi8 gene
3166	15780		3.27	2.4E-01	U72726.1	NT	Bovine adenovirus 3 complete genome
3182	15795	28267	1.38	2.4E-01	X74208.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3724	16325	28792	1.26	2.4E-01	AF169793.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
3824	16424	28886	0.83	2.4E-01	AE000312.1	NT	Podospira anserina HET-C protein (Het-c) gene, complete cds
4103	16697		0.6	2.4E-01	D29960.1	NT	Escherichia coli K-12 MG1655 section 202 of 400 of the complete genome
5008	17581	30024	1.08	2.4E-01	AE000305.1	NT	Rattus norvegicus mRNA for alphaB crystallin-related protein, complete cds
5220	17785	30203	0.93	2.4E-01	BE737592.1	EST_HUMAN	Escherichia coli K-12 MG1655 section 195 of 400 of the complete genome
5302	17864		1.55	2.4E-01	K02402.1	NT	601572862F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839775 5'
5653	18280	30758	0.83	2.4E-01	A1925707.1	EST_HUMAN	Human coagulation factor IX gene, complete cds
5653	18280	30759	0.83	2.4E-01	A1925707.1	EST_HUMAN	wc33d05.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5676	18303	30785	0.85	2.4E-01	D50871.1	NT	wc33d05.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457129 3'
5836	18460	31182	7.92	2.4E-01	AF091216.1	NT	Glycine max mRNA for mitotic cyclin b1-type, complete cds
5836	18460	31183	7.92	2.4E-01	AF091216.1	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
6050	24754		1.02	2.4E-01	AJ133836.2	NT	Mus musculus Wrm protein (Wrm) gene, complete cds
						NT	Branchiostoma floridae mRNA for calmodulin 2 (calM2 gene)
6054	18872	31411	2.36	2.4E-01	BF592336.1	EST_HUMAN	7154d04.x1 NCL_CGAP_Br16 Homo sapiens cDNA clone IMAGE:3338503 3' similar to SW:SFR4_HUMAN
6138	18752	31510	2.5	2.4E-01	AF035546.1	NT	Q08170 SPLICING FACTOR, ARGININE/SERINE-RICH 4 ;contains element TART1 TART1 repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6240	18849	31619	2.28	2.4E-01	7661801	NT	Homo sapiens HSPC142 protein (HSPC142), mRNA
6290	18898	31669	0.8	2.4E-01	AV733787.1	EST_HUMAN	AV733787 cDNA Homo sapiens cDNA clone cDAAD11 5'
6656	19252	32055	2.43	2.4E-01	AI698989.1	EST_HUMAN	w62c11.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to gb.J03484 PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN);
7381	19907	32772	8.84	2.4E-01	L43001.1	NT	Bos taurus guanylyl cyclase-activating protein 2 (guca2) mRNA, complete cds
7709	20218	33106	1.08	2.4E-01	AF229644.1	NT	Mus musculus DXImx48e protein (DXImx48e) mRNA, complete cds
8139	20680	33591	0.71	2.4E-01	AJ008397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8139	20680	33592	0.71	2.4E-01	AJ008397.1	NT	Streptococcus pneumoniae r08 and h08 genes; two component system 08
8290	20831	33752	1.66	2.4E-01	AJ012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
8535	21074	33994	0.97	2.4E-01	BF242794.1	EST_HUMAN	601877679F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106288 5'
8588	21127		0.58	2.4E-01	BF678275.1	EST_HUMAN	602086188F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250372 5'
9059	21596	34528	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9059	21596	34527	0.58	2.4E-01	AL139077.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 4/6
9482	21881	34826	6.84	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330806 3' similar to contains MER22 b1 TAR1 repetitive element;
9620	22120	35083	0.8	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
9620	22120	35084	0.6	2.4E-01	AF220087.1	NT	Drosophila melanogaster SKPB gene, complete cds
10335	22829	35823	1.95	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
10647	23179	36192	3.25	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
10715	23243	36260	2.9	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
11081	23583		2.28	2.4E-01	Z21847.1	NT	P. asiatica mosaic virus genomic RNA
11665	24089	37145	1.91	2.4E-01	AF217491.1	NT	Homo sapiens fragile T6D oxido reductase (FOR) gene, exon 6
11807	24853		2.65	2.4E-01	AF004213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
11866	24220		2.02	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
12086	24838		2.18	2.4E-01	V01507.1	NT	Gallus gallus gene coding for a-actin
12320	25081		1.5	2.4E-01	BF229975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
12562	24682		2.31	2.4E-01	AL162881.2	NT	Homo sapiens chromosome 21 segment HS21C081
412	13047	25538	0.91	2.3E-01	S75898.1	NT	aromatase [Poephila guttata-zebra finches, ovary, mRNA, 3188 nt]
665	13289		4.4	2.3E-01	U9713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
695	13318	25903	17.02	2.3E-01	U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
969	13580	26092	3.44	2.3E-01	BF311893.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1647	14239	26774	1.19	2.3E-01	AJ245490.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
1674	14286	26800	2.75	2.3E-01	Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
2089	14699		1.29	2.3E-01	AJ235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FEL gene

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2489	15054	27626	2.03	2.3E-01	BE297718.1	EST_HUMAN	60117562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531015 5'
2878	15238	27803	1.18	2.3E-01	MT11319.1	NT	Human erythropoietin gene, complete cds
2851	14024	28552	1.42	2.3E-01	AB015033.1	NT	Marinilabilla agarovorans gyb gene for DNA gyrase subunit B, partial cds, strain:IFO 14957
2990	15606	28086	0.93	2.3E-01	AA601379.1	EST_HUMAN	no16d06.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element; contains element THIR repetitive element;
3120	15734		6.98	2.3E-01	R21732.1	EST_HUMAN	y121b07.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130357 3'
3417	16025	28507	0.78	2.3E-01	H68836.1	EST_HUMAN	y97h10.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213283 5'
3908	16507	28969	1.02	2.3E-01	S82821.1	NT	GSTA5-glutathione S-transferase Yc2 subunit (5' region, intron 1) [rats, Morris hepatoma cell line, Genomic, 2212 nt, segment 1 of 3]
4009	16807		5.14	2.3E-01	7862133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4442	17028	23468	0.83	2.3E-01	R8252.1	EST_HUMAN	y1701.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149017 5'
4489	17074		2.4	2.3E-01	L78789.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4548	17131	29578	0.87	2.3E-01	D90899.1	NT	Synechocystis sp. PCC6803 complete genome, 1/27, 1-133859
4586	17169	29613	2.18	2.3E-01	AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PRKM13) mRNA, complete cds
4652	17234	29690	6.13	2.3E-01	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
5180	17585	30028	0.62	2.3E-01	J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5202	17767	30191	0.62	2.3E-01	AB032400.1	NT	Mus musculus tulip 1 mRNA, complete cds
5403	17981	30372	0.9	2.3E-01	AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5507	18140	30552	2.39	2.3E-01	AB040845.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
							7130b06.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3476899 3' similar to SW:GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]. ;
5821	18250	30718	2.05	2.3E-01	BF058381.1	EST_HUMAN	C.familialis rom1 gene
5721	18347	31050	4.56	2.3E-01	X96587.1	NT	Vitiforma corneum small subunit ribosomal RNA gene
5831	18455		1.19	2.3E-01	L39112.1	NT	23S rRNA [Leuconostoc carnosum, Genomic, 2866 nt]
5926	18548	31274	0.78	2.3E-01	S60371.1	NT	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6096	18712	31451	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6096	18712	31462	2.34	2.3E-01	A1708840.1	EST_HUMAN	as27e12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2318446 3' similar to gb:U13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6782	19355	32184	0.76	2.3E-01	AF198099.1	NT	Oryctolagus cuniculus cytochrome oxidase subunit Via (coxVia2) mRNA, complete cds; nuclear gene for mitochondrial product
6959	19538	32380	4.1	2.3E-01	A1718148.1	EST_HUMAN	as42f12.x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Alu repetitive element;
7165	19697	32544	0.7	2.3E-01	8923323	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7331	19858	32721	0.69	2.3E-01	AF000227.1	NT	Secale cereale omega secalin gene, complete cds
7445	19969	32837	2.42	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
7603	20116		3.63	2.3E-01	8754779	NT	Mus musculus myosin XV (Myo15), mRNA
7608	20121	32998	1.63	2.3E-01	BE898071.1	EST_HUMAN	601511573F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
7732	20240		2.86	2.3E-01	N80983.1	EST_HUMAN	z12908.r1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:292359 5'
7793	20336	33243	0.58	2.3E-01	AL161568.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 58
7835	20477	33387	1.93	2.3E-01	M68931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tel-alpha alanine version) gene, complete cds
8430	20970	33882	0.6	2.3E-01	U57999.1	NT	Mus musculus prosaposin (psap/SGP-1) gene, complete cds
9067	21604	34534	0.87	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9067	21604	34535	0.87	2.3E-01	AA372164.1	EST_HUMAN	EST84061 Rhabdomyosarcoma Homo sapiens cDNA 5' end similar to DnaJ homolog (GB:X63368)
9501	22001	34958	0.65	2.3E-01	6679318	NT	Mus musculus phosphatidylinositol 3-kinase catalytic subunit delta (Pik3cd), mRNA
9644	22144	35112	0.51	2.3E-01	BE277860.1	EST_HUMAN	601120110F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2988739 5'
9697	22196	35169	0.76	2.3E-01	AW984460.1	EST_HUMAN	EST376533 MAGE resequences, MAGH Homo sapiens cDNA
9746	22244	35225	1.22	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HincII restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HincII endonuclease (EC 3.1.21.4))
9781	22279	35264	0.56	2.3E-01	AW364633.1	EST_HUMAN	PM2-DT0036-281298-001-04 DT0036 Homo sapiens cDNA
9847	22345	35326	2.6	2.3E-01	BE173060.1	EST_HUMAN	MR0-HT0569-240400-014-g11 HT0569 Homo sapiens cDNA
9903	22400	35373	1.93	2.3E-01	AJ293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
10339	22833	35828	0.94	2.3E-01	AF201929.1	NT	Murine hepatitis virus strain 2, complete genome
10351	22845		5.86	2.3E-01	BF133577.1	EST_HUMAN	601646155R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
10893	23414	36432	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
10893	23414	36433	1.85	2.3E-01	AF004833.1	NT	Mus musculus tissue factor pathway inhibitor (TFPI) mRNA, complete cds
11088	23560	36619	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11088	23580	36620	1.85	2.3E-01	AJ250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
11230	23761	36817	2.49	2.3E-01	AE002167.2	NT	Chlamydia pneumoniae AR39, section 4 of 94 of the complete genome
11624	24066		1.6	2.3E-01	AV709736.1	EST_HUMAN	AV709736 ADC Homo sapiens cDNA clone ADCAGH01 5'
11768	24172		2.82	2.3E-01	U45428.1	NT	Borrelia burgdorferi 2-9-6 locus, ORF-A-D genes, complete cds and REP+ gene, partial cds
11876	24226		57.94	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCOE44 5'
11899	24804		1.31	2.3E-01	AA089819.1	EST_HUMAN	ch1424 seq F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
11908	24246		1.61	2.3E-01	AW863940.1	EST_HUMAN	PM4-SJN0012-030400-001-506 SJN0012 Homo sapiens cDNA
11989	25002	30810	3.1	2.3E-01	AW303823.1	EST_HUMAN	xv21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR:Q9Z175 Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2, contains PTR5.62 TAR1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12007	25053	30511	10.96	2.3E-01	BE882484.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
12057	24340		1.94	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
12107	24369		3.11	2.3E-01	AJ005519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12205	24429		1.36	2.3E-01	U49645.1	NT	Pleurodeles welli distal-less like protein PwDlx-3 (PwDlx-3) mRNA, complete cds
12211	24369		1.67	2.3E-01	AJ005519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
12480	24614		2.57	2.3E-01	BF475611.1	EST_HUMAN	nec39h12.x1 Lupski_sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
12668	24888	30710	1.26	2.3E-01	AA094108.1	EST_HUMAN	MER38 repetitive element;
93	12769	25252	0.91	2.2E-01	AJ052190.1	EST_HUMAN	g1864.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
1611	14204	26736	2.85	2.2E-01	AF187850.1	NT	oz14a10.x1 Scores_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to
2063	14643		3.89	2.2E-01	AF171801.1	NT	TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
2136	14714	27287	3.16	2.2E-01	M34640.1	NT	Homo sapiens PPAR delta gene, promoter region
2447	15014	27586	5.61	2.2E-01	BF677538.1	EST_HUMAN	Trimeresurus malabaricus cyb gene, partial cds; mitochondrial gene for mitochondrial product
2623	15185	27751	1.27	2.2E-01	BE618258.1	EST_HUMAN	Fresh-water sponge Emf1 alpha collagen (COLF1) gene
2703	15250		1.17	2.2E-01	AL163218.2	NT	602085609F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249989 5'
2906	15523	27993	4.28	2.2E-01	BE155625.1	EST_HUMAN	601462628F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3866190 5'
2906	15523	27994	4.28	2.2E-01	BE155625.1	EST_HUMAN	601462628F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:3866190 5'
2947	15563		1.64	2.2E-01	AF020503.1	NT	Homo sapiens chromosome 21 segment HS21C018
3439	16047		2.67	2.2E-01	AL161562.2	NT	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
3886	16484		1.18	2.2E-01	AF155728.1	NT	PM2-HT0353-281299-003-a12 HT0353 Homo sapiens cDNA
4281	16877		1.26	2.2E-01	AF119102.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4300	16886	29330	7.03	2.2E-01	AF155142.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
4350	16937	29378	2.59	2.2E-01	AF117340.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4350	16937	29379	2.59	2.2E-01	AF117340.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4447	17033	29475	1.36	2.2E-01	U01307.1	NT	Mus musculus mixed lineage kinase 3 (Mlks3) and two pore domain K+ channel subunit (Kcnk6) genes, complete cds
4447	17033	29476	1.36	2.2E-01	U01307.1	NT	Mus musculus MAP kinase kinase 1 (Mek11) mRNA, complete cds
4952	17527		1.35	2.2E-01	D50804.1	NT	Mus musculus MAP kinase kinase 1 (Mek11) mRNA, complete cds
4957	17532	29974	2.86	2.2E-01	AA21216.1	EST_HUMAN	Human scRNA (BC200 beta) pseudogene
5196	17761		1.33	2.2E-01	L13299.1	NT	Human scRNA (BC200 beta) pseudogene
5203	17768		1.79	2.2E-01	AE001137.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
							z087c05.r1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:648968 5'
							Mus musculus vinculin gene, exon 3
							Borrelia burgdorferi (section 23 of 70) of the complete genome

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5291	17853	30277	1.2	2.2E-01	BE141035.1	EST_HUMAN	MR0-HT0067-201099-002-c10 HT0067 Homo sapiens cDNA
5316	17878		0.9	2.2E-01	S57565.1	NT	histamine H2-receptor [rats, Genomic, 1928 nt]
5919	18541	31267	2.46	2.2E-01	5803002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5930	18552		3.53	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6150	18763	31525	0.73	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6150	18763	31526	0.73	2.2E-01	U67087.1	NT	Gallus gallus T-box containing protein (Ch-Tbx1) mRNA, complete cds
6807	19398	32212	0.85	2.2E-01	AB038490.1	NT	Homo sapiens gene for fukutin, complete cds
7093	19664	32503	9.14	2.2E-01	AV756238.1	EST_HUMAN	AV756238 BM Homo sapiens cDNA clone BMFAHC08 5'
7183	19715	32562	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7183	19715	32563	1.46	2.2E-01	AF082738.1	NT	Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes
7333	19860	32723	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7333	19860	32724	2.01	2.2E-01	M24136.1	NT	Human glycophorin B gene, exon 4
7698	20197	33085	0.68	2.2E-01	AF267967.1	NT	Homo sapiens homeobox B7 (HOXB7) gene, partial cds; and homeobox B6 (HOXB6), homeobox B5 (HOXB5), homeobox B4 (HOXB4), and homeobox B3 (HOXB3) genes, complete cds
7963	20505		3.06	2.2E-01	AF155143.1	NT	Mus musculus mm23-M1 gene, promoter region
8032	20574	33479	0.84	2.2E-01	Z49833.1	NT	E. coli sepA and sepB genes
8815	21354	34277	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8815	21354	34278	0.57	2.2E-01	L23312.1	NT	Mouse HD protein mRNA, complete cds
8827	21366	34290	3.48	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome
8847	21388	34310	1.02	2.2E-01	U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
8952	21490		3.12	2.2E-01	AW85039.1	EST_HUMAN	PM3-CT0263-241299-009-b07 CT0263 Homo sapiens cDNA
9043	21580	34509	1.82	2.2E-01	8393247	NT	Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Deaf1), mRNA
9126	21661	34604	1.95	2.2E-01	BF376354.1	EST_HUMAN	MR1-TN0045-110900-008-c02 TN0045 Homo sapiens cDNA
9213	21730	34673	1.24	2.2E-01	W02988.1	EST_HUMAN	z6408.11 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE.291591 5'
9231	21953	34603	14.03	2.2E-01	P49634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED TRANSCRIPT 2)
9274	21800	34750	0.74	2.2E-01	AJ009839.1	NT	Xenopus laevis mRNA for kinesin-like protein 3 (xklp3)
9285	21865	34830	0.71	2.2E-01	7657428	NT	Mus musculus osteoblast specific factor 2 (OSF-2), mRNA
9288	21868	34845	3.69	2.2E-01	M89843.1	NT	Brachydanio rerio ependymin beta and gamma chains (Epd) gene, complete cds
9539	22039	35000	0.59	2.2E-01	Q80980	SWISSPROT	CYCIC NUCLEOTIDE GATED CHANNEL, ROD PHOTORECEPTOR, ALPHA SUBUNIT (CNG CHANNEL 3) (CNG-3) (CNG3)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9729	22227	35204	3.1	2.2E-01	AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPsHSP21) mRNA, complete cds;
9864	22361	35341	2.23	2.2E-01	BF206507.1	EST_HUMAN	nuclear gene for chloroplast product
10079	22574	35569	0.87	2.2E-01	682587.1	NT	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
10340	22834		0.81	2.2E-01	AF071001.1	NT	Human herpesvirus 5, complete genome
10384	22878	35870	0.72	2.2E-01	AE001582.1	NT	Mus musculus PHR1 (Phr1) gene, partial cds
10384	22878	35871	0.72	2.2E-01	AE001582.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11005	23518	36554	1.6	2.2E-01	AF257772.1	NT	Helicobacter pylori, strain J99 section 123 of 132 of the complete genome
11299	23751	36808	5.56	2.2E-01	X01918.1	NT	Homo sapiens RNA binding protein MCG10 gene, complete cds, alternatively spliced
11335	23033	36042	3.18	2.2E-01	7706215	NT	Drosophila 68C glue gene cluster
11715	24125		1.8	2.2E-01	BE870959.1	EST_HUMAN	Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
11827	25065						601448957F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850870 5'
11910	24248		6.34	2.2E-01	U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and L1>
12024	18029	30491	5.37	2.2E-01	AF188843.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
12025	24317		1.7	2.2E-01	AW381098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
12575	25058		1.85	2.2E-01	AW681922.1	EST_HUMAN	h17b02.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2972523 3'
12659	24730	30855	4.05	2.2E-01	AV694801.1	EST_HUMAN	AV694801 GK6 Homo sapiens cDNA clone GKCAHB02 5'
1006	13617	26132	2.44	2.2E-01	BF243095.1	EST_HUMAN	601876452F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104988 5'
1009	13619	26134	1.36	2.1E-01	AA589289.1	EST_HUMAN	nm31e11.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1051804
1163	13765		1.27	2.1E-01	AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1240	13838	26354	2.41	2.1E-01	AE002314.2	NT	Chlamydia muridarum, section 45 of 85 of the complete genome
1240	13838	26355	0.85	2.1E-01	6754299	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1557	14149	26881	0.85	2.1E-01	6754289	NT	Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1937	14541	27097	3.45	2.1E-01	AJ248985.1	NT	Mus musculus mas proto-oncogene and Igf2r gene for insulin-like growth factor type 2 and L41ps and Au76 pseudogenes
2201	14777	27350	1.84	2.1E-01	AA906824.1	EST_HUMAN	ck73a02.s1 NCI_CGAP_GCA Homo sapiens cDNA clone IMAGE:1518610 3' similar to gb:K02765
2386	14954	27526	3.39	2.1E-01	BF695073.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2851	15567	28041	2.01	2.1E-01	6753235	NT	602083128F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
3879	16477						Mus musculus calcium channel, voltage dependent, alpha2/delta subunit 3 (Caena2d3), mRNA
4129	16721	29176	2.53	2.1E-01		NT	Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
			6.58	2.1E-01	6912445	NT	Beta vulgaris mitochondrion, complete genome
			1.22	2.1E-01	P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180

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4129	16721	29177	1.22	2.1E-01	P11875	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4336	16923		1.38	2.1E-01	AF124526.1	NT	Orchestria cavimana calcium-binding protein BP23 precursor (BP23) gene, complete cds
4465	17051		1.51	2.1E-01	AB033041.1	NT	Homo sapiens mRNA for KIAA1215 protein, partial cds
4676	17258	29709	1.83	2.1E-01	AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
5083	17656	30097	1.63	2.1E-01	U76409.1	NT	Lycopodium esculentum homeobox 1 protein (THox1) mRNA, partial cds
5434	17890	30396	0.98	2.1E-01	J05082.1	NT	Vampire bat (D. rotundus) plasminogen activator mRNA, complete cds
5504	18138	30548	6.55	2.1E-01	BF672695.1	EST_HUMAN	602152001F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283001 5'
6987	19544	32369	1.16	2.1E-01	AJ233392.1	NT	Doto fragilis mitochondrial 16S rRNA gene, partial
6979	19477	32299	2.04	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds
7436	19980	32825	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7436	19980	32826	1.24	2.1E-01	Q01956	SWISSPROT	VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)
7447	19971		2.17	2.1E-01	AE000972.1	NT	Archaeoglobus fulgidus section 135 of 172 of the complete genome
7692	20201	33088	2.02	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds
7731	20239	33130	1.14	2.1E-01	AF068697.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7731	20239	33131	1.14	2.1E-01	AF068697.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7765	20273		0.68	2.1E-01	T87354.1	EST_HUMAN	yt83b01.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:114793 5'
8017	20559		1.19	2.1E-01	7305030	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.13), mRNA
8439	20979	33894	4.93	2.1E-01	U88399.1	NT	Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds
8732	21271	34190	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8732	21271	34191	0.82	2.1E-01	AL040537.1	EST_HUMAN	DKFZp434H0814_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434H0814 5'
8898	21426		0.47	2.1E-01	AB022524.1	NT	Homo sapiens APC gene, exon 9
8987	21505	34426	5.93	2.1E-01	235788.1	NT	S. cerevisiae chromosome II reading frame ORF YBLO28w
9423	21932	34880	0.6	2.1E-01	N42536.1	EST_HUMAN	yt11e10.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:270954 5'
9423	21932	34881	0.6	2.1E-01	N42536.1	EST_HUMAN	yt11e10.r1 Soares melanocyte 2Nbl-HM Homo sapiens cDNA clone IMAGE:270954 5'
9432	21958	34906	2.95	2.1E-01	X87378.1	NT	A. thaliana mRNA for ARRLBP1b protein
9536	22036	34996	1.57	2.1E-01	AB036529.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 8
10232	22727	35719	1.04	2.1E-01	297067.1	NT	Beta vulgaris mRNA for elongation factor 1-beta
10263	22758	35745	1.96	2.1E-01	P52824	SWISSPROT	DIACYLGLYCEROL KINASE, DELTA (DGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)
10269	22764	35751	0.67	2.1E-01	BF574254.1	EST_HUMAN	602131427F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270831 5'

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Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10505	22889	36007	0.5	2.1E-01	AF294286.1	NT	Anolis lineatopus isolate NG NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
11438	23888		2.24	2.1E-01	11036647	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA
11451	23901	36969	2.34	2.1E-01	BE180422.1	EST_HUMAN	RC3-HIT0622-040500-013-b11 HT0622 Homo sapiens cDNA
11641	24602		1.39	2.1E-01	X57024.1	NT	Drosophila melanogaster ALA-E8 DNA, repeat region
12183	24418		1.46	2.1E-01	AF217490.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12465	24593		1.72	2.1E-01	BE622149.1	EST_HUMAN	601440712F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915675 5'
12607	24691	30858	2.08	2.1E-01	BE672330.1	EST_HUMAN	7a59a02.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3223034 3'
12812	24695	30861	1.26	2.1E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
214	12875	25362	1.86	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avian, complete cds
559	13190		2.2	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
728	13348	25840	1.24	2.0E-01	M77085.1	NT	O. cuniculus germline IgH heavy chain V-H pseudogene, allotype VHa2
843	13459	25968	1.76	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region
1049	13656	26167	0.72	2.0E-01	D80905.1	NT	Synechocystis sp. PCC6803 complete genome, 7/27, 781449-920915
1104	13766	26276	3.24	2.0E-01	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
1297	13881	26414	1.37	2.0E-01	AJ132695.5	NT	Homo sapiens rac1 gene
1351	13946	26470	1.22	2.0E-01	AW384937.1	EST_HUMAN	PM1-HT0422-261269-002-c08 HT0422 Homo sapiens cDNA
1507	14089		1.22	2.0E-01	AJ243957.1	NT	Plum pox virus strain M, complete genome, isolate PS
1534	14126	26663	23.08	2.0E-01	4503408	NT	Homo sapiens dystrobrevin, alpha (DTNA), mRNA
1589	14181	26722	3.03	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1604	14196	26728	1.23	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1735	14326	26868	1.17	2.0E-01	U23246.1	NT	Human bradykinin B1 receptor (bradyb1) gene, complete cds
1755	14345		1.83	2.0E-01	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
1795	14385		1.99	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 87 of 150 of the complete genome
1834	14518	27073	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1934	14518	27074	1.14	2.0E-01	BE871330.1	EST_HUMAN	601449441F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853330 5'
1937	14521	27077	1	2.0E-01	8922238	NT	Homo sapiens hypothetical protein FLJ10120 (FLJ10120), mRNA
2386	14955		1.64	2.0E-01	X82877.1	NT	H. sapiens Na+-D-glucose cotransport regulator gene
2915	15532		0.66	2.0E-01	AF074990.1	NT	Homo sapiens full length insert cDNA YH85A11
3534	16139	28621	0.7	2.0E-01	P46607	SW/ISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3626	16229		0.82	2.0E-01	AW238005.1	EST_HUMAN	xp15b02.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2740395 3' similar to contains element MER21 repetitive element
3768	16369	28835	0.8	2.0E-01	P34641	SW/ISSPROT	GED-11 PROTEIN

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4028	16828	29098	0.76	2.0E-01	Z46906.1	NT	Sus scrofa
4102	16696	29152	0.66	2.0E-01	X83997.1	NT	C.parasitica espC gene
4522	17106	29552	0.76	2.0E-01	AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Naip6) gene, complete cds; and Naip3 gene, exons 2-9 and 11-16
4665	17247	30186	8.43	2.0E-01	BE820165.1	EST_HUMAN	QV4-EN0032-190500-223-403 EN0032 Homo sapiens cDNA
5192	17757	30186	7.09	2.0E-01	8922080	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5226	16139	28621	0.62	2.0E-01	P46607	SWISSPROT	HOMEOBOX PROTEIN GLABRA2 (HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
5636	18265	30737	2.36	2.0E-01	X56800.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5916	18538	31263	2	2.0E-01	11432540	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
6006	18628	31361	0.69	2.0E-01	X91856.1	NT	F.rubripes DNA encoding for valyl-tRNA synthetase
6210	18920	31591	6.46	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hef5p (HAL5) mRNA, complete cds
6321	18928	31591	0.71	2.0E-01	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
6560	19158	31955	3.94	2.0E-01	X61033.1	NT	M.aureus mu class glutathione transferase gene
6650	19246	32049	3.63	2.0E-01	AW360865.1	EST_HUMAN	PM1-CT0247-141099-001-g08 CT0247 Homo sapiens cDNA
7251	19780	32636	0.68	2.0E-01	U39724.1	NT	Mycoplasma genitalium section 48 of 51 of the complete genome
7336	19863	32727	1.18	2.0E-01	AF250371.1	NT	Mus musculus phosphofructokinase-1 C isozyme (Pfkce) gene, exons 3 through 7
7775	20284	33181	1.53	2.0E-01	AK024427.1	NT	Homo sapiens mRNA for FLJ00016 protein, partial cds
7895	20437	33595	6.45	2.0E-01	AF028026.1	NT	Andes virus strain OI23133 glycoprotein G1 and G2 precursor, gene, partial cds
8142	20683	33595	2.91	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
8658	21197	34749	0.53	2.0E-01	BE562247.1	EST_HUMAN	601344648F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677794 5'
9273	21799	34749	1.03	2.0E-01	U82511.1	NT	Dichytetium discoidium random slug cDNA19 protein (rsc19) mRNA, partial cds
9312	21826	34775	0.65	2.0E-01	U71122.1	NT	Arabidopsis pyruvate decarboxylase-2 (Pdc2) gene, complete cds
9475	21874	35132	4.35	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
9661	22160	35132	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9661	22160	35133	0.51	2.0E-01	P11420	SWISSPROT	DAUGHTERLESS PROTEIN
9808	22304	35431	1.98	2.0E-01	AF146892.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
9854	22449	35431	1.79	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
9854	22449	35432	1.79	2.0E-01	AF086907.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
10072	22567	35562	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10072	22567	35563	0.53	2.0E-01	AF157814.1	NT	Homo sapiens cAMP specific phosphodiesterase (PDE4C) gene, exons 2 through 12
10115	22610	35789	0.72	2.0E-01	X78398.1	NT	D.melanogaster DNA mobile element (hoppe)
10304	22798	35789	0.88	2.0E-01	X97121.1	NT	R.novgigius mRNA for NTR2 receptor
10720	23248	36263	2.77	2.0E-01	D89088.1	NT	Salvelinus pluvius mRNA for transferrin, complete cds

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10720	23248	38264	2.77	2.0E-01	D89088.1	NT	Salvelinus plusvius mRNA for transferrin, complete cds
12162	24402		1.34	2.0E-01	AF206637.2	NT	Pimephales promelas liver glucose-6-phosphate-1-dehydrogenase mRNA, partial cds
12374	24887		1.95	2.0E-01	AF302773.1	NT	Homo sapiens ninenin-Lm isoform (ninenin) mRNA, complete cds
12386	24807	30788	2.81	2.0E-01	AW975297.1	EST_HUMAN	EST387405 MAGC resequences; MAGN Homo sapiens cDNA
12425	24610	30888	3.97	2.0E-01	AD23592.1	EST_HUMAN	ov80a10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643610 3'
12449	24584		17.06	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds
115	12786		6.22	1.9E-01	7549743	NT	Rattus norvegicus Aryl hydrocarbon receptor nuclear translocator 1 (Ahr1), mRNA
374	13023	25509	5.4	1.9E-01	AF004353.1	NT	Mus musculus pale ear (ep) gene, wild type allele, 3' region, partial cds
684	13308	25792	1.47	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
684	13308	25793	1.47	1.9E-01	U32581.2	NT	Homo sapiens lambda/ota protein kinase C-interacting protein mRNA, complete cds
691	13315	25800	6.8	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
692	13315	25800	6.82	1.9E-01	BE070801.1	EST_HUMAN	RC3-BT0502-251199-011-d01 BT0502 Homo sapiens cDNA
1023	13633		1.92	1.9E-01	7305180	NT	Mus musculus interleukin 2 receptor, gamma chain (Il2rg), mRNA
1143	13746	26256	10.04	1.9E-01	AA358813.1	EST_HUMAN	EST87784 Fetal lung II Homo sapiens cDNA 5' end
1413	14006	26534	2.41	1.9E-01	AF081282.1	NT	Sorghum bicolor 22 kDa kafirin cluster
1482	14075		4.02	1.9E-01	AF184623.1	NT	Plasmodium vivax reticulocyte binding protein-2 (rpb-2) gene, complete cds
2185	14761	27331	1.29	1.9E-01	AA816492.1	EST_HUMAN	644409.s1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:1526369 3' similar to gb:A03911
2422	14900	27563	3.27	1.9E-01	8922533	NT	GLIA DERIVED NEXIN PRECURSOR (HUMAN);
2949	15565	28039	4.1	1.9E-01	U66066.1	NT	Homo sapiens hypothetical protein FLJ10581 (FLJ10581), mRNA
2965	15580		6.58	1.9E-01	J00922.1	NT	Sigmodon hispidus p53 gene, partial cds
3033	15649	28128	1.05	1.9E-01	U25148.1	NT	Gallus gallus ovalbumin (Y) gene, complete cds
3442	16050	28528	4.19	1.9E-01	D13197.1	NT	Rattus norvegicus brush border myosin-I (BBMI) mRNA, partial cds
3526	16131	28611	5.24	1.9E-01	RT6467.1	NT	Mouse gene for immunoglobulin diversity region D1
3877	16475	28839	0.76	1.9E-01	AF264017.1	EST_HUMAN	y42710.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128547 5'
4084	16681	29123	3.85	1.9E-01	AB008784.1	NT	Rattus norvegicus arylacetamide deacetylase gene, complete cds
4157	16749	29202	1.86	1.9E-01	AW754106.1	EST_HUMAN	Schizosaccharomyces pombe DNA for cytoplasmic dynein heavy chain, complete cds
4315	16901	29345	1.17	1.9E-01	BE834943.1	EST_HUMAN	CM3-CT0315-271199-045-b11 CT0315 Homo sapiens cDNA
4568	17151	29597	0.69	1.9E-01	AL161483.2	EST_HUMAN	MR1-FN0010-280700-007-404 FN0010 Homo sapiens cDNA
5156	17726		1.11	1.9E-01	AF223642.1	NT	Arahidopsis thaliana DNA chromosome 4, contig fragment No. 5
						NT	Rattus norvegicus chemokine receptor CXCR3 mRNA, complete cds
5789	18414		5.46	1.9E-01	AW130149.1	EST_HUMAN	x29807.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2619444 3' similar to gb:M73779 RETINOIC
5826	18450	31173	7.81	1.9E-01	AF127837.1	NT	ACID RECEPTOR ALPHA-1 (HUMAN);
6005	18625	31360	0.73	1.9E-01	AF091216.1	NT	Homo sapiens DNA polymerase epsilon catalytic subunit protein (POLE1) gene, exon 1a
						NT	Mus musculus Wrm protein (Wrm) gene, complete cds

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6046	18665		2.52	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP4001328 5'
6469	19070	31855	1.07	1.9E-01	AI762391.1	EST_HUMAN	wf54h02.x1 NCL_CGAP_Cot6 Homo sapiens cDNA clone IMAGE:2394099 3'
6523	19123	31915	1.23	1.9E-01	AW148452.1	EST_HUMAN	xf14c08.x1 NCL_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618030 3' similar to gb:X03559 ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (HUMAN);
7050	18069	30480	1.37	1.9E-01	R43212.1	EST_HUMAN	y909a12.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13 repetitive element;
7072	19644	32481	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7072	19644	32482	0.91	1.9E-01	AF034920.1	NT	Homo sapiens tubby like protein 1 (TULP1) gene, exons 9-11
7503	20025	32889	1.3	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds
7543	20063	32937	2.89	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme 1 (sbe1) gene, complete cds
7927	20469	33378	1.71	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57
8620	21159	34074	12.12	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds
8875	21414	34337	1.36	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
8875	21414	34338	1.36	1.9E-01	M14568.1	NT	Marsupial cat beta-globin gene mRNA, partial cds
9789	22287	35271	0.72	1.9E-01	AA912488.1	EST_HUMAN	cl96g10.s1 NCL_CGAP_PNS1 Homo sapiens cDNA clone IMAGE:1537506 3' similar to contains Alu repetitive element
10140	22635	35626	0.71	1.9E-01	BE830353.1	EST_HUMAN	RCS-E T0082-060700-022-A02 E T0082 Homo sapiens cDNA
10140	22635	35627	0.71	1.9E-01	BE830353.1	EST_HUMAN	RCS-E T0082-060700-022-A02 E T0082 Homo sapiens cDNA
10523	23081	36071	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10523	23081	36072	2.02	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15
10635	23167	36178	2.06	1.9E-01	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11377	23829	36891	1.68	1.9E-01	M22253.1	NT	Rattus norvegicus sodium channel I mRNA, complete cds
11571	24018	37088	2.69	1.9E-01	AJ249213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
12207	24431		1.33	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds
12582	24874		3.69	1.9E-01	AF001169.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds
34	12713	25172	2.56	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds
281	15412	25423	1.67	1.8E-01	AB022090.1	NT	Mus musculus Cctg gene for chaperonin containing TCP-1 gamma subunit, partial cds
393	13039	25530	1.76	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products
776	13395	25896	0.77	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OIGC1, complete cds
1018	13628	28141	0.78	1.8E-01	AI912212.1	EST_HUMAN	wf1102.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3'
1130	13732	26242	1.26	1.8E-01	AF000580.1	NT	Dicystelium discoideum plasmid Dap5, complete genome
1332	13926	26447	6.97	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1

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1551	14143	26676	1.31	1.8E-01	8753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1551	14143	26677	1.31	1.8E-01	8753947	NT	Mus musculus guanylate nucleotide binding protein 1 (Gbp1), mRNA
1887	14472		2.79	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA
1907	14492		2.22	1.8E-01	A1733708.1	EST_HUMAN	qg22d10.x6 NCI CGAP_K1d3 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR:O75936 O75936 GAMMA BUTYROBETAINE HYDROXYLASE;
1958	14542	27098	1.52	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
2716	15273		2.26	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0016-081299-036-g04 DT0018 Homo sapiens cDNA
2923	15540		2.36	1.8E-01	AF184589.1	NT	Junosidum acaule LEAFY protein (LEAFY2) gene, partial cds
2928	15544	28020	1.18	1.8E-01	AW182300.1	EST_HUMAN	x41a03.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3'
3158	15772	28239	1.31	1.8E-01	AW995178.1	EST_HUMAN	QV0-BN0041-070300-147-g04 BN0041 Homo sapiens cDNA
3413	16021	28501	0.71	1.8E-01	BF183582.1	EST_HUMAN	601809723R1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040621 3'
3683	16284	28752	0.79	1.8E-01	H03369.1	EST_HUMAN	Y445e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
3683	16284	28753	0.79	1.8E-01	H03369.1	EST_HUMAN	Y445e01.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:151704 3' similar to contains Alu repetitive element
4333	16920	29362	0.78	1.8E-01	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4426	17012		4.07	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BdLA-DQB), complete cds
4654	17236	29691	6.59	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4896	17481	29914	2.51	1.8E-01	AB051897.1	NT	Mus musculus Scya6, Scya9, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
4928	17503	29950	1.03	1.8E-01	X92179.1	NT	S.tubercuam mRNA for alcohol dehydrogenase
5198	17763	30188	2.18	1.8E-01	AW814270.1	EST_HUMAN	MR3-ST0203-151299-112-g06 ST0203 Homo sapiens cDNA
5216	17781	30200	1.59	1.8E-01	A1792382.1	EST_HUMAN	en28g07.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700028 5'
5237	17820	30245	1.5	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5281	17843	30270	1.07	1.8E-01	AI439881.1	EST_HUMAN	t57e04.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5288	17850	30276	0.59	1.8E-01	AF132115.1	NT	Arabidopsis thaliana cytochrome b-561 (CYTB561) gene, partial cds
5338	17899	30314	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5338	17899	30315	0.78	1.8E-01	AJ132844.1	NT	Broad bean wilt virus 2 genes encoding 119kDa protein, 104kDa protein, large coat protein, small coat protein
5398	17956	30387	2.04	1.8E-01	AW809402.1	EST_HUMAN	MR4-ST0121-041199-019-b01 ST0121 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5976	18596	31331	1	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
6082	18689	31446	1.01	1.8E-01	N28629.1	EST_HUMAN	Y38H08.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:264063 5'
6277	18865	31653	1.1	1.8E-01	6878428	NT	Mus musculus Trf receptor-associated factor 6 (Traf6), mRNA
6277	18865	31654	1.1	1.8E-01	6878428	NT	Mus musculus Trf receptor-associated factor 6 (Traf6), mRNA
6635	19231	32035	2.03	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
6675	19271		2.24	1.8E-01	N94853.1	EST_HUMAN	Y62H02.r1 Soares multiple_sclerosis_2NbhMSP Homo sapiens cDNA clone IMAGE:278163 5'
7077	19649	32487	1.22	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7077	19649	32488	1.22	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
7177	19457	32272	0.71	1.8E-01	BE981353.1	EST_HUMAN	607648361R2 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3932247 3'
8547	21068	34008	0.47	1.8E-01	AW966118.1	EST_HUMAN	EST378191 MAGE resequences, MAGI Homo sapiens cDNA
9268	21792	34741	1.13	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
9296	21896	34843	1.39	1.8E-01	9626232	NT	Bacteriophage Ika, complete genome
9412	21921		0.55	1.8E-01	AA493751.1	EST_HUMAN	h02a05.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943088 similar to contains L1.13 L1 repetitive element
9494	21694	34950	1.13	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9494	21694	34951	1.13	1.8E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9532	22032	34980	0.95	1.8E-01	M26019.1	NT	S. commune crodine-5'-phosphate decarboxylase (URA1) gene, complete cds
9532	22032	34991	0.95	1.8E-01	M26019.1	NT	S. commune crodine-5'-phosphate decarboxylase (URA1) gene, complete cds
9694	22193	35168	0.62	1.8E-01	P08123	SWISSPROT	COLLAGEN ALPHA 2(I) CHAIN PRECURSOR
9698	22187	35170	0.69	1.8E-01	U67548.1	NT	Methanococcus jannaschii section 90 of 150 of the complete genome
10039	22534		0.64	1.8E-01	AF200262.1	NT	Aquarius amplus cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial gene for mitochondrial product
10271	22768	35753	1.22	1.8E-01	X63440.1	NT	M. musculus mRNA for P19-protein tyrosine phosphatase
10516	23054	36066	2.37	1.8E-01	X77336.1	NT	A. thaliana mRNA for ribonucleotide reductase R2
10558	23094	36106	7.47	1.8E-01	U38906.1	NT	Bacteriophage r11 integrase, repressor protein (ro), dUTPase, holin and lysin genes, complete cds
10615	19649	32487	3.07	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10615	19649	32488	3.07	1.8E-01	AB018561.1	NT	Citullus lanatus mRNA for wsus, complete cds
10616	23148	36160	4.49	1.8E-01	AF019107.1	NT	Dicystostellium discoidium unknown (DG1041) gene, complete cds
10897	23417	36434	1.84	1.8E-01	M59257.1	NT	Human carcinoembryonic antigen (CEA) gene, exon 4
11337	23035	36045	4.3	1.8E-01	X57033.1	NT	B. taurus mRNA for potassium channel
11599	24042	37111	2.74	1.8E-01	8394421	NT	Rattus norvegicus Thromboxane receptor (Tbx2r), mRNA
11628	24068	37132	1.6	1.8E-01	U40487.1	NT	Mycobacterium smegmatis proton antiporter efflux pump (PRA), complete cds
11748	24146		2.04	1.8E-01	10086561	NT	Bovine ephemeral fever virus, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11814	24186	31032	1.41	1.8E-01	BF348623.1	EST_HUMAN	602019828F1 NCJ_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155318 5'
12218	13926	28447	1.3	1.8E-01	AL117180.1	NT	Yersinia pestis plasmid pCD1
12291	24491		5.61	1.8E-01	Q86682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN)(PTP PROTEIN)
12416	24569		23.47	1.8E-01	R24494.1	EST_HUMAN	YH49H10.r1 Soares placenta N52HP Homo sapiens cDNA clone IMAGE:133027 5'
12459	24590		2.75	1.8E-01	Y11114.1	NT	E dispar mRNA for hexokinase (hdx1)
12502	25045	30507	1.58	1.8E-01	9506952	NT	Rattus norvegicus procollagen C-proteinase enhancer protein (Pcolce), mRNA
603	13232	26705	5.53	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'
898	13454	25964	2.99	1.7E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
996	13608		8.63	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE)(NF-L)
1096	13701	28210	0.67	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1096	13701	28211	0.67	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolydnavirus, complete genome
1853	14441	28998	0.95	1.7E-01	AL181573.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 69
2025	14607		2.84	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product
							Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
2885	15503	27973	1.98	1.7E-01	AF000716.1	NT	
2885	15503	27974	1.98	1.7E-01	AF000716.1	NT	
2953	15569	28044	1.53	1.7E-01	AA336909.1	EST_HUMAN	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL VIBCO gene, partial cds
3027	15643	28121	1.9	1.7E-01	AJ238736.1	NT	EST41651 Endometrial tumor Homo sapiens cDNA 5' end
3027	15643	28122	1.9	1.7E-01	AJ238736.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3139	15753	28220	1.91	1.7E-01	AF081514.1	NT	Naja naja atra cbx-1 gene, exons 1-3
3412	16020	28500	1.11	1.7E-01	N55763.1	EST_HUMAN	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds
3494	16099	28574	1.26	1.7E-01	AJ289505.1	NT	J2348F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2348 5'
4012	16610	29083	4.99	1.7E-01	AJ235377.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene
4658	17240		1.63	1.7E-01	X52936.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL/HRX gene fused to intron 5 of the AF-4/FEL gene
4877	17452	28904	0.84	1.7E-01	AF217460.1	NT	Schistosoma gregaria alpha repetitive DNA
4965	17539	29981	1.07	1.7E-01	AJ247635.1	EST_HUMAN	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
5210	17775		0.88	1.7E-01	U28376.1	NT	qh57e09.x1 Soares fetal liver spleen, 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to contains ORF.b1 ORF repetitive element;
5242	17806	30227	1.02	1.7E-01	BF689719.1	EST_HUMAN	Zee mays calcium-dependent protein kinase (MZECDPK2) mRNA, complete cds

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5297	17859		1.08	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme 1b (ae) gene, complete cds
5342	17903	30319	0.6	1.7E-01	BF030010.1	EST_HUMAN	601557266F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827197 5'
5421	17978	30386	7.82	1.7E-01	J04479.1	NT	S.pneumoniae DNA polymerase I (polA) gene, complete cds
5604	18233	30683	1.92	1.7E-01	AA470886.1	EST_HUMAN	ne13a02.st1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb.M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5604	18233	30684	1.92	1.7E-01	AA470886.1	EST_HUMAN	ne13a02.st1 NCL CGAP_C03 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb.M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
5779	18404	31120	0.7	1.7E-01	U43599.1	NT	Brugia pahangi microfilarial sheath protein SHP3 (shp3) gene, complete cds
6471	19072	31856	20.9	1.7E-01	H72118.1	EST_HUMAN	ys02g08.st1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:213658 3'
6522	19122	31913	1.33	1.7E-01	A1370976.1	EST_HUMAN	ta28c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6522	19122	31914	1.33	1.7E-01	A1370976.1	EST_HUMAN	ta28c11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:2045492 3'
6937	18045	30467	0.71	1.7E-01	BE300286.1	EST_HUMAN	600944067T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2980248 3'
6960	19537		2.26	1.7E-01	AF026523.3	NT	Mesocricetus auratus oviductin precursor (OVI) gene, complete cds
7074	19646		0.87	1.7E-01	Z92910.1	NT	Homo sapiens HFE gene
7272	19800	32857	2.83	1.7E-01	AP000422.1	NT	Escherichia coli O157:H7 genomic DNA, Sakai-VT2 prophage inserted region
7339	19866	32730	8.92	1.7E-01	BE734179.1	EST_HUMAN	601565022F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
7494	20017	32862	1.16	1.7E-01	P16724	SWISSPROT	PROBABLE PROCESSING AND TRANSPORT PROTEIN UL56 (HLEF0 PROTEIN)
7508	24784	32893	0.73	1.7E-01	O01955	SWISSPROT	COLLAGEN ALPHA 3(V) CHAIN PRECURSOR
7802	20345	33253	1.26	1.7E-01	AF000573.1	NT	Homo sapiens homocitrate 1,2-dioxygenase gene, complete cds
7804	20446	33332	0.54	1.7E-01	AF150689.1	NT	Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds
8219	20760	33674	6.82	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8219	20760	33675	6.82	1.7E-01	7708428	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
8631	21170	34087	0.58	1.7E-01	AW992873.1	EST_HUMAN	RC2-BN0032-120200-011-a10 BN0032 Homo sapiens cDNA
8682	21201	34119	3.28	1.7E-01	D00384.1	NT	Rat (SHR strain) SX1 gene
8778	21317	34239	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
8778	21317	34240	0.68	1.7E-01	AF217413.1	NT	Homo sapiens neuroigin 3 isoform gene, complete cds, alternatively spliced
9095	21631	34569	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9095	21631	34570	0.46	1.7E-01	BE253142.1	EST_HUMAN	601116672F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357184 5'
9509	22009	34687	7.72	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
9614	22114	35077	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9614	22114	35078	0.56	1.7E-01	AW977455.1	EST_HUMAN	EST389564 IMAGE resequences, MAGO Homo sapiens cDNA
9631	22131	35096	2.47	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
9704	22203	35174	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)
9704	22203	35175	1.27	1.7E-01	Z34508.1	NT	Human immunodeficiency virus type 1 (B7.05) env gene (partial)

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9722	22220	35195	0.81	1.7E-01	AJ251749.1	NT	Drosophila melanogaster mRNA for serine protease inhibitor (serpin-6), (sp6 gene)
10132	22627		2.24	1.7E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
10283	22787	35777	0.99	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
10295	22789	35779	1.72	1.7E-01	AA827972.1	EST_HUMAN	ng60e07.s1 NCI CGAP_C09 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081
10560	23096	36109	9.23	1.7E-01	BE390835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN);
10885	23215	36227	2.63	1.7E-01	AA814617.1	EST_HUMAN	601286547F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
10991	23505	36536	8.7	1.7E-01	71063300	NT	d43a03.s1 NCI CGAP_ONS1 Homo sapiens cDNA clone IMAGE:1426924 3'
10991	23505	36537	8.7	1.7E-01	71063300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11558	24006		2.18	1.7E-01	P15272	SWISSPROT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
11643	24604		1.45	1.7E-01	AJ272584.1	NT	AMP NUCLEOSIDASE
11647	24079	37143	4.09	1.7E-01	11418157	NT	Biobella aurantiaca mitochondrial partial COII gene for cytochrome c oxidase subunit II
11782	25004		1.94	1.7E-01	AL163278.2	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
12333	24517		1.38	1.7E-01	N40825.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
12381	24548	30905	12.95	1.7E-01	U01317.1	NT	yw62c12.1 Soares_placenta_8to9weeks_2NbpHP8to9W Homo sapiens cDNA clone IMAGE:258742 5'
12609	24693		1.33	1.7E-01	AJ132510.1	NT	Human beta globin region on chromosome 11
131	12798	25285	1.57	1.8E-01	AF217532.1	NT	Sus scrofa c-fos gene, exons 1-4
708	15388	25818	1.56	1.8E-01	R31497.1	EST_HUMAN	Homo sapiens mevalonate kinase gene, exon 6 and 7
1569	14161	26992	4.35	1.8E-01	AF288117.1	NT	y175f12.1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:135598 5'
1968	14552	27108	2.8	1.8E-01	P22063	SWISSPROT	Homo sapiens homeobox protein OTX2 gene, complete cds
2028	14610		1.08	1.8E-01	U10334.1	NT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
2427	15466	27569	0.96	1.8E-01	X94232.1	NT	Crossostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2535	15099	27672	1.12	1.8E-01	AB037729.1	NT	H.sapiens mRNA for novel T-cell activation protein
2917	15534	28006	11.95	1.8E-01	AF185689.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2917	15534	28007	11.95	1.8E-01	AF185689.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3041	15657	28137	1.17	1.8E-01	AE001862.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3695	16298	28765	1.35	1.8E-01	AJ003165.1	NT	Deinococcus radiodurans R1 section 1 of 2 of the complete chromosome 2
3695	16298	28765	1.35	1.8E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
3940	16439	28901	0.71	1.8E-01	AE000962.1	NT	Populus trichocarpa cv. Trichobel ABI3 gene
4072	16668		2.65	1.8E-01	AE004413.1	NT	Archaeoglobus fulgidus section 145 of 172 of the complete genome
4422	17007	29450	11.02	1.8E-01	AF179680.1	NT	Vibrio cholerae chromosome II, section 70 of 93 of the complete chromosome
4554	17137		3.42	1.8E-01	AW968601.1	EST_HUMAN	Homo sapiens apelin gene, complete cds
							EST380677 MAGE resequences, MAG1 Homo sapiens cDNA

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4563	17146		4.68	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Cct3), mRNA
5057	17630	30074	0.84	1.6E-01	P40631	SWISSPROT	MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) (CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA)
5080	17653	30093	1.45	1.6E-01	AA088343.1	EST_HUMAN	z84h09.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR:E221855
5101	17673	30112	1.26	1.6E-01	AJ006356.1	NT	E221955 38,855 BP SEGMENT OF CHROMOSOME XIV.
5101	17673	30113	1.26	1.6E-01	AJ006356.1	NT	Lycopodium esculentum RsaI fragment 2, satellite region
5358	17918		1.81	1.6E-01	BF209302.1	EST_HUMAN	Lycopodium esculentum RsaI fragment 2, satellite region
5359	17919	30333	1.23	1.6E-01	AJ074074.1	EST_HUMAN	601872523F1 NIH_MGC_64 Homo sapiens cDNA clone IMAGE:4096885 5'
5587	18218	30688	0.76	1.6E-01	L40608.1	NT	wm48c08.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2439182 3'
5713	18339	30844	2.76	1.6E-01	AW197498.1	EST_HUMAN	Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds
5713	18339	30845	2.76	1.6E-01	AW197498.1	EST_HUMAN	xm43f01.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2886969 3' similar to TR:O75984 O75984
5725	18351	31054	2.12	1.6E-01	AF034716.1	NT	HYPOTHETICAL 127.6 KD PROTEIN
6179	18789	31558	0.84	1.6E-01	BE255803.1	EST_HUMAN	HYPOTHETICAL 127.6 KD PROTEIN
6559	19157	31953	2	1.6E-01	AL161588.2	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebpe) gene, complete cds
6559	19157	31954	2	1.6E-01	AL161588.2	NT	RC3-BN0034-310800-113-h01 BN0034 Homo sapiens cDNA
7043	18063	30453	3.49	1.6E-01	AW291215.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
7753	20261	33157	1.44	1.6E-01	AW246359.1	EST_HUMAN	UI-H-B12-egl-b-06-O-U.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724418 3'
7770	20278		0.75	1.6E-01	AU136525.1	EST_HUMAN	2822248.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
7810	20353	33262	1.43	1.6E-01	L49349.1	NT	AU136525 PLACE1 Homo sapiens cDNA clone PLACE1004466 5'
7988	20510		0.55	1.6E-01	BE244087.1	EST_HUMAN	Gorilla gorilla androgen receptor gene, partial exon
8062	20604	33515	0.76	1.6E-01	U36243.1	NT	TCBAP1E0607 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0607
8567	21106	34025	0.77	1.6E-01	Z99119.1	NT	Bacteroides vulgatus beta-lactamase (cbxA) gene, complete cds and mobilization protein (mobA) gene, complete cds
8760	21289	34220	0.65	1.6E-01	R13673.1	EST_HUMAN	Bacillus subtilis complete genome (section 18 of 21): from 2697771 to 3213410
8863	21402		0.64	1.6E-01	L36881.1	NT	Y60h08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:26873 5'
8901	21439	34362	1.91	1.6E-01	Z49501.1	NT	Homo sapiens guanylate cyclase activating protein (GCAP) gene exons 1-4, complete cds
9039	21576		0.8	1.6E-01	AF111167.2	NT	S.cerevisiae chromosome X reading frame ORF YJR001W
9569	22069		1.93	1.6E-01	BF375171.1	EST_HUMAN	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
9572	22072	35033	1.86	1.6E-01	Z49501.1	NT	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
							S.cerevisiae chromosome X reading frame ORF YJR001W

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	22107		1.06	1.6E-01	BE155684.1	EST_HUMAN	PM2-HT0353-270100-004-f11 HT0353 Homo sapiens cDNA
10536	23073	36087	2.7	1.6E-01	AW850853.1	EST_HUMAN	IL3-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
10880	23401	36418	1.55	1.6E-01	BE259649.1	EST_HUMAN	601145793F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161183 5'
10984	23508		8.03	1.6E-01	AF106084.1	NT	Plasmodium falciparum calcium-dependent protein kinase-3 (cdpk3) gene, complete cds
11289	23741	36798	10.88	1.6E-01	5871552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Aptb1), mRNA
11680	25019		1.72	1.6E-01	5879468	NT	Mus musculus protein kinase, cGMP-dependent, type II (Prkg2), mRNA
11784	24189	36776	5.34	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
12095	24362	30968	1.55	1.6E-01	L14933.1	NT	Rat convertase PC5 mRNA, 5' end
12126	24392		1.75	1.6E-01	AW839711.1	EST_HUMAN	RC1-LT0074-120200-014-h01_1 LT0074 Homo sapiens cDNA
12229	24821		11.74	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
12407	24584		5.11	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds
12497	24625		3.96	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Qiu 94208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
12521	24637	30896	1.88	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
269	12926	25412	1.76	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
269	12926	25413	1.76	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
613	15387		2.16	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCAADH06 5'
815	13433	25938	1.04	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1131	13734	26244	0.84	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGG522 myosin heavy chain, 3'UTR
1152	13765	26248	2.28	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1258	13855	26371	0.79	1.5E-01	AW195516.1	EST_HUMAN	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1318	13912	26432	3.12	1.5E-01	D26535.1	NT	xn39d11.x1 NCI CGAP_K1d11 Homo sapiens cDNA clone IMAGE:2696085 3'
1318	13912	26433	3.12	1.5E-01	D26535.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1529	14121	26650	1.84	1.5E-01	AF117340.1	NT	Human gene for dihydrolipoamide succinyltransferase, complete cds (exon 1-15)
1951	14535	27091	1.62	1.5E-01	AW444451.1	EST_HUMAN	Mus musculus MAP kinase kinase kinase 1 (Mek1) mRNA, complete cds
2736	15291	27859	1.17	1.5E-01	BF695381.1	EST_HUMAN	U1-H-B19-akb-b-09-0-U1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733641 3'
2938	15554		1.01	1.5E-01	AW572516.1	EST_HUMAN	602083289F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
3070	15685	28157	0.62	1.5E-01	M81441.1	NT	xx56a02.x2 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2831978 3' similar to gb:X55072_rna1
3395	16003	28484	6.87	1.5E-01	AA935049.1	EST_HUMAN	THYROID HORMONE RECEPTOR ALPHA-1 (HUMAN); Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3415	16023	28504	0.65	1.5E-01	Z23104.1	NT	oo68d05.s1 NCI CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:M11433
3415	16023	28505	0.65	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); L. stagnalis mRNA for G protein-coupled receptor
						NT	L. stagnalis mRNA for G protein-coupled receptor

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3474	16080	28553	0.99	1.5E-01	AW612237.1	EST_HUMAN	hh:29f02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2956539 3' similar to contains element MER16 repetitive element;
3819	18419	28881	2.13	1.5E-01	U09984.1	NT	Mus musculus CR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3835	18434	28896	0.94	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3849	18447	28908	0.58	1.5E-01	M97882.1	NT	XYNA, Thermotoga bacterium; xynA, 4182 base-pairs
3934	18532	28999	2.74	1.5E-01	AW805983.1	EST_HUMAN	h10908.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3951	18549	29017	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
3951	18549	29018	0.9	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichobol ABI3 gene
4124	18717	29173	0.82	1.5E-01	AW36659.1	EST_HUMAN	RC2-HT0149-191099-012-c09 HT0149 Homo sapiens cDNA
4262	18848	29286	9.62	1.5E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C0B4
4833	17411	29864	1.29	1.5E-01	BF687665.1	EST_HUMAN	602087192F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4066223 5'
4863	15291	27859	2.03	1.5E-01	BF686381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4906	17481	29838	0.92	1.5E-01	BE173796.1	EST_HUMAN	GM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4906	17481	29939	0.92	1.5E-01	BE173796.1	EST_HUMAN	GM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
5139	17711	30141	1.59	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5461	18098	30414	1.96	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5489	18123	30530	0.8	1.5E-01	AF256662.1	NT	Caiman crocodilus MHC class II beta chain (hclbeta) gene, complete cds
5531	18163		5.6	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (ABP)
5729	18355	31059	4.68	1.5E-01	AW850754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5767	18393	31106	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
5767	18393	31107	6.97	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGfa) mRNA, complete cds
6156	18769	31532	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6156	18769	31533	1.4	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dnmt2), mRNA
6194	18804	31573	1.96	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
6342	18948	31725	3.23	1.5E-01	BE727688.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
6394	18997		1.86	1.5E-01	4506398	NT	Homo sapiens RAD54 (S cerevisiae)-like (RAD54L) mRNA
6484	19085	31887	1.75	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuraminidase gene, partial cds
6628	24765	32027	1.94	1.5E-01	AE001039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
6652	19248	32050	4.63	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (OSORF3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6663	19259	32063	1.5	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
6702	19297	32101	2.16	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6786	19377	32192	0.95	1.5E-01	AA714760.1	EST_HUMAN	hw30d10.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241971 3'
6813	19404	32220	1.59	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TALB INTERGENIC REGION (ORF6)
7055	18074	30464	6.39	1.5E-01	AW970295.1	EST_HUMAN	EST382376 IMAGE: resseques, MAGK Homo sapiens cDNA
7268	19786		1.9	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
7423	19947	32813	1.5	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
7589	20104	32978	1.02	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7589	20104	32980	1.02	1.5E-01	AF299073.1	NT	Bos taurus Niemann-Pick type C1 disease protein (NPC1) mRNA, complete cds
7586	20110	32984	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BND-akk-4-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7596	20110	32985	1.71	1.5E-01	AW500611.1	EST_HUMAN	UI-HF-BND-akk-4-05-0-U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
7722	20230	33119	0.71	1.5E-01	U46560.1	NT	Saccharomyces cerevisiae weak multicopy suppressor of los1-1 (SOL3) gene, complete cds
8002	20544	33448	1.1	1.5E-01	P21303	SWISSPROT	MEROZOITE RECEPTOR PK66 PRECURSOR (66 KD PROTECTIVE MINOR SURFACE ANTIGEN)
8181	20702	33617	0.95	1.5E-01	AA970317.1	EST_HUMAN	cd59g12.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573030 3' similar to gb:M26062
8254	20785		1.11	1.5E-01	BE884789.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN)
8339	20880		11.5	1.5E-01	C16800.1	EST_HUMAN	601510523F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912004 5'
8372	20912	33832	1.82	1.5E-01	L27835.1	NT	C16800 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-529H09 5'
8529	21068	33987	2.04	1.5E-01	DB4476.1	NT	Pangasanodon gigas growth hormone (GH) mRNA, complete cds
8550	21089		0.86	1.5E-01	P43446	SWISSPROT	Homo sapiens mRNA for ASK1, complete cds
8772	21311	34234	1.23	1.5E-01	4501972	NT	WNT-10A PROTEIN PRECURSOR
9033	21570	34499	2.46	1.5E-01	N74226.1	EST_HUMAN	Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
9121	21657	34598	1.06	1.5E-01	BF585485.1	EST_HUMAN	zaf5e06.s1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:296866 3' similar to
9128	21683		2.63	1.5E-01	AV754819.1	EST_HUMAN	PIR:S444443 S44443 RAD23 protein homolog2 - human ;
9326	21840		0.94	1.5E-01	AU130007.1	EST_HUMAN	GV0000404 Human Psoriasis Differential Display Homo sapiens cDNA
9374	20313	33215	7.21	1.5E-01	U00455.1	NT	AV754819 TP Homo sapiens cDNA clone TPAAHB12 5'
9731	22229	35208	0.48	1.5E-01	M77144.1	NT	AU130007 NT2RP3 Homo sapiens cDNA clone NT2RP3000080 5'
9835	22333	35314	8.51	1.5E-01	AF007570.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
9835	22333	35315	8.51	1.5E-01	AF007570.1	NT	Human type II 3-beta hydroxysteroid dehydrogenase/ 5-delta - 4-delta isomerase gene, complete cds
10104	22599	35591	2.54	1.5E-01	X8852.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
10188	22683		3.34	1.5E-01	AB027759.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
						NT	P1enisculus mRNA for integrin beta subunit
						NT	Mesocricetus auratus mRNA for collagen type XVII, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10210	22705	35698	2.82	1.5E-01	AB14048.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10210	22705	35699	2.82	1.5E-01	AB14048.1	EST_HUMAN	wk53h12.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
10288	22783	35775	1.75	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax9b (Pax9) mRNA, complete cds
10433	22927	35933	1.97	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10433	22927	35934	1.97	1.5E-01	AJ011984.1	NT	Claviceps purpurea ps1 gene
10704	23233	36245	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10704	23233	36246	5.45	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
10954	23469	36494	1.71	1.5E-01	AW841915.1	EST_HUMAN	IL5-CH0024-030300-025-D04 CH0024 Homo sapiens cDNA
11045	19947	32813	2.44	1.5E-01	A1973157.1	EST_HUMAN	wf52c08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
11739	24875		79.5	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
12125	24381		1.43	1.5E-01	AF030358.2	NT	Rattus norvegicus chemokine CX3C mRNA, complete cds
12190	24898		7.05	1.5E-01	R83077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
12288	24920		3.12	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDAIGD04 5'
12406	24824	30794	18.12	1.5E-01	AL139074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/8
12621	24699	30892	3	1.5E-01	Q9Z078	SWISSPROT	VOLTAGE-DEPENDENT T-TYPE CALCIUM CHANNEL ALPHA-1I SUBUNIT (CAVT.3)
12832	24709	30865	11.33	1.5E-01	AJ276242.1	NT	Sus scrofa mRNA for sodium iodide symporter
321	12975		1.48	1.4E-01	AF009683.1	NT	Homo sapiens T cell receptor beta locus, TCRBV85P to TCRBV21S2A2 region
943	13556		2.71	1.4E-01	D78838.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-)methyltransferase, complete cds
1302	13896		1.59	1.4E-01	T81884.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1784	14374		1.35	1.4E-01	6670980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1787	14377	26921	1.39	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
2028	14611		10.08	1.4E-01	AA720615.1	EST_HUMAN	ny72d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 3'
2514	15078	27650	1.4	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)
2818	15370	27940	4.1	1.4E-01	AB93498.1	EST_HUMAN	wm74d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
4253	16841	29290	10.32	1.4E-01	AF69094.1	EST_HUMAN	b65c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4253	16841	29291	10.32	1.4E-01	AF69094.1	EST_HUMAN	b65c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4321	16907	29349	3.71	1.4E-01	AE001710.1	NT	Thermotoga maritima section 22 of 136 of the complete genome
4501	17085		0.61	1.4E-01	AA776287.1	EST_HUMAN	z50b01.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453873 3' similar to gb:X01057_maf1 INTERLEUKIN-2 RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);contains Alu repetitive element;
4784	17364	29815	0.59	1.4E-01	5453881	NT	Homo sapiens phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2) (PDE4A), mRNA

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5329	17890		1.74	1.4E-01	BE910013.1	EST_HUMAN	801498056F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900157 5'
5509	18142	30554	4.49	1.4E-01	T60977.1	EST_HUMAN	ye15c11.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:117812 3'
5532	18164	30577	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5532	18164	30578	4.24	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
6440	19042	31850	2.7	1.4E-01	BE328991.1	EST_HUMAN	h87c02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133538 3'
6808	19205	32012	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6808	19205	32013	6.4	1.4E-01	AU117147.1	EST_HUMAN	AU117147 HEMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
6886	19282	32085	3.78	1.4E-01	AW082796.1	EST_HUMAN	xb71d12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2581751 3'
6899	19295		1.53	1.4E-01	BE266536.1	EST_HUMAN	801193523F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537581 5'
6718	19312	32115	2.07	1.4E-01	BF376533.1	EST_HUMAN	QV1-UM00036-080300-103-d09 UM0036 Homo sapiens cDNA
7160	19712		0.81	1.4E-01	AL118568.1	EST_HUMAN	DKFZp761A0910.r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A0910 5'
7419	18943		1.83	1.4E-01	AW015373.1	EST_HUMAN	UIH-B10-sat-c-09-0.U1.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
7617	20130	33005	1.94	1.4E-01	U95845.1	NT	Oryctolagus cuniculus fructose 1,6-bisphosphate aldolase (AldB) gene, complete cds
7733	20241	33132	1.77	1.4E-01	AI305182.1	EST_HUMAN	ql90b12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1879583 3'
8410	20950		1.28	1.4E-01	AV658047.1	EST_HUMAN	AV658047 GLC Homo sapiens cDNA clone GLGFSH06 3'
8719	21258		0.62	1.4E-01	AI436093.1	EST_HUMAN	th92b12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126111 3' similar to
8844	21383	34308	4.58	1.4E-01	AA307073.1	EST_HUMAN	TR:O02710 O02710 GAG POLYPROTEIN ;
8924	21482	34379	0.62	1.4E-01	AW023636.1	EST_HUMAN	EST1178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
9050	21587	34518	1.21	1.4E-01	R62746.1	EST_HUMAN	df58b03.y1 Morton Feal Cochlea Homo sapiens cDNA clone IMAGE:2487485 5'
9050	21587	34519	1.21	1.4E-01	R62746.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9114	21650	34591	8.46	1.4E-01	BF310959.1	EST_HUMAN	y10h05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138873 5'
9199	21716	34680	1.09	1.4E-01	W93411.1	EST_HUMAN	601895465F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124824 5'
9280	21806	34757	1.47	1.4E-01	Y10196.1	NT	z094a04.r1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element ;
9280	21806	34758	1.47	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
9371	20310	33213	1.95	1.4E-01	AF121361.1	NT	Homo sapiens PHEX gene
9898	22395	35371	1.18	1.4E-01	AF023813.1	NT	Drosophila melanogaster signal transducing adaptor protein (STAM), serine threonine kinase Ial (IAL), and zinc finger protein (DNZ1) genes, complete cds
10000	22495	35484	0.51	1.4E-01	AW021908.1	EST_HUMAN	Macromitrium levatum small ribosomal protein 4 (rps4) gene, chloroplast gene encoding chloroplast protein, partial cds
10000	22495	35485	0.51	1.4E-01	AW021908.1	EST_HUMAN	df29h08.y1 Morton Feal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22652	35645	0.72	1.4E-01	BF375285.1	EST_HUMAN	df29h08.y1 Morton Feal Cochlea Homo sapiens cDNA clone IMAGE:2485094 5'
10157	22652	35646	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA
10157	22652	35648	0.72	1.4E-01	BF375285.1	EST_HUMAN	MR3-ST0218-211299-013-a08 ST0218 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10360	22854		0.73	1.4E-01	T84293.1	EST_HUMAN	y447d03.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:111365 5'
10489	22983	35981	0.7	1.4E-01	Z99117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2599481 to 2812870
10587	23122		1.89	1.4E-01	AA811480.1	EST_HUMAN	os69a03.st NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1320364 3'
10722	23250	36265	3.2	1.4E-01	R53400.1	EST_HUMAN	y70c05.r1 Soares breast 2NbHBst Homo sapiens cDNA clone IMAGE:154088 5'
10974	23489	36519	1.56	1.4E-01	P08648	SWISSPROT	INTEGRIN ALPHA-5 PRECURSOR (FIBRONECTIN RECEPTOR ALPHA SUBUNIT) (INTEGRIN ALPHA-5) (VLA-5) (CD49E)
11172	23679	36724	1.82	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein
11210	19943		1.96	1.4E-01	AW015373.1	EST_HUMAN	UI-H-BID-aat-c-08-0-UJ.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710289 3'
11344	23042	36052	2.4	1.4E-01	U28760.1	NT	Borrelia burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
12061	24344	30963	4.44	1.4E-01	X74773.1	NT	P. salina plastid gene secY
12074	24352		3.65	1.4E-01	11868117	NT	Rattus norvegicus desmin (Des), mRNA
12123	25082		1.52	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634328 5'
12223	24444		9.33	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycineamide ribonucleotide transferase (GART) genes, complete cds
12235	24451		1.96	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
12315	25098		1.77	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN ABL
12340	24522		2.01	1.4E-01	AA452305.1	EST_HUMAN	z30a12.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788014 5' similar to contains Alu repetitive element
12545	24800		3.55	1.4E-01	D82983.1	NT	Mus musculus mRNA for prolidase, complete cds
12627	24705		1.33	1.4E-01	AW377998.1	EST_HUMAN	MRO-HT0208-221299-204-c08 HT0208 Homo sapiens cDNA
344	12698	25481	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
344	12998	25482	2.28	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
555	13186	25664	3.25	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
664	13288	25769	3.03	1.3E-01	AJ277806.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
664	13288	25770	3.03	1.3E-01	AJ277806.1	NT	Human calicivirus HUJNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUJNLV/Girlington/93/UK
877	13491	26009	0.78	1.3E-01	X53330.1	NT	P. dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4
927	13540	26058	1.44	1.3E-01	AF139518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1084	13669	26179	1.36	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1168	13768		2.03	1.3E-01	AL115265.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1257	13854	26370	1.36	1.3E-01	AV712467.1	EST_HUMAN	AV712467 DCA Homo sapiens cDNA clone DCAAF05 5'
1493	14085		0.97	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2002	14584	27143	2.32	1.3E-01	AL117078.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2215	14790		1.21	1.3E-01	AJ243578.1	NT	Rhodospseudomonas acidophila pucB5, pucA5, pucB6, pucA7, pucB7, pucA8 and pucC genes and ORF151
2329	14900		1.56	1.3E-01	AW812104.1	EST_HUMAN	RC4-S10173-191089-032-412 ST0173 Homo sapiens cDNA
2421	14989		3.74	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2822	15184	27750	1.55	1.3E-01	MB6918.1	NT	Carassius auratus keratin type I mRNA, complete cds
3402	16011	28490	0.61	1.3E-01	AF196779.1	NT	Homo sapiens transcription factor 1GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α
3498	16103	28578	0.99	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolylase mRNA, complete cds
3785	16385	28850	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3785	16385	28851	1.19	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3791	16391	28856	0.8	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodialdehyde dehydrogenase 4 [AKR1C4], exon 2
3848	16385	28850	0.62	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3848	16385	28851	0.62	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt. position (177)
3875	16473	28937	0.74	1.3E-01	6978840	NT	Rattus norvegicus Fibrinogen, gamma polypeptide (F89), mRNA
4060	16657		1.3	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77
4125	13288	25769	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4125	13288	25770	1.65	1.3E-01	AJ277606.1	NT	Human calicivirus HUNLV/Girlington/93/UK RNA for capsid protein (ORF2), strain HUNLV/Girlington/93/UK
4218	16806		0.95	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome
4238	16826		4.04	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081299-036-a03 DT0018 Homo sapiens cDNA
4246	16834	26285	2.25	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose biphosphate aldolase mRNA, complete cds
4285	16851	26299	21.7	1.3E-01	AW273741.1	EST_HUMAN	xx23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995.3
4404	16989		1.55	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4577	17160	28603	0.62	1.3E-01	M21572.1	NT	Bovine branched chain alpha-keto acid dihydrolylase mRNA, complete cds
4631	17214	29665	2.35	1.3E-01	BE272339.1	EST_HUMAN	601128096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2960063.5
4998	18009		0.94	1.3E-01	BE884017.1	EST_HUMAN	601610347F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987.5
5056	17629	30073	1.05	1.3E-01	D78842.1	EST_HUMAN	HUM520C02B Human placenta polyA+ (Tfujwara) Homo sapiens cDNA clone GEN-520C02.5
5279	17841	30268	4.06	1.3E-01	A432531.1	EST_HUMAN	th38c10.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2120562.3
5396	17954	30365	0.65	1.3E-01	AP000005.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 994001-1166000 nt. position (517)

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5444	17999	30402	13.66	1.3E-01	AA991841.1	EST_HUMAN	ot45e07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5444	17999	30403	13.66	1.3E-01	AA991841.1	EST_HUMAN	ot45e07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1619748 3' similar to SW:YEY6_YEAST P40093 HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION. [1];
5528	18160	30575	0.69	1.3E-01	AW466988.1	EST_HUMAN	ha07b08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872979 3' similar to contains L1.b1 L1
5565	18196	30642	2.76	1.3E-01	AW604417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA
5692	18318		0.78	1.3E-01	AF107793.1	NT	Emeritella nidulans DNA-dependent RNA polymerase II RPB140 (RPB2) gene, partial cds
5772	18397		0.76	1.3E-01	AF056890.1	NT	Hepatitis C virus 68_CL10 genome polyprotein gene, partial cds
5809	18521	31246	0.89	1.3E-01	BF210920.1	EST_HUMAN	601874891F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101119 5'
6009	19208	32014	15.81	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds
6684	19280	32083	2.07	1.3E-01	X68891.1	NT	Cjaechus intron 4 of visual pigment gene (red allele)
6883	19618		0.82	1.3E-01	W26367.1	EST_HUMAN	26f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
7305	19833		1.94	1.3E-01	H48664.1	EST_HUMAN	Y333d02.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:207075 5'
7900	20442		0.67	1.3E-01	BE272339.1	EST_HUMAN	601126096F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2960063 5'
7914	20456	33362	1.62	1.3E-01	11423294	NT	Homo sapiens PRO0611 protein (PRO0611), mRNA
7945	20487	33397	0.99	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286074 3'
8180	20721		0.47	1.3E-01	BE562526.1	EST_HUMAN	601335829F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3689934 5'
8286	20827		4.61	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YDL054c
8325	20866		3.78	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A2.2 (MACROH2A2), mRNA
8465	21005	33923	1.05	1.3E-01	BF690522.1	EST_HUMAN	602187015T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4286074 3'
8878	21416	34339	0.52	1.3E-01	R11172.1	EST_HUMAN	SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
8878	21416	34340	0.52	1.3E-01	R11172.1	EST_HUMAN	Y39g11.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:129284 5' similar to
9146	21681	34625	1.64	1.3E-01	11068003	NT	SP:RL2B_RAT P29316 60S RIBOSOMAL PROTEIN ;
9146	21681	34626	1.64	1.3E-01	11068003	NT	Plutella xylostella granulovirus, complete genome
9393	21816	34766	5.08	1.3E-01	AF023126.1	NT	Oryctolagus cuniculus H+K+ATPase alpha 2c subunit mRNA, complete cds
9686	22185		0.8	1.3E-01	N86348.1	EST_HUMAN	J7837F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J7837 5' similar to B-CELL
9964	22459		0.8	1.3E-01	8393940	NT	RECEPTOR ASSOCIATED PROTEIN (BAP) 29
10036	22531	35528	0.83	1.3E-01	AW851569.1	EST_HUMAN	Rattus norvegicus peptidyl arginine deiminase, type IV (Pd4), mRNA
							MR2-CT0222-201089-001-e01 CT0222 Homo sapiens cDNA

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10292	24797	35776	0.9	1.3E-01	AL183246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10417	22911	35911	0.82	1.3E-01	AU121237.1	EST_HUMAN	AU121237 HEMBB1 Homo sapiens cDNA clone HEMBB:1002387 5'
10511	23049		3.33	1.3E-01	BF330699.1	EST_HUMAN	MR4-BT0358-130700-010-H08 BT0358 Homo sapiens cDNA
10975	23490	36520	1.58	1.3E-01	AF119117.1	NT	Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
11130	23638		5.15	1.3E-01	6671745	NT	Mus musculus cofilin 2, muscle (Cif2), mRNA
11488	23916	36984	3.61	1.3E-01	BE279449.1	EST_HUMAN	601158052F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504804 5'
11902	24241	31007	1.84	1.3E-01	BE818346.1	EST_HUMAN	601462741F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866003 5'
12048	24332		3.27	1.3E-01	AJ242780.1	NT	Gallus gallus sox1 gene for lympholactin, exons 1-3
12486	24594		1.53	1.3E-01	AW001114.1	EST_HUMAN	wu24d09.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2520977 3' similar to TR:O60287 KIAA0539 PROTEIN. ;
12647	24721		1.84	1.3E-01	BE958903.1	EST_HUMAN	601644622R2 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3929880 3'
406	13081	25573	10.81	1.2E-01	AK421744.1	EST_HUMAN	tf39b02.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098539 3' similar to gb:U05760_mn1
449	12678		1.43	1.2E-01	U66912.1	NT	ANNEXIN V (HUMAN); Dictyostelium discoideum ORF DG1016 gene, partial cds
573	13203		2.58	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
1419	14012	26541	2.31	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001891 3'
1419	14012	26542	2.31	1.2E-01	AU149146.1	EST_HUMAN	AU149146 NT2RM4 Homo sapiens cDNA clone NT2RM4001891 3'
1426	14019		3.26	1.2E-01	AV735249.1	EST_HUMAN	AV735249 cda Homo sapiens cDNA clone cdaAJB11 5'
1431	14023		6.69	1.2E-01	AL445066.1	NT	Thermoplasma acidophilum complete genome, segment 4/5
1554	14146		1.19	1.2E-01	AA887474.1	EST_HUMAN	el48609.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460584 3' similar to TR:Q16671
1673	14265	26799	1.48	1.2E-01	Q14934	SWISSPROT	Q16671 ANTH-MULLERIAN HORMONE TYPE II RECEPTOR PRECURSOR. ;
1691	14283	26819	2.77	1.2E-01	AI285402.1	EST_HUMAN	NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC 4 (T CELL TRANSCRIPTION FACTOR NFAT3) (NF-ATC4) (NF-AT3)
1805	14395		21.02	1.2E-01	X89211.1	NT	q169709.x1 NCI CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1960553 3'
1964	14548		2.23	1.2E-01	AW449368.1	EST_HUMAN	H.sapiens DNA for endogenous retroviral like element
2226	14801	27373	1.31	1.2E-01	BF246490.1	EST_HUMAN	UI-H-B13-akl-e-10-Q-UI.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734554 3'
2325	14896	27470	1.08	1.2E-01	AL163213.2	NT	601821667F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4046224 5'
2416	14984		1.05	1.2E-01	221405.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C0013
2625	15187	27754	1.38	1.2E-01	AW996556.1	EST_HUMAN	HSAAAE8ZT TEST11, Human adult Testis tissue Homo sapiens cDNA
							QV3-BN0046-220300-129-110 BN0046 Homo sapiens cDNA
2754	15309	27875	1.11	1.2E-01	AI623388.1	EST_HUMAN	ts18g07.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2228988 3' similar to TR:Q14048 Q14048
2866	15486	27959	1.22	1.2E-01	U18018.1	NT	COLLAGEN VI ALPHA-2 ALTERNATIVE C-TERMINAL DOMAIN. [1] ;contains element PTR5 repetitive element ;
							Human E1A enhancer binding protein (E1A-F) mRNA, partial cds

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2927	15543	28019	2.37	1.2E-01	AF20470.1	EST_HUMAN	as80c09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335024 3' similar to gb.L05095
2981	15577	28056	3.29	1.2E-01	M16364.1	NT	60S RIBOSOMAL PROTEIN L30 (HUMAN);
3037	15653	28132	0.83	1.2E-01	X56882.1	NT	Human creatine kinase-B mRNA, complete cds
3267	15879	28362	2.08	1.2E-01	AW370668.1	EST_HUMAN	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3296	15907		1.19	1.2E-01	U67600.1	NT	QV1-BT0259-261069-021-405 BT0259 Homo sapiens cDNA
3525	16130		0.62	1.2E-01	Z99118.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
3573	16177	28659	0.82	1.2E-01	X56882.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
3573	16177	28660	0.82	1.2E-01	X56882.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3666	16130		1.09	1.2E-01	Z99118.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3833	16432	29294	0.64	1.2E-01	BF128551.1	EST_HUMAN	Bacillus subtilis complete genome (section 15 of 21); from 2795131 to 3013540
4261	16847	29295	1.98	1.2E-01	Z54255.1	NT	3' end of 3' UTR of P. clarkei mRNA; repeat region (ID 2MRT17)
4402	16987	29431	0.6	1.2E-01	M15861.1	NT	P. clarkei mRNA; repeat region (ID 2MRT17)
4830	17408	29862	0.98	1.2E-01	Z48183.1	NT	Chicken neural cell-adhesion molecule (N-CAM) gene, exon 19
4909	17484		2.93	1.2E-01	AF221633.1	NT	L. esculentum mRNA for glycylase-1
5163	17732	30159	1.06	1.2E-01	BF577357.1	EST_HUMAN	Rana ridibunda pituitary adenylylate cyclase-activating polypeptide variant 2 precursor, mRNA, complete cds, alternatively spliced
5275	17836	30262	10.23	1.2E-01	AL163227.2	NT	602135185F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4290165 5'
5275	17836	30263	10.23	1.2E-01	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5423	17980		1.99	1.2E-01	AL162757.2	NT	Homo sapiens chromosome 21 segment HS21C027
5457	18092	30408	0.71	1.2E-01	AA744369.1	EST_HUMAN	Neisseria meningitidis serogroup A strain Z2491 complete genome, segment 617
5503	18137	30547	1.13	1.2E-01	AF223391.1	NT	ny63c04.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1282950 3'
5513	18146	30557	2.28	1.2E-01	W33035.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CAONA1E) gene, exons 7-49, and partial cds, alternatively spliced
5671	18202	30652	2.3	1.2E-01	Z98266.1	NT	z08d02.r1 Soares_parrathyroid_tumor_NbH-IPA Homo sapiens cDNA clone IMAGE:321699 5'
5696	18322	30822	0.89	1.2E-01	Z48234.1	NT	Homo sapiens gene encoding plakophilin (exons 1-13)
6347	18952	31731	1.81	1.2E-01	BE20945.1	EST_HUMAN	M. domestica Borkh. Granny Smith adh mRNA for alcohol dehydrogenase
6395	18998	31777	0.81	1.2E-01	P10842	SW/ISSPROT	601493318F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
6441	19043	31831	2.38	1.2E-01	AW845275.1	EST_HUMAN	MATING-TYPE P-SPECIFIC POLYPEPTIDE PI
6502	19102	31887	1.59	1.2E-01	M29925.1	NT	ILO-GT0031-221099-113-e04 CT0031 Homo sapiens cDNA
6755	19348	32157	0.98	1.2E-01	BF347985.1	EST_HUMAN	Mouse galactosyltransferase mRNA, complete cds
7833	20375		1.31	1.2E-01	BE007072.1	EST_HUMAN	602023112F1 NCI_CGAP_Brm67 Homo sapiens cDNA clone IMAGE:4158386 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7803	20445	33351	3.58	1.2E-01	A1913753.1	EST_HUMAN	wc99g03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326804 3' similar to SW:GST2_HUMAN
7950	20492	33401	0.72	1.2E-01	Q02369	SWISSPROT	Q99735 MICROSOMAL GLUTATHIONE S-TRANSFERASE II
8251	20792	33709	0.9	1.2E-01	A1832681.1	EST_HUMAN	NADH-UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT (COMPLEX I-B22) (CI-B22)
8335	20876		9.03	1.2E-01	AW083652.1	EST_HUMAN	at71b10.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2377435 3'
							xc49d07.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2887597 3' similar to gb:M13452 LAMIN A (HUMAN);
8355	20895		4.17	1.2E-01	AF083772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds; and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (qacB) genes, complete cds
8392	20932	33852	0.92	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8392	20932	33853	0.92	1.2E-01	J03956.1	NT	N.crassa vacuolar ATPase 57-Kd subunit (vma-2) gene, complete cds
8537	21076		0.83	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
8623	21192		2.14	1.2E-01	U32714.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
8637	21198		0.85	1.2E-01	X15191.1	NT	M.musculus DNA fragment of Apolipoprotein B gene
9491	21947	34896	2.68	1.2E-01	X77981.1	NT	S.cerevisiae HXT5 gene
9918	22414	35389	2.65	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CjAAKE08 5'
10155	22850	35644	0.48	1.2E-01	AI718395.1	EST_HUMAN	as59g09.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2333056 3'
10766	23280		3.58	1.2E-01	D26184.1	NT	Yeast MP T5 gene for suppressor protein, complete cds
10944	23460		3.87	1.2E-01	BE962324.2	EST_HUMAN	601655578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846283 3'
11026	23540		1.62	1.2E-01	BF314481.1	EST_HUMAN	601600763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
11134	23642	36882	2.67	1.2E-01	AF190493.1	NT	Homo sapiens dynein intermediate chain DNA11 (DNA11) gene, exon 17
11193	23698	36748	1.57	1.2E-01	R40249.1	EST_HUMAN	Y80c02.s1 Soeies infant brain 1N1B Homo sapiens cDNA clone IMAGE:28880 3'
11382	23834		1.8	1.2E-01	M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
11687	24090		4.22	1.2E-01	AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCF1B12 3'
12029	24319		4.43	1.2E-01	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
12109	25038	30503	3.9	1.2E-01	Q04912	SWISSPROT	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON) (CDW136) (CD136 ANTIGEN)
12228	24447		1.95	1.2E-01	AF188892.1	NT	Drosophila melanogaster strain Oregon R potential RNA-binding protein gene, complete cds; and syntaxin gene, partial cds
12230	13203		17.94	1.2E-01	AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
12345	24528		1.81	1.2E-01	X53981.1	NT	R.norvegicus NF68 gene for 68kDa neurofilament
12440	24577	30815	6.5	1.2E-01	AI289903.1	EST_HUMAN	gn20g05.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
12463	24591		2.19	1.2E-01	L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
12468	24972		9.71	1.2E-01	O98433	SWISSPROT	CYCLIN T

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12649	16130		1.65	1.2E-01	Z99118.1	NT	Bacillus subtilis complete genome (section 15 of 21) from 2795131 to 3013540
590	13220	25696	0.8	1.1E-01	AI561003.1	EST_HUMAN	tn18408.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'
643	13266	25743	2.98	1.1E-01	AA569006.1	EST_HUMAN	nm08g11.s1 NCI_CGAP_Co10 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_mel1
1092	13697	26207	1.54	1.1E-01	BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);
1124	13727		1.48	1.1E-01	AL161560.2	NT	602128847F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286771 5'
1201	15435	26314	3.68	1.1E-01	AW972158.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
1292	13887	28411	1.89	1.1E-01	D64004.1	NT	EST1384142 MAGE resequences, MAGL Homo sapiens cDNA
1568	14160	26691	2.94	1.1E-01	AL140363.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965
2353	14924		3.72	1.1E-01	6755215	NT	AU140363 PLAGE2 Homo sapiens cDNA clone PLAGE2000403 5'
2576	15401		1.24	1.1E-01	6978676	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra), mRNA
2602	15164		1.06	1.1E-01	AW821909.1	EST_HUMAN	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA
2680	15498	27968	1.17	1.1E-01	S82418.1	NT	RCO-ST0378-210100-032-g04 ST0378 Homo sapiens cDNA
3068	15683	28155	0.78	1.1E-01	F03265.1	EST_HUMAN	interleukin-12 p35 subunit [mice, Genomic, 700 nt, segment 4 of 5]
3365	15894		1.87	1.1E-01	6753231	NT	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1f02 3'
3488	16075	28548	2.27	1.1E-01	BE383188.1	EST_HUMAN	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Cacna1g), mRNA
3499	16104	28579	1.59	1.1E-01	X62135.1	NT	601308679F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3827086 5'
3538	16143	28626	0.59	1.1E-01	R6948.1	EST_HUMAN	C.reinhardtii nuclear gene on linkage group XIX
3842	16245	28720	0.8	1.1E-01	Y07695.1	NT	y082g08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:200414 3' similar to contains
3763	16364		1.35	1.1E-01	P97384	SWISSPROT	Alu repetitive element;
3771	16372	28837	1.61	1.1E-01	X52708.1	NT	A.immersus gene for transposase
4188	16778	29223	1.61	1.1E-01	AW819412.1	EST_HUMAN	ANNEXIN XI (CALCYCLIN-ASSOCIATED ANNEXIN 50) (CAP-50)
4188	16778	29224	1.61	1.1E-01	AW819412.1	EST_HUMAN	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5
4339	16926		12.27	1.1E-01	AF157066.1	NT	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4374	16961	29407	0.63	1.1E-01	AW802056.1	EST_HUMAN	MR3-ST0280-280100-025-g07 ST0280 Homo sapiens cDNA
4745	17328	29768	1.11	1.1E-01	S44857.1	NT	Drosophila melanogaster klarsicht protein (klar) mRNA, complete cds
4958	17533	29975	1.21	1.1E-01	Y07695.1	NT	IL5-UM0070-020500-088-a08 UM0070 Homo sapiens cDNA
5169	16784		0.78	1.1E-01	AF030001.1	NT	Tape-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
5431	17988	30392	4.82	1.1E-01	AV730599.1	EST_HUMAN	A.immersus gene for transposase
5431	17988	30393	4.82	1.1E-01	AV730599.1	EST_HUMAN	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophosphatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and tenascin X (TNX) genes, complete>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5435	16245	28720	0.57	1.1E-01	Y07695.1	NT	A.immerus gene for transposase
5850	18474		4.49	1.1E-01	AA747216.1	EST_HUMAN	nx76a03.s1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5914	18536	31261	1.17	1.1E-01	AF020927.1	NT	6 Homo sapiens diacylglycerol kinase 3 (DAGK3) gene, exon 6
5974	18594	31328	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4186818 5'
5974	18594	31329	0.84	1.1E-01	BF339519.1	EST_HUMAN	602039176F1 NCI_CGAP_Brm84 Homo sapiens cDNA clone IMAGE:4186818 5'
6001	18621	31356	2	1.1E-01	X68651.1	NT	S.pombe ste8 gene encoding protein kinase
6031	18650	31391	5.02	1.1E-01	M86533.1	NT	Providencia rettgeri penicillin G amidase gene
6177	18787	31555	1.75	1.1E-01	AJ007973.1	NT	Homo sapiens LGMD2B gene
6197	18807	31576	1.6	1.1E-01	BE769152.1	EST_HUMAN	PM3.FT0024-130600-004.f12 FT0024 Homo sapiens cDNA
6216	18826	31598	7.81	1.1E-01	AW853699.1	EST_HUMAN	RC3-CT0254-280999-011-a01 CT0254 Homo sapiens cDNA
6562	19160	31958	1.38	1.1E-01	AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
6599	19196	32001	0.84	1.1E-01	AI216307.1	EST_HUMAN	qg76d06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841099 3'
6721	19315	32118	3.92	1.1E-01	Q69635	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE-COA LIGASE) (ACYL-ACTIVATING ENZYME)
6805	19396		3.07	1.1E-01	AF032922.1	NT	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6888	19823	32458	2.36	1.1E-01	11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB), mRNA
7238	25119		0.97	1.1E-01	BF382758.1	EST_HUMAN	601816524F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050653 5'
7345	24780	32737	0.92	1.1E-01	AF000008.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (8/7)
7542	20062	32835	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7542	20062	32836	7.24	1.1E-01	BF684628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019 5'
7651	20163	33051	1.85	1.1E-01	P41067	SWISSPROT	TRAB PROTEIN
7682	20163		0.7	1.1E-01	Z14098.1	NT	B.subtilis gene encoding hypothetical polyketide synthase
7683	20194	33082	3.53	1.1E-01	AA788784.1	EST_HUMAN	ah31b06.s1 Soares_parathyroid_tumor_Nbi-IPA Homo sapiens cDNA clone 1240403 3' similar to gb.J03483
7909	20451	33358	1.41	1.1E-01	U67492.1	NT	CHROMOGRANIN A PRECURSOR (HUMAN);
8149	20690	33603	1.6	1.1E-01	AA495574.1	EST_HUMAN	Methanococcus jannaschii section 34 of 150 of the complete genome
8149	20690	33604	1.6	1.1E-01	AA495574.1	EST_HUMAN	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8197	20738	33650	1.18	1.1E-01	X91233.1	NT	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
8235	20776		1.15	1.1E-01	AW817918.1	EST_HUMAN	H.sapiens IL15 gene
8292	20833	33755	1.54	1.1E-01	AL134349.1	EST_HUMAN	PMT-ST0270-080200-001-f09 ST0270 Homo sapiens cDNA
8752	21291	34211	8.48	1.1E-01	U02482.1	NT	DKFZp547P194.1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547P194 5'
8843	21382	34307	0.87	1.1E-01	A1807474.1	EST_HUMAN	Pedococcus acidilactici H plasmid pSMB74 pediocin ACh production (pap) gene cluster papA, papB, papC and papD genes, complete cds
							wf48c01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358816 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8938	21478	34397	0.48	1.1E-01	AF050081.1	NT	Homo sapiens C16orf3 large protein mRNA, complete cds
8973	21511	34433	2.22	1.1E-01	AA192153.1	EST_HUMAN	z93b12.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
8973	21511	34434	2.22	1.1E-01	AA192153.1	EST_HUMAN	z93b12.r1 Strategene muscle 937209 Homo sapiens cDNA clone IMAGE:627743 5'
9082	21589	34529	0.82	1.1E-01	Y12727.1	NT	P.furiosus partial dph5 gene and argf gene
9092	21628	34565	2.28	1.1E-01	T72675.1	EST_HUMAN	y19h03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
9119	21655		0.87	1.1E-01	BE893260.1	EST_HUMAN	601436972F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922048 5'
9343	21857		1.13	1.1E-01	BE142305.1	EST_HUMAN	CN3-HT0142-271099-028-g11 HT0142 Homo sapiens cDNA
9417	21926		2.2	1.1E-01	BF085149.1	EST_HUMAN	MR2-GN0027-040900-005-a08 GN0027 Homo sapiens cDNA
9824	22322		0.5	1.1E-01	AL161543.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 43
10107	22602		1.03	1.1E-01	R60590.1	EST_HUMAN	y98a09.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147084 3'
10240	22735	35727	0.86	1.1E-01	U60529.1	NT	Ceratitis capitata yoyo retrotransposon gag-like, pol-like and env-like genes, complete cds
10554	23090	38104	1.6	1.1E-01	AF245277.1	NT	Dictyostelium discoideum kinesin Unc104/KIF1a homolog (Unc104) mRNA, complete cds
10684	15683	28155	2.12	1.1E-01	F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'
10802	23325		3.23	1.1E-01	AF168032.1	NT	Carassius auratus actin beta A precursor, mRNA, complete cds
10923	23442	36463	3.76	1.1E-01	R23708.1	EST_HUMAN	yh35f12.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element ;
10931	23449	36470	1.85	1.1E-01	6981351	NT	Rattus norvegicus Phosphofructokinase, liver, B-type (Pfkf), mRNA
10947	18587	31298	1.56	1.1E-01	AL110985.1	NT	Borhytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
11060	23572	36809	1.74	1.1E-01	X70058.1	NT	M.musculus cytokine gene
11085	23597	36833	3.35	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11085	23597	36834	3.35	1.1E-01	Z11910.1	NT	Z.mobilis tgt and lig genes encoding tRNA guanine transglycosylase and DNA ligase
11186	23691	36738	2.99	1.1E-01	P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
11884	24231		4.61	1.1E-01	BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-f03 NT0112 Homo sapiens cDNA
12143	24835		3.29	1.1E-01	BE974556.1	EST_HUMAN	601680551R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950604 3'
12597	24694	30880	1.99	1.1E-01	BF238753.1	EST_HUMAN	601906350F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134085 5'
1243	13841		2.35	1.0E-01	O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1315	13908	26429	1.92	1.0E-01	AB95499.1	EST_HUMAN	ws04d01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2466577 3' similar to contains MER7 f3
1436	14028	26557	2.23	1.0E-01	AL161504.2	NT	MER7 repetitive element ;
2531	15095	27687	0.97	1.0E-01	AW451365.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
3563	16167	28849	1.04	1.0E-01	BF033991.1	EST_HUMAN	UH-HB13-alc-d-07-Q.U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3782	16382	28847	0.82	1.0E-01	BF239818.1	EST_HUMAN	601456301F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3859849 5'
3904	16503	28964	1.41	1.0E-01	AF270970.1	NT	601906489F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
							Escherichia coli enterotoxin EspC (espC) gene, complete cds; and unknown genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3904	16503	28965	1.41	1.0E-01	AF297081.1	NT	Escherichia coli enterobidin EspC (espC) gene, complete cds; and unknown genes
4027	16626	29097	2.82	1.0E-01	BF365703.1	EST_HUMAN	QV2-NT0048-160800-318-e05 NT0048 Homo sapiens cDNA
4486	17080	29529	1.62	1.0E-01	AE002285.2	NT	Chlamydomonas reinhardtii AR39, section 91 of 94 of the complete genome
4653	17235		0.97	1.0E-01	AF792349.1	EST_HUMAN	an32c04.y5 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700358 5'
4822	17400	29853	1.8	1.0E-01	U50450.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fer) mRNA, complete cds
4920	17495	29946	0.96	1.0E-01	AA765434.1	EST_HUMAN	oa05h03.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1304117 3'
5050	17623	30068	2.12	1.0E-01	AW952344.1	EST_HUMAN	EST364414 IMAGE resequences, MAGB Homo sapiens cDNA
5408	17965	30375	1.06	1.0E-01	AV721471.1	EST_HUMAN	AV721471 HTB Homo sapiens cDNA clone HTBQ610 5'
5415	17972		0.88	1.0E-01	AV763960.1	EST_HUMAN	zh62h04.s1 Soares fetal liver spleen_1INFLS_S1 Homo sapiens cDNA clone IMAGE:416895 3'
5524	18196		8.57	1.0E-01	W86490.1	EST_HUMAN	Homo sapiens mRNA for FLJ00065 protein, partial cds
6040	18659		0.95	1.0E-01	AK024472.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6175	18786	31554	11.01	1.0E-01	AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds
6477	19078	31861	0.98	1.0E-01	AA481879.1	EST_HUMAN	L1.13 L1 repetitive element
6489	19090	31873	0.82	1.0E-01	AA408039.1	EST_HUMAN	yu67c12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:743062 3'
7091	19662		1.71	1.0E-01	R23821.1	EST_HUMAN	yu34h06.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element
7717	20225		2.33	1.0E-01	Y12488.1	NT	M.musculus whn gene
7874	20416	33324	0.53	1.0E-01	AA861091.1	EST_HUMAN	ak32g01.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407696 3' similar to gb:U34182 CAMP-DEPENDENT PROTEIN KINASE, GAMMA-CATALYTIC SUBUNIT (HUMAN);
8107	20648		0.6	1.0E-01	4758365	NT	Homo sapiens fibroblast growth factor 13 (FGF13) mRNA
8429	20869		0.83	1.0E-01	AW189797.1	EST_HUMAN	xi09b01.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675689 3' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); contains TAR1.3 TAR1 repetitive element
9113	21649	34590	1.08	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP-interacting protein Synemon mRNA, complete cds
9416	21925	34873	0.49	1.0E-01	R44693.1	EST_HUMAN	yu33h04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34549 3'
9426	21935		2.05	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
9469	21868		2.67	1.0E-01	AE001501.1	NT	Helicobacter pylori strain J99 section 62 of 132 of the complete genome
9483	21940	34888	0.71	1.0E-01	W01955.1	EST_HUMAN	z66c10.s1 Soares fetal heart_NbHH19W Homo sapiens cDNA clone IMAGE:327282 3'
9735	22233	35211	1.67	1.0E-01	BF240154.1	EST_HUMAN	601905661F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4133487 5'
9848	22346	35327	8.17	1.0E-01	AB046789.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
9848	22346	35328	8.17	1.0E-01	AB046789.1	NT	Homo sapiens mRNA for KIAA1579 protein, partial cds
10048	22543		2.05	1.0E-01	AW957425.1	EST_HUMAN	EST368615 IMAGE resequences, MAGC Homo sapiens cDNA
10053	22548	35542	0.61	1.0E-01	T51952.1	EST_HUMAN	yu29a06.s1 Striatogene fetal spleen (#837205) Homo sapiens cDNA clone IMAGE:72562 3' similar to contains Alu repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10234	22729	35720	1.08	1.0E-01	BE792750.1	EST_HUMAN	601584604F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939098 5'
10537	23074		2.11	1.0E-01	AU159127.1	EST_HUMAN	AU159127 THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
10910	23429	36448	3.33	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
10910	23429	36449	3.33	1.0E-01	BF242946.1	EST_HUMAN	601877703F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
11278	23731	36786	5.03	1.0E-01	BE790543.1	EST_HUMAN	601582558F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939734 5'
11870	24581		3.49	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12104	24366		1.74	1.0E-01	7602165	NT	Homo sapiens KIAA0514 gene product (KIAA0514), mRNA
12122	24380		1.36	1.0E-01	X00854.1	NT	Drosophila melanogaster fz gene
12336	24518		2.27	1.0E-01	AA737891.1	EST_HUMAN	rx11c08.x1 NC1_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1255780 3'
12413	25031		4.74	1.0E-01	U52891.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
12445	24581		2.17	1.0E-01	BE537719.1	EST_HUMAN	601065554F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451933 5'
12485	24623		1.93	1.0E-01	BE158905.1	EST_HUMAN	QV4-HT0401-211288-064-g03 HT0401 Homo sapiens cDNA
12511	25001		41.15	1.0E-01	U66834.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
12578	24674		7.73	1.0E-01	AP001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
2806	15358	27825	0.93	9.8E-02	AF274008.1	NT	Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-R1) mRNA, complete cds
2813	15385	27834	1.95	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
2813	15385	27835	1.95	9.8E-02	BE545554.1	EST_HUMAN	601070219F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456385 5'
3305	15916	28393	1.98	9.9E-02	AF098810.1	NT	Homo sapiens neurxin III-alpha gene, partial cds
4025	16823	28095	0.64	9.8E-02	AB21637.1	EST_HUMAN	zu45c03.x8 Scores ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:740932 3'
7049	18088	30459	9.12	9.8E-02	DB3710.1	NT	Aspergillus terreus BSD mRNA for blastidin S deaminase, complete cds
7856	20398	33304	0.65	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
7856	20398	33305	0.65	9.9E-02	AW103088.1	EST_HUMAN	xd43c09.x1 NC1_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2596528 3' similar to contains Alu repetitive element; contains element MIR MIR repetitive element ;
9181	21758	34704	1.1	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Pltp), mRNA
589	13219		1.48	9.8E-02	X56338.1	NT	O. sativa RAmY3C gene for alpha-amylase
3179	15792	28263	4.23	9.8E-02	AF184274.1	NT	Daucus carota leucoanthocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds
4308	16894	29337	8.69	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
4308	16894	29338	8.69	9.8E-02	AF257329.1	NT	Leptospira maculans beta-tubulin mRNA, complete cds
7495	20018		0.99	9.8E-02	X54133.1	NT	Human HPTP delta mRNA for protein tyrosine phosphatase delta
9178	21755		1.05	9.8E-02	M61943.1	NT	Human laminin B1 chain gene, exon 28
11334	23032	36041	2.27	9.8E-02	BF037421.1	EST_HUMAN	601460793F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3864287 5'
11840	24203		1.46	9.8E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1394	13988	26516	1.24	9.7E-02	AB005808.1	NT	Alce arborescens mRNA for NADP-malic enzyme, complete cds
1629	14221		1.75	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2301	14874	27450	2.11	9.7E-02	BE169660.1	EST_HUMAN	QV1-HT0518-070300-095-a04 HT0518 Homo sapiens cDNA
4055	16652		4.78	9.7E-02	Q99795	SWISSPROT	CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
5548	18180	30594	1.01	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
5548	18180	30595	1.01	9.7E-02	AF098189.1	NT	Caulobacter crescentus thymidylate kinase (tmk) and DNA polymerase III delta prime subunit (dnaC) genes, complete cds
6165	18777	31541	1.29	9.7E-02	AW954478.1	EST_HUMAN	EST366546 MAGE resequences, MAGEC Homo sapiens cDNA
7340	19857	32731	3.26	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (section 18 of 21); from 2897771 to 3213410
7924	20466	33374	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
7924	20466	33375	1.29	9.7E-02	N22798.1	EST_HUMAN	yw41c03.s1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:254788 3'
8783	21322	34246	1.47	9.7E-02	A1953984.1	EST_HUMAN	wx78b06.x1 NCI CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_ma1
11076	23598		2.34	9.7E-02	U56337.1	NT	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A (HUMAN);
2060	14640	27213	1.33	9.6E-02	A080721.1	EST_HUMAN	Mus musculus ligatin (Lgth) mRNA, partial cds
2060	14640	27214	1.33	9.6E-02	A080721.1	EST_HUMAN	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4437	17023	29463	7.54	9.6E-02	Z52888.2	NT	oz47d11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
5142	17713	30144	1.03	9.6E-02	AW969230.1	EST_HUMAN	Proteus mirabilis fimbrial operon, strain HI4320
6254	18863		2.74	9.6E-02	BE910039.1	EST_HUMAN	EST378303 MAGE resequences, MAGEI Homo sapiens cDNA
8317	20858		0.61	9.6E-02	AU137084.1	EST_HUMAN	601498088F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
9463	21988	34944	1.34	9.6E-02	AV887898.1	EST_HUMAN	AU137084 PLACE1 Homo sapiens cDNA clone IMAGE:1005740 5'
9786	22284		1.35	9.6E-02	BE894895.1	EST_HUMAN	AV887898 GKC Homo sapiens cDNA clone GKCAAH02 5'
9952	22447	35429	1.21	9.6E-02	AJ243211.1	NT	601434080F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
10055	22550	35544	1.26	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10055	22550	35545	1.26	9.6E-02	AB013985.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
10159	22654	35649	3.43	9.6E-02	P08174	SWISSPROT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
10621	23153	36165	7.28	9.6E-02	Z79702.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
11568	24013	37082	1.81	9.6E-02	AA825755.1	EST_HUMAN	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55)
12486	24617		1.55	9.6E-02	H14596.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome; segment 102/162
4177	16768	29217	2.24	9.5E-02	AW992395.1	EST_HUMAN	zu91g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
5286	17848	30274	1.12	9.5E-02	U63374.1	NT	ym19h03.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
							GM2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
							Lycopodium obscurum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5846	18470	31196	0.82	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7344	19871	32736	4.47	9.5E-02	AB003473.1	NT	Trimeresurus flaviviridis DNA for phospholipase A2 inhibitor, complete cds
7569	20066	32863	6.95	9.5E-02	AL161538.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 38
7685	18470	31196	0.9	9.5E-02	P51854	SWISSPROT	TRANSKETOLASE 2 (TK 2) (TRANSKETOLASE RELATED PROTEIN)
7821	20363	33271	2.04	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
7821	20363	33272	2.04	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23085	36107	3.19	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
10559	23095	36108	3.19	9.5E-02	BF035861.1	EST_HUMAN	601453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
12557	24658		2.4	9.5E-02	AF272732.1	NT	Arabidopsis thaliana putative transcription factor (MYB110) mRNA, complete cds
1873	14459	27015	3.67	9.4E-02	BF671063.1	EST_HUMAN	602150882F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4281917 5'
1904	14489	27050	1.36	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1904	14489	27051	1.36	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3949	16547	29015	5.59	9.4E-02	Z33059.1	NT	M. capricolum DNA for CONTIG MC073
5383	17942		0.93	9.4E-02	X98106.1	NT	Lactobacillus bacteriophage phig1e complete genomic DNA
6459	19060	31846	0.73	9.4E-02	AF097363.1	NT	Triticum aestivum heat shock protein 101 (Hsp101a) mRNA, complete cds
8536	21075		2.32	9.4E-02	Z46863.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
10813	20107	32682	2.33	9.4E-02	L78833.1	NT	Human BRCA1, Rho7 and vati genes, complete cds, and lpr35 gene, partial cds
11722	24934		6.48	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
12645	24719	30869	3.54	9.4E-02	U27699.1	NT	Human pepHBT-1 betaine-GABA transporter mRNA, complete cds
3018	15634		1.68	9.3E-02	4809280	NT	Homo sapiens BAI1-associated protein 3 (BAIAP3) mRNA
3063	15679		7.31	9.3E-02	6912525	NT	Homo sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3295	15906	28387	2.05	9.3E-02	BF575511.1	EST_HUMAN	602133086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4232	16820	29269	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4232	16820	29270	4.11	9.3E-02	BE391943.1	EST_HUMAN	601286082F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607653 5'
4840	17418		1.28	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
5843	18467		0.73	9.3E-02	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
8190	20731	33643	0.52	9.3E-02	AW568007.1	EST_HUMAN	EST89 Human Fetal Brain MATCHMAKER cDNA Library Homo sapiens cDNA
9052	21589		0.5	9.3E-02	AL113179.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9626	22126	35090	2.1	9.3E-02	BE962631.2	EST_HUMAN	60165588R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855881 3'
10094	22589	35581	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10094	22589	35582	3.16	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
10222	22717		3.82	9.3E-02	AJ206117.1	EST_HUMAN	U1-HB1-afx-h-05-0-UJ.s1 NCI_GCAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
11892	24854		2.27	9.3E-02	AJ249850.1	NT	Photobacterium damselae subsp. damselae partial gyrB gene for DNA gyrase B subunit

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12379	24886		16.03	9.3E-02	AW468850.1	EST_HUMAN	hd28h12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
12599	24933						Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; Bing1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr>
249	12809	25390	3.18	9.3E-02	AF100956.1	NT	
249	12809	25391	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
249	12809	25392	5.24	9.2E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
2269	14843		1.58	9.2E-02	R54156.1	EST_HUMAN	Y989107.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:41618 5'
3213	15826	26302	3.92	9.2E-02	Q28631	SWISSPROT	MAJOR EPIDIDYMYMIS-SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3345	15955	28430	0.86	9.2E-02	AA534354.1	EST_HUMAN	nt79e01.s1 NCI_CGAP_C63 Homo sapiens cDNA clone IMAGE:926136 3'
3646	16249		1.16	9.2E-02	6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Ptra). mRNA
4322	16908		1.42	9.2E-02	U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4398	16981		0.65	9.2E-02	BE299722.1	EST_HUMAN	600943365F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2660176 5'
4744	17325	29767	1.44	9.2E-02	X96402.1	NT	G.gallus Mia-CK gene
7951	20493	33402	1.75	9.2E-02	T49920.1	EST_HUMAN	y99c09.r1 Stragene placenta (#337225) Homo sapiens cDNA clone IMAGE:68808 5' similar to similar to gb:X56009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
8117	20658	33567	2.11	9.2E-02	X95256.1	NT	H.vulgaris xylose isomerase gene
12656	24930		2.09	9.2E-02	Z22150.1	NT	S.dysgalactiae fnbA gene
448	12677	25134	2.83	9.1E-02	X77665.1	NT	O. cuniculus k12 keratin gene
3733	16334		0.95	9.1E-02	AW372569.1	EST_HUMAN	PM2-BT0349-161289-001-402 BT0349 Homo sapiens cDNA
4582	17165	29608	1.55	9.1E-02	AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
5605	18527	31253	1.5	9.1E-02	AF128756.1	NT	Homo sapiens MSH55 gene, partial cds; and GLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
7420	19944	32809	11.98	9.1E-02	AW160658.1	EST_HUMAN	au74a05.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781968 5'
7668	20180	33067	0.89	9.1E-02	AP000081.1	NT	Aeropyrum pernix genomic DNA, section 4/7
7695	20204	33091	0.68	9.1E-02	U39073.1	NT	Mus musculus thymopoietin zeta mRNA, complete cds
8855	21394	34317	1.05	9.1E-02	Y14378.1	NT	Homo sapiens gamma adducin gene, exon 9
10325	22819		1.39	9.1E-02	T02884.1	EST_HUMAN	FB19F10 Fetal brain, Stragene Homo sapiens cDNA clone FB19F10 3' end
10354	22848	35842	1.52	9.1E-02	ST4059.1	NT	Tg616-Cyl actin [Tripneustes gratilla=sea urchins, embryos, Genomic, 5275 nt]
10380	22874	35867	0.73	9.1E-02	Y11187.1	NT	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes
11656	24083		2.35	9.1E-02	9633494	NT	Bacteriophage Mu, complete genome
11898	25036		1.62	9.1E-02	AA179901.1	EST_HUMAN	zp38h12.s1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11978	24289		2.21	9.1E-02	AF052693.1	NT	Rattus norvegicus cell cycle protein p55CDC gene, complete cds
12467	24877		17.53	9.1E-02	AJ291390.1	NT	Homo sapiens partial MUG3B gene for MUG3B much, exons 1-11
12672	24740		1.5	9.1E-02	AF226888.1	NT	Bombax mori fibrin heavy chain Fib-H (fib-H) gene, complete cds
774	13393	25893	3.92	9.0E-02	P15328	SWISSPROT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
1676	14268	26801	6.34	9.0E-02	BE220482.1	EST_HUMAN	h39g10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element;
2829	15381	27951	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2829	15381	27952	1.76	9.0E-02	AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
3380	15989	28468	0.83	9.0E-02	AF279135.1	NT	Dictyostelium discoideum spore coat structural protein SP85 (coE) gene, complete cds
4387	16973	29422	0.59	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4387	16973	29423	0.59	9.0E-02	S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4775	17356	29808	1.68	9.0E-02	X65740.2	NT	Plasmodium falciparum P-type ATPase 3 gene
5401	17959	30370	1.12	9.0E-02	Q24597	SWISSPROT	REGULATORY PROTEIN ZEST
6146	18760	31519	18.48	9.0E-02	W58037.1	EST_HUMAN	z68a12.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694 5' similar to
6820	19410		1.1	9.0E-02	BF062651.1	EST_HUMAN	PIR-S52171 S52171 small G protein - human ;
6864	19598	32428	0.77	9.0E-02	R62805.1	EST_HUMAN	7h63d03.x1 NCI_CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3320845 3' similar to contains Alu repetitive element;
12300	24497		2.42	9.0E-02	AF022238.1	NT	y11b08.s1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
1486	14079	26617	1.46	8.9E-02	BF701593.1	EST_HUMAN	Escherichia coli strain E2348/69 pathogenicity island, rOf1 (orf1), rOf2 (orf2), EscR (escR), EscS (escS), EscT (escT), EscU (escU), CesD (cesD), EscC (escC), EscJ (escJ), SepZ (sepZ), EscV (escV), EscN (escN), SepQ (sepQ), Tir (tir), OrfU (orfU), >
1486	14079	26618	1.46	8.9E-02	BF701593.1	EST_HUMAN	602129030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951 5'
2430	14897	27571	9.68	8.9E-02	BE153572.1	EST_HUMAN	PMO-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4277	18863		1.79	8.9E-02	AF286055.1	NT	Atrichum angustatum AtranFlo2 protein (AtranFlo2) gene, partial cds
4741	17322	29762	1.91	8.9E-02	AA424887.1	EST_HUMAN	zw03d04.s1 Soares_NhrIMPu_S1 Homo sapiens cDNA clone IMAGE:768199 3'
6014	18634	31370	3.35	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f08-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6014	18634	31371	3.35	8.9E-02	AW452122.1	EST_HUMAN	UI-H-B13-alc-f08-Q-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068294 3'
6026	18645	31387	3.24	8.9E-02	11433478	NT	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
7244	19773	32630	1.76	8.9E-02	P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE; METHYLENETETRAHYDROFOLATE CYCLOHYDROLASE]
7559	20077		2.15	8.9E-02	Z78021.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20F8

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7994	20536	33439	0.99	8.9E-02	P28475	SWISSPROT	NITRIC-OXIDE SYNTHASE, BRAIN (NOS, TYPE I) (NEURONAL NOS) (N-NOS) (NNOS) (CONSTITUTIVE NOS) (NC-NOS) (BNOS)
8072	20614	33528	0.69	8.9E-02	BF701665.1	EST_HUMAN	802129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8072	20614	33529	0.69	8.9E-02	BF701665.1	EST_HUMAN	802129111F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285827 5'
8534	21073	33963	4.81	8.9E-02	AA309319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9538	22038	34998	0.83	8.9E-02	A1285627.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_1_ym6 Homo sapiens cDNA clone IMAGE:1969680 3' similar to contains MER10.b1 MER10 repetitive element;
9538	22038	34999	0.83	8.9E-02	A1285627.1	EST_HUMAN	qu55c05.x1 NCL_CGAP_1_ym6 Homo sapiens cDNA clone IMAGE:1969680 3' similar to contains MER10.b1 MER10 repetitive element;
9848	22147	35118	0.55	8.9E-02	AA339356.1	EST_HUMAN	EST44454 Fetal brain 1 Homo sapiens cDNA 5' end
11721	24884		2.61	8.9E-02	P19524	SWISSPROT	MYOSIN-2 ISOFORM
11872	24224		4.62	8.9E-02	BF696918.1	EST_HUMAN	802129882F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180 5'
12044	24330		3.07	8.9E-02	6680220	NT	Mus musculus hippocampus abundant gene transcript 1 (Hiat1), mRNA
12307	25104		1.57	8.9E-02	U40493.1	NT	Ceratitis capitata mariner transposon transposase gene, complete cds
1416	14009	26538	1.36	8.8E-02	Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3871	16589	29038	1.08	8.8E-02	AA299128.1	EST_HUMAN	EST11595 Uterus Homo sapiens cDNA 5' end
4106	16700		4.3	8.8E-02	Q00288	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIIID 135 KDA SUBUNIT (TAFII-135) (TAFII-130) (TAFII130)
4390	16976		0.86	8.8E-02	4580423	NT	Homo sapiens paired box gene 6 (enitridia, keratitis) (PAX6), isoform b, mRNA
8918	21456	34376	1.18	8.8E-02	AA151872.1	EST_HUMAN	zr98a05.s1 Stralagene clone (#837204) Homo sapiens cDNA clone IMAGE:566288 3'
10897	23511	36543	3.11	8.8E-02	BE284465.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
10897	23511	36544	3.11	8.8E-02	BE284465.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535648 5'
11142	23690	36692	10.91	8.8E-02	AL040129.1	EST_HUMAN	DKFZp434D1313_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434D1313 5'
11948	24277	31019	1.73	8.8E-02	Z71561.1	NT	S. cerevisiae chromosome XIV reading frame ORF YNL285w
3756	16357	28826	3.9	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3756	16357	28827	3.9	8.7E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
4816	17394	29847	1.42	8.7E-02	AF178638.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5264	17826		1.2	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1189406 (section 101 of 148) of the complete genome
5517	18149	30561	5.18	8.7E-02	AA288875.1	EST_HUMAN	zs55g08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5517	18149	30562	5.18	8.7E-02	AA286875.1	EST_HUMAN	zs55g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701438 3'
6931	19590	32421	0.75	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
6931	19590	32422	0.75	8.7E-02	AJ271885.2	NT	Mus musculus partial Kcnq1 gene for potassium channel protein, exons 10-14
7803	20346	32422	0.46	8.7E-02	AA284532.1	EST_HUMAN	420e03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:713692 3'
8452	20992	33910	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 528 of the complete genome
8452	20992	33911	0.64	8.7E-02	AE004787.1	NT	Pseudomonas aeruginosa PAO1, section 348 of 528 of the complete genome
10590	23125	36745	2.71	8.7E-02	LO4758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' and
11191	23688	36745	1.77	8.7E-02	AJ007763.1	NT	Glucobacter oxydans tRNA-ile and tRNA-Ala genes
11835	24289		2.35	8.7E-02	X17116.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
12142	24389		2.72	8.7E-02	6879057	NT	Mus musculus nidogen 2 (Nid2), mRNA
1295	13899	26412	6.51	8.6E-02	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
2286	14860	27435	2.47	8.6E-02	BE408687.1	EST_HUMAN	601304018F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638643 5'
3222	15834	28312	2.42	8.6E-02	LO5468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3708	16307		4.02	8.6E-02	AF153362.1	NT	Dicystidium discoidaleum adenylyl cyclase (accA) gene, complete cds
4584	17197	29610	0.59	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galectin-3 gene, untranslated exon and 5' flanking region
6244	18853	31624	5.78	8.6E-02	Y10828.1	NT	Homo sapiens LCN1b gene
6512	19112	31899	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6512	19112	31900	1.56	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
7581	20096	32974	1.14	8.6E-02	P14616	SWISSPROT	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR)
7871	20413	33319	1.23	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
7871	20413	33320	1.23	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8015	20557	33460	0.76	8.6E-02	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8073	20615		0.65	8.6E-02	U60188.1	NT	Dictyostelium discoideum proteasome subunit C2 homolog PrtC (prtC) gene, complete cds
9852	22151	35121	1.18	8.6E-02	AF11170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
9888	22187		1.27	8.6E-02	AW662153.1	EST_HUMAN	hi20c08.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2872846 3'
10057	22552	35547	0.74	8.6E-02	AF026504.1	NT	Rattus norvegicus SPA-1 like protein p1294 mRNA, complete cds
10824	23345	36360	1.68	8.6E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
10824	23345	36361	1.68	8.6E-02	AF208551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
11128	23636	36677	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11128	23636	36678	4.74	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5'
11315	23013	36022	7.58	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
2440	15007	27579	2.52	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5985	18507		1.91	8.5E-02	P08089	SWISSPROT	M PROTEIN, SEROTYPE 6 PRECURSOR
6162	18775	31537	5.64	8.5E-02	AF233885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
8542	21081	34002	1.76	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
9750	22248	35230	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
9750	22248	35231	3.08	8.5E-02	BE833054.1	EST_HUMAN	RC4-OT0037-200700-014-e05 OT0037 Homo sapiens cDNA
10379	22873	35868	0.92	8.5E-02	11418108	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
11035	23549		12.56	8.5E-02	AF155510.1	NT	Homo sapiens heparanase precursor, mRNA, complete cds
11050	23563	36598	4.42	8.5E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
12354	24814		5.89	8.5E-02	AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
12536	24647		2.27	8.5E-02	AA362834.1	EST_HUMAN	EST72736 Ovary II Homo sapiens cDNA 5' end
2690	15474	27816	3.71	8.4E-02	W69330.1	EST_HUMAN	z444e11.1 r1 Soares fetal heart NBHH19W Homo sapiens cDNA clone IMAGE:343532 5'
5200	17765		1	8.4E-02	X01472.1	NT	Drosophila melanogaster copia-like element 17.6
5369	17929	30343	0.88	8.4E-02	5453817	NT	Homo sapiens nucleobindin 1 (NUCB1), mRNA
5515	18147	30559	9.46	8.4E-02	BE287153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534393 5'
6791	19382	32197	1.67	8.4E-02	AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
7972	20514	33421	7.35	8.4E-02	BE095074.1	EST_HUMAN	CM3-BT0760-260400-182-d05 BT0760 Homo sapiens cDNA
8776	21315	34237	1.13	8.4E-02	AF218890.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 2
10265	22760	35747	1.61	8.4E-02	AI735194.1	EST_HUMAN	as88g10.x1 Barstead codon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:O88312
11858	24217	31042	1.92	8.4E-02	R79408.1	EST_HUMAN	O88312 GOB-4;
2056	14637	27208	2.06	8.3E-02	5835680	NT	y83h12.1 r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145895 5'
2056	14637	27209	2.06	8.3E-02	5835680	NT	lxodes hexagonus mitochondrion, complete genome
3652	16255	28728	8.88	8.3E-02	P78334	SWISSPROT	lxodes hexagonus mitochondrion, complete genome
3680	16281	28748	0.68	8.3E-02	AI436797.1	EST_HUMAN	HYPOTHETICAL LIPOPROTEIN MCG309 HOMOLOG PRECURSOR
3680	16281	28749	0.68	8.3E-02	AI436797.1	EST_HUMAN	th82g06.x1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5416	17973		1.71	8.3E-02	AW902857.1	EST_HUMAN	th82g06.x1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
6406	19009	31791	0.89	8.3E-02	AI942338.1	EST_HUMAN	QV3-NN1025-030500-173-e04 NN1025 Homo sapiens cDNA
6504	19104	31889	3.05	8.3E-02	AF052683.1	NT	w07811.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2461581 3'
7922	20464	33371	3.57	8.3E-02	AF195787.1	NT	Homo sapiens protocadherin 43 gene, exon 1
7955	20497		1.31	8.3E-02	AA865285.1	EST_HUMAN	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Dp2) mRNA, complete cds
8241	20782		4.14	8.3E-02	AA987873.1	EST_HUMAN	cg81f10.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1592779 3'
9457	21983	34835	1.55	8.3E-02	AW593503.1	EST_HUMAN	la05h10.x1 Human Pancreatic islets Homo sapiens cDNA 3' similar to TR:Q15332 Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9470	21869		1.94	8.3E-02	AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
10244	22739		0.56	8.3E-02	AF020409.1	NT	Dictyostellium discoideum DocA (docA) mRNA, complete cds
11550	23998	37070	1.7	8.3E-02	AA700756.1	EST_HUMAN	262204.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:435367 3' similar to contains element MER22 repetitive element;
11953	25040		1.36	8.3E-02	BE958458.1	EST_HUMAN	601644770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928993 5'
1421	14014		9.32	8.2E-02	Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1542	14134	26668	1.79	8.2E-02	AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3109	15724		2.23	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3874	16472		1.66	8.2E-02	AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
4079	16875	29136	1.29	8.2E-02	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
4371	16958	29400	7.76	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29401	7.76	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4371	16958	29402	7.76	8.2E-02	P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
5240	17804	30225	3.53	8.2E-02	U76009.1	NT	Mus musculus zinc transporter (ZnT-3) gene, complete cds
5400	17958	30369	0.9	8.2E-02	AU119830.1	EST_HUMAN	AU119830 HEMBA1 Homo sapiens cDNA clone HEMBA1006744 5'
5538	18170	30585	1.62	8.2E-02	BE897030.1	EST_HUMAN	601439576F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924523 5'
7092	19663	32502	3.11	8.2E-02	AF309555.1	NT	Bos taurus connective tissue growth factor precursor (CTGF) gene, complete cds
8707	21246	34169	2.98	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-031289-011-d05 PT0004 Homo sapiens cDNA
9517	22017	34974	4.96	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
9678	22177	35152	2.2	8.2E-02	BE254318.1	EST_HUMAN	601115055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355598 5'
11959	24281	31029	5.69	8.2E-02	AE002246.2	NT	Chlamydia pneumoniae AR39, section 73 of 94 of the complete genome
12383	24806		4.6	8.2E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
5929	18551	31278	1.08	8.1E-02	AE004008.1	NT	Xylella fastidiosa, section 152 of 229 of the complete genome
6516	19116	31906	0.97	8.1E-02	T11532.1	EST_HUMAN	A1484F Heart Homo sapiens cDNA clone A1484
7248	19777		0.72	8.1E-02	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
7582	20097		1.03	8.1E-02	A1632681.1	EST_HUMAN	wd8608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338503 3'
8281	20822	33741	0.62	8.1E-02	11426974	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
8281	20822	33742	0.62	8.1E-02	AL163202.2	NT	Homo sapiens hypothetical protein FLJ10060 (FLJ10060), mRNA
9826	22324		1.7	8.1E-02	AY005150.1	NT	Homo sapiens extracellular glycoprotein lactrin precursor, gene, complete cds
11371	23823	36886	1.87	8.1E-02	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
6	15405	25143	9.1	8.0E-02	AW654653.1	EST_HUMAN	EST366723 IMAGE resequences, MAGC Homo sapiens cDNA
971	13582	26095	1.13	8.0E-02	U60315.1	NT	Molluscum contagiosum virus subtype 1, complete genome
1738	15449	26869	10.86	8.0E-02	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1736	15449	26870	10.86	8.0E-02	D26535.1	NT	Human gene for dihydriolipamide succinyltransferase, complete cds (exon 1-15)
1947	14531	27087	3.32	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-170200-001-b08 BT0347 Homo sapiens cDNA
2413	14981	27556	1.14	8.0E-02	D60915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2413	14981	27557	1.14	8.0E-02	D60915.1	NT	Synechocystis sp. PCC6803 complete genome, 17/27, 2137259-2267259
2509	15073		4.66	8.0E-02	BF246744.1	EST_HUMAN	601855548F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4075619 5'
2847	13733	26243	0.87	8.0E-02	M23449.1	NT	Dichoselium discoidium cyclic nucleotide phosphodiesterase gene, complete cds
2825	15541	28016	0.64	8.0E-02	AL445067.1	NT	Thermoplasma acidophilum complete genome, segment 5/5
3889	16487	28948	0.59	8.0E-02	AW966118.1	EST_HUMAN	EST378191 IMAGE resequences, MAGI Homo sapiens cDNA
4146	16736		0.95	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
4890	17465	29920	2.28	8.0E-02	AI434202.1	EST_HUMAN	931902.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2132114 3'
4939	17514		5.81	8.0E-02	X72794.1	NT	M.musculus gene for gelatinase B
6051	18669	31408	3.07	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
7232	18669	31408	1.42	8.0E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
8069	20611	33524	3.68	8.0E-02	AL114993.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
9311	21825	34773	1.22	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
9311	21825	34774	1.22	8.0E-02	X74208.1	NT	H.sapiens AGT gene, intron 4
10063	22558		0.57	8.0E-02	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10671	23203	36216	3.69	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M88, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
11993	24302	30988	3.6	8.0E-02	AJ005375.1	NT	Drosophila arena hunchback region
12695	16738		3.88	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
2218	14793	27366	4.15	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5'
3007	15623	28101	11.7	7.9E-02	AI582028.1	EST_HUMAN	ar98c08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb.Z26876 60S RIBOSOMAL PROTEIN L38 (HUMAN)
3865	16463	28927	0.92	7.9E-02	AF030694.2	NT	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), putative chloroquine resistance transporter (crt), CG9 (cg9), CG1 (cg1), CG6 (cg6), CG2 (cg2), and CG7 (cg7) genes, complete cds
3917	16515	28978	3	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
3917	16515	28979	3	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csf1r), mRNA
4834	17509		1.36	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
5390	17948	30360	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
5390	17948	30361	0.58	7.9E-02	AF035672.1	NT	Mus musculus MHC class I related protein 1 (MR1) gene, complete cds
6798	19389		1.08	7.9E-02	BF368016.1	EST_HUMAN	RC3-GN0042-310800-024-411 GN0042 Homo sapiens cDNA
7675	20517	33424	3.32	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of Mif2 Smk4p (SMT4) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9941	22436	35412	4.71	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2 CE08611;
9941	22436	35413	4.71	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP.C37A2.2 CE08611;
12479	24613		1.42	7.9E-02	A1761639.1	EST_HUMAN	wg66h01.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2370097 3' ce59d02.y6 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;
1252	13849	26365	1.36	7.8E-02	A1793275.1	EST_HUMAN	ce59d02.y6 NCI_CGAP_Lu8 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L1.13 L1 repetitive element;
1252	13849	26366	1.36	7.8E-02	A1793275.1	EST_HUMAN	PM3-FND058-140700-005-f09 FN0058 Homo sapiens cDNA 600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
4812	17487	29943	0.67	7.8E-02	BE936331.1	EST_HUMAN	
5247	18412		2.77	7.8E-02	BE250048.1	EST_HUMAN	
7136	19475	32287	1.34	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
7136	19475	32288	1.34	7.8E-02	U82895.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
8720	21259	34179	1.46	7.8E-02	BE97947.1	EST_HUMAN	601440439F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925449 5' S.cerevisiae CAT8 gene
8813	21352	34274	0.6	7.8E-02	X78344.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FVE-DSP1b mRNA, complete cds
8983	21521	34447	0.83	7.8E-02	AF233437.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FVE-DSP1b mRNA, complete cds
8983	21521	34448	0.83	7.8E-02	AF233437.1	NT	nc68b06.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731 Bacillus subtilis complete genome (section 21 of 21): from 3999281 to 4214814
9283	21883	34828	1.08	7.8E-02	AA469354.1	EST_HUMAN	Human interleukin-11 receptor alpha chain gene, complete cds
9717	22215	35189	0.5	7.8E-02	Z96124.1	NT	Homo sapiens envoplakin (EVPL) gene, exons 15 through 18
10544	23081	36094	1.87	7.8E-02	U32323.1	NT	Homo sapiens WRN (WRN) gene, complete cds
12384	24550	30506	1.95	7.8E-02	U72847.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1444	15442	26568	0.91	7.7E-02	AF181897.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 13
3647	16250		2.62	7.7E-02	AJ238093.1	NT	zu53d11.r1 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR.G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;
5129	17701	30135	0.92	7.7E-02	AL161501.2	NT	PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR059C
7850	20392	33265	5.56	7.7E-02	AA402949.1	EST_HUMAN	
9749	22247	35229	5.97	7.7E-02	P38080	SWISSPROT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10037	22532	35527	0.75	7.7E-02	A1318662.1	EST_HUMAN	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S
10037	22532	35528	0.76	7.7E-02	A1318662.1	EST_HUMAN	RIBOSOMAL PROTEIN L38 (HUMAN);
10889	23410	36428	4.97	7.7E-02	11422757	NT	ta80b08.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050359 3' similar to gb:Z26876 60S
12194	24894		1.91	7.7E-02	11436859	NT	RIBOSOMAL PROTEIN L38 (HUMAN);
3434	16042	28523	3.08	7.6E-02	BE514432.1	EST_HUMAN	Homo sapiens KIAA0828 gene product (KIAA0828), mRNA
3455	16062	28537	0.67	7.6E-02	AA298447.1	EST_HUMAN	Homo sapiens interferon regulatory factor 7 (IRF7), mRNA
3615	16218	28697	0.67	7.6E-02	AJ400877.1	NT	601316426F1 NIH_MGC 8 Homo sapiens cDNA clone IMAGE:3634903 5'
4993	17567		2.04	7.6E-02	AW858844.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to similar to protobocaderin 43
6247	18856	31627	0.7	7.6E-02	A1061275.1	EST_HUMAN	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17
6497	19098	31882	0.83	7.6E-02	BE379328.1	EST_HUMAN	gene
9292	21892	34839	1.24	7.6E-02	AJ131018.1	NT	RC3-CT0347-110300-014-a05 CT0347 Homo sapiens cDNA
9811	22309		1.7	7.6E-02	AL139078.2	NT	an25602.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1699730 3'
10120	22815	35605	0.52	7.6E-02	BE708002.1	EST_HUMAN	601236402F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3608401 5'
10251	22746		0.49	7.6E-02	BE959638.2	EST_HUMAN	Homo sapiens SCL gene locus
10480	22874	35981	0.72	7.6E-02	X92856.1	NT	Campylobacter jejuni NCTC11168 complete genome; segment 5/6
10480	22874	35982	0.72	7.6E-02	X92856.1	NT	RC1-HT0545-020800-017-d06 HT0545 Homo sapiens cDNA
11526	23974	37044	2.58	7.6E-02	AW698645.1	EST_HUMAN	601654915R1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:3839810 3'
817	13435	25940	1.18	7.5E-02	5902093	NT	L. esculentum mRNA for triose phosphate translocator
817	13435	25941	1.18	7.5E-02	5902093	NT	L. esculentum mRNA for triose phosphate translocator
4606	17189	29636	0.57	7.5E-02	AB015961.1	NT	QV3-EN0046-150400-151-a04 BN0046 Homo sapiens cDNA
8280	20821	33740	1.15	7.5E-02	A1864397.1	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
8444	20984	33899	1.18	7.5E-02	AU118913.1	EST_HUMAN	Homo sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
9845	22440		0.5	7.5E-02	BF221730.1	EST_HUMAN	Homo sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
10387	22881	35875	0.9	7.5E-02	BF206809.1	EST_HUMAN	w52b02.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb:M14328 ALPHA ENOLASE (HUMAN);
10481	22975	35883	0.71	7.5E-02	X79480.1	NT	AU118913 HEMBA1 Homo sapiens cDNA clone HEMBA100264 5'
503	13135	25623	1.23	7.4E-02	AW838547.1	EST_HUMAN	7661c05.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3578504 3' similar to contains element
1509	14101		0.97	7.4E-02	AF030027.1	NT	MER27 repetitive element;
							601870205F1 NIH_MGC 19 Homo sapiens cDNA clone IMAGE:4100449 5'
							C.fiml DSM 20113 16S rDNA
							RC5-LT0054-280100-011-H09 LT0054 Homo sapiens cDNA
							Equine herpesvirus 4 strain NS60567, complete genome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2616	15178		1.04	7.4E-02	6755089	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pibx1), mRNA
3654	16257	28729	0.84	7.4E-02	A1807885.1	EST_HUMAN	wf43h01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358385 3'
4814	17392	29844	1.33	7.4E-02	L78810.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4911	17486	29942	2.82	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvrl1), mRNA
5052	17825		1.65	7.4E-02	AE000886.1	NT	Methanobacterium thermoautotrophicum from bases 1076134 to 1086763 (section 92 of 148) of the complete genome
5076	17649	30090	1.67	7.4E-02	6878492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchrlp), mRNA
5393	17851	30364	0.93	7.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6621	19218		1.64	7.4E-02	R17477.1	EST_HUMAN	wf14g08.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:32339 5'
7485	20008	32874	0.68	7.4E-02	AA605132.1	EST_HUMAN	nc71402.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112259 3'
7842	20384	33288	1.23	7.4E-02	BE880112.1	EST_HUMAN	601493368F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
8438	20978	33893	1.2	7.4E-02	U56089.1	NT	Human periodic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9093	21629	34566	0.92	7.4E-02	AW628605.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9093	21629	34567	0.92	7.4E-02	AW628605.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2. ;
9360	20289	33197	0.72	7.4E-02	A1672939.1	EST_HUMAN	hh67d11.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2867861 5' similar to SW:SCA2_HUMAN
9360	20289	33198	0.72	7.4E-02	A1672939.1	EST_HUMAN	O15127 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2. ;
9728	22226	35203	0.85	7.4E-02	U62293.1	NT	wf74d02.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
11600	24043		1.57	7.4E-02	U8282.1	NT	wf74d02.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2346819 3'
11812	24250		1.28	7.4E-02	11525893	NT	Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds
12187	25015		4.44	7.4E-02	AW379431.1	EST_HUMAN	Rattus norvegicus telomerase protein component 1 (TLP1) mRNA, complete cds
12351	24531	30926	2.8	7.4E-02	BF035099.1	EST_HUMAN	Homo sapiens histone deacetylase 5 (NY-CO-9), mRNA
12361	24535	30901	1.37	7.4E-02	AJ223459.2	NT	GM4-HT0243-081199-037-411 HT0243 Homo sapiens cDNA
494	13127	25613	1.42	7.3E-02	BE964961.2	EST_HUMAN	601453813F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3857738 5'
494	13127	25614	1.42	7.3E-02	BE964961.2	EST_HUMAN	Aspergillus nidulans pmD, prnX, prnA genes
713	13334	25820	2.68	7.3E-02	AE001789.1	NT	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1528	15444	26659	4.47	7.3E-02	AW600281.1	EST_HUMAN	601658738R1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'
1885	15453		16.16	7.3E-02	AL163302.2	NT	Thermotoga maritima section 101 of 136 of the complete genome
							GM0-NIN1004-130300-284-g08 NN1004 Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C102
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV25S1A2N1T, TCRBV6S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2P, TCRBV7S2A1N4T, TCRBV13S9/13S>
3838	16437		0.59	7.3E-02	U66059.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 6-10 and complete cds
5137	17709		1.11	7.3E-02	U12283.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6580	19178	31978	1.56	7.3E-02	AA779877.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb.L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
7484	20007	32872	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
7484	20007	32873	4.36	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8109	20850		1.06	7.3E-02	7682107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8137	21672		1.38	7.3E-02	AB011090.1	NT	Homo sapiens mRNA for KIAA0518 protein, partial cds
11095	19178	31978	3.07	7.3E-02	AA779877.1	EST_HUMAN	z24a02.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb.L02426 26S PROTEASE SUBUNIT 4 (HUMAN);
125	12794	25279	1.36	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
125	12794	25280	1.36	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1524	14116	26652	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1524	14116	26653	2.11	7.2E-02	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2585	15148		2.76	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3054	16552	29021	0.59	7.2E-02	AW298322.1	EST_HUMAN	UI-H-BW0-aj-e-05-0-U1.s1 NCI_CGAP_Sub66 Homo sapiens cDNA clone IMAGE:2732049 3'
4438	17024	29464	3.65	7.2E-02	BF572307.1	EST_HUMAN	60207757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
5223	17788	30207	0.89	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5491	18125	30533	2.8	7.2E-02	U87531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5492	18126	30534	8.6	7.2E-02	P11120	SWISSPROT	CALMODULIN
6265	18873		0.93	7.2E-02	BF217598.1	EST_HUMAN	601883905F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4086224 5'
7220	19751	32607	1.27	7.2E-02	BF216086.1	EST_HUMAN	601883588F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4085710 5'
7261	19789		1.54	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
8128	20663	33578	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8128	20669	33579	0.69	7.2E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
8904	21532		0.5	7.2E-02	Y1217.1	NT	Lactococcus lactis cspe gene
9495	21995		0.57	7.2E-02	X16349.1	NT	Human gene for sex hormone-binding globulin (SHBG)
9529	22029	34968	2.28	7.2E-02	AV12452.1	EST_HUMAN	AV12452 DCA Homo sapiens cDNA clone DCAAUG01 5'
9874	22173	35149	4.69	7.2E-02	L14581.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
9828	22326	35307	1.01	7.2E-02	BF125399.1	EST_HUMAN	601763523F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026436 5'
9914	22410	35386	2.73	7.2E-02	AW873187.1	EST_HUMAN	h24111.x1 NCI_CGAP_Adr1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q92340 Q92340 ATYPICAL PKC SPECIFIC BINDING PROTEIN. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10254	22749	35737		7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
10370	22864	35857	5.88	7.2E-02	BE56003.1	EST_HUMAN	601343928F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685951 5'
10382	22886		3.22	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
10782	23315	36324	6.18	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
11822	24192	31033	1.54	7.2E-02	AA773698.1	EST_HUMAN	af81a04.r1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
11857	24216		4.88	7.2E-02	AJ230786.1	EST_HUMAN	AJ230786 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
11914	24252		2.01	7.2E-02	AA584465.1	EST_HUMAN	nc05108.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1099839 3'
11979	24280		3.59	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
11895	24858		7.52	7.2E-02	AW900982.1	EST_HUMAN	CM4-NN1009-200300-116-c11 NN1009 Homo sapiens cDNA
12514	24833		1.85	7.2E-02	AA401779.1	EST_HUMAN	z57c12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726454 5'
1948	14532	27088	1.42	7.1E-02	L02280.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2331	14902	27473	4.53	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4092981 5'
7848	20390	33282	0.84	7.1E-02	A1125284.1	EST_HUMAN	q492a10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1736922 3'
11700	24113		6.04	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051234 5'
554	13185	25663	0.97	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR
1547	14139		1.43	7.0E-02	X96677.1	NT	M.artellia Mitc1-1 gene
1798	14388	26833	0.94	7.0E-02	AA056343.1	EST_HUMAN	z166104.s1 Stralagene colon (#837204) Homo sapiens cDNA clone IMAGE:509599 3'
3064	15680	28153	2.03	7.0E-02	AW138152.1	EST_HUMAN	UI-H-B11-acyc-c-07-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
3966	16584	29033	1.71	7.0E-02	AA815438.1	EST_HUMAN	af65a12.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 60S
4118	16712	29168	1.11	7.0E-02	BE070264.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
4219	16807		1.11	7.0E-02	AW792862.1	EST_HUMAN	QV4-BT0407-280100-090-e10 BT0407 Homo sapiens cDNA
4294	16880	29027	1.28	7.0E-02	AF077821.1	NT	CMO-UM0001-060300-270-e12 UM0001 Homo sapiens cDNA
5063	17636	30079	6.56	7.0E-02	BF381987.1	EST_HUMAN	Genis familiaris inducible nitric oxide synthase mRNA, complete cds
5580	18211		0.84	7.0E-02	Y08143.2	NT	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7431	19955	32820	0.88	7.0E-02	AV689285.1	EST_HUMAN	Lumbricus rubellus mRNA for cyclophilin B
9027	21564	34493	1.41	7.0E-02	9628113	NT	AV689285 GK Homo sapiens cDNA clone GKCCAE08 5'
9515	22015	34973	1.25	7.0E-02	K02801.1	NT	African swine fever virus, complete genome
9863	22360	35340	0.73	7.0E-02	U27266.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
11251	23781	36837	2.68	7.0E-02	AA724285.1	EST_HUMAN	Human myosin binding protein H (MyBP-H) gene, complete cds
							ah99a05.s1 Soares_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:U14837
							TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
540	13171	25649	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
540	13171	25650	11.84	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1378	13971		1.34	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signaling (ZGAP1) mRNA, and translated products
3860	16458	28921	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
3860	16458	28922	1.16	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
5381	17940	30354	3.58	6.9E-02	AF121254.1	NT	Enterococcus faecium cysteine aminopeptidase (pepC) gene, partial cds; phospho-beta-glucosidase BglB (bglB), beta-glucoside specific transport protein (bglS), transcription antiterminator (bglR), enterocin B precursor (entB), enterocin B immunity protease
7996	20538		1.13	6.9E-02	U12022.1	NT	Human calmodulin (CALM1) gene, exons 2,3,4,5 and 6, and complete cds
8488	21027	33944	1.1	6.9E-02	BE567435.1	EST_HUMAN	601340861F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
8488	21027	33945	1.1	6.9E-02	BE567435.1	EST_HUMAN	601340861F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3683030 5'
9048	21585	34516	0.61	6.9E-02	U22967.1	NT	Barbarte duck parvovirus REP protein (rep) and three capsid protein VP (vp) genes, complete cds
11853	24213		17.91	6.9E-02	X74315.1	NT	Xlaevis XFD2 mRNA for fork head protein
12031	24321		1.96	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFH HOMOLOG
12258	24468		3.68	6.9E-02	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (MNP2) gene, complete cds
1926	14511	27065	1.83	6.8E-02	AA496759.1	EST_HUMAN	es30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1926	14511	27068	1.83	6.8E-02	AA496759.1	EST_HUMAN	es30f02.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1950	14534	27090	3.99	6.8E-02	AF156673.1	NT	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (HUMAN);
2023	14605	27170	1.68	6.8E-02	BE263781.1	EST_HUMAN	Homo sapiens putative hepatic transcription factor (WBSCR14) gene, complete cds
4651	17233		0.66	6.8E-02	BE141076.1	EST_HUMAN	601194141F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537706 5'
6980	19478		4.63	6.8E-02	BE061890.1	EST_HUMAN	MRO-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
7324	19851	32713	8.08	6.8E-02	AL163268.2	NT	RC1-BT0254-090300-017-d09 BT0254 Homo sapiens cDNA
8230	20771	33690	5.36	6.8E-02	AJ248287.1	NT	Homo sapiens chromosome 21 segment HS21C068
8230	20771	33691	5.36	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome; segment 516
11646	25064		2.46	6.8E-02	T03214.1	EST_HUMAN	Pyrococcus abyssi complete genome; segment 516
11783	24168		2.42	6.8E-02	AA758014.1	EST_HUMAN	FB4A8 Fetal brain, Stratiene Homo sapiens cDNA clone FB4A8 3' end similar to LINE-1
12380	24547		1.37	6.8E-02	AW875839.1	EST_HUMAN	en67R05.s1 Soares_NHT Homo sapiens cDNA clone 1320705 3'
12444	24580		2.87	6.8E-02	6910585	NT	EST387948 MAGe resequences, MAGN Homo sapiens cDNA
12650	25008	30614	1.54	6.8E-02	6978885	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1578	14169		1.51	6.7E-02	AF115536.1	NT	Rattus norvegicus Growth factor independent-1 (Gfi1), mRNA
1938	14522	27078	3.82	6.7E-02	A1220285.1	EST_HUMAN	Oncofyrchilus mykiss TAP1 protein (OnmyTAP1) mRNA, OnmyTAP1*01 allele, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3780	16380	28844	4.61	6.7E-02	P17278	SWISSPROT	HOMEOBOX PROTEIN HOX-D4 (CHOXA)
4842	17420	28873	3.51	6.7E-02	AP001514.1	NT	Bacillus halodurans genomic DNA, section 8/14
7792	20335	33241	0.63	6.7E-02	X62695.1	NT	H sapiens DNA for cGMP phosphodiesterase (exons 4-22)
7792	20335	33242	0.63	6.7E-02	X62695.1	NT	H sapiens DNA for cGMP phosphodiesterase (exons 4-22)
9518	22018	34975	0.75	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-aer-g-01-O-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
9518	22018	34976	0.75	6.7E-02	AW137359.1	EST_HUMAN	UI-H-B11-aer-g-01-O-UI.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2715433 3'
2225	14800	27372	3	6.8E-02	AJ280241.1	NT	Mus musculus Capn12 gene for calpain 12, exons 1-21, three alternative transcripts
3510	16115	28594	9.7	6.8E-02	R64306.1	EST_HUMAN	yt18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139579 3'
3524	16129	28609	3.24	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3524	16129	28610	3.24	6.8E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
4154	16746	29200	1.83	6.8E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
5114	17686	30122	11.2	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5114	17686	30123	11.2	6.8E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
5164	17733	30160	0.57	6.8E-02	AA393244.1	EST_HUMAN	z74a07.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:728052 5' similar to gb:104270 TUMOR
5164	17733	30161	0.57	6.8E-02	AA393244.1	EST_HUMAN	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
6098	19294	32099	4.11	6.8E-02	X08411.1	NT	NECROSIS FACTOR RECEPTOR 2 RELATED PROTEIN PRECURSOR (HUMAN);
7888	20430	33339	1.58	6.8E-02	AF052572.1	NT	P. vulgaris mRNA for chalcone synthase
8409	20949	33869	0.72	6.8E-02	AF006055.1	NT	Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds
8714	21253		0.49	6.8E-02	O80673	SWISSPROT	Dicystostellum discoideum darlin (darA) gene, complete cds
8852	21391	34312	0.52	6.8E-02	9629198	NT	DNA POLYMERASE ZETA CATALYTIC SUBUNIT (HREV3)
8852	21391	34313	0.52	6.8E-02	9629198	NT	Human respiratory syncytial virus, complete genome
8862	22359	35339	0.58	6.8E-02	AI458752.1	EST_HUMAN	Human respiratory syncytial virus, complete genome
9999	22494	35483	1.54	6.8E-02	Y07848.1	NT	g97g06.xt NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2149488 3'
10029	22524		0.53	6.8E-02	11430559	NT	Homo sapiens EWS, ger22, rrp22 and balm22 genes
10842	23063	36379	7.09	6.8E-02	BF374248.1	EST_HUMAN	Homo sapiens vinculin (VCL), mRNA
12251	24462		2.87	6.8E-02	9637991	NT	MR1-SN0064-010600-008-s12 SN0064 Homo sapiens cDNA
12585	24678		1.36	6.8E-02	AF167430.1	NT	Mus musculus DIPB gene (Dipb), mRNA
608	13238	25710	1.65	6.5E-02	BF027639.1	EST_HUMAN	Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region
1024	13635	26151	2.61	6.5E-02	7706088	NT	601671046F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3954178 5'
1435	14028	26556	3.4	6.5E-02	U47624.1	NT	Homo sapiens E2F-like protein (LOC51270), mRNA
1770	14360	26905	1.42	6.5E-02	AE000764.1	NT	Xenopus laevis alpha(E)-catenin mRNA, complete cds
5349	17909	30324	0.88	6.5E-02	D45899.1	NT	Aquifex aeolicus section 96 of 109 of the complete genome
							Caenorhabditis elegans DNA for ryanodine receptor, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5747	18373	31081	1.79	6.5E-02	AA443991.1	EST_HUMAN	z44h12.s1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:756743 3' similar to gb-M26038
6684	19260	32084	0.89	6.5E-02	BF665340.1	EST_HUMAN	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-5 BETA CHAIN (HUMAN);
7051	18070	30461	0.96	6.5E-02	U22681.1	NT	602118687F1 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4276029 5'
9854	22352	35332	0.65	6.5E-02	BE963200.2	EST_HUMAN	Azotobacter vinelandii ATCC 9048 negative regulator MucB (mucB) gene, partial cds
9854	22352	35333	0.85	6.5E-02	BE963200.2	EST_HUMAN	601656817R1 NIH_MGC 67 Homo sapiens cDNA clone IMAGE:3865637 3'
10363	22857	35849	0.59	6.5E-02	BF106300.1	EST_HUMAN	601823511F1 NIH_MGC 77 Homo sapiens cDNA clone IMAGE:4043138 5'
10518	23056	36067	5.86	6.5E-02	AA195648.1	EST_HUMAN	z32g05.s1 Soares NIHMPU_S1 Homo sapiens cDNA clone IMAGE:665144 3'
11669	24091		5.28	6.5E-02	M21496.1	NT	Rabbit microsomal epoxide hydrolase
12040	24327		3.84	6.5E-02	AF102990.1	NT	Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds
601	13230	25703	1.74	6.4E-02	X94549.1	NT	A. carterae precursor of penicillin-chlorophylla-protein (PCP) gene
5641	18270	30743	1.21	6.4E-02	AI191956.1	EST_HUMAN	q607b01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element;
6261	18869	31639	5.4	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6261	18869	31640	5.4	6.4E-02	AF052733.1	NT	Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-eng-1) gene, complete cds
6534	19134	31927	0.68	6.4E-02	AI872898.1	EST_HUMAN	w673g12.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2346790 3'
6907	19841	32477	4.7	6.4E-02	BE974448.1	EST_HUMAN	601690425R2 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:3950503 3'
8278	20819		2.66	6.4E-02	6753328	NT	Mus musculus chaperonin subunit 8a (zeta) (Cct8a), mRNA
8599	21138	34052	3.59	6.4E-02	AA093305.1	EST_HUMAN	K1419.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9055	21592	34522	0.85	6.4E-02	AF150195.1	EST_HUMAN	AF150195 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAIA10
9506	22006		0.61	6.4E-02	BE834083.1	EST_HUMAN	RC1-OT0083-150600-014-g08 OT0083 Homo sapiens cDNA
9633	22133	35098	1.79	6.4E-02	AB011128.1	NT	Homo sapiens mRNA for KIAA0564 protein, partial cds
10162	22657	35652	0.68	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
10162	22657	35653	0.68	6.4E-02	AF087150.1	NT	Homo sapiens DNA topoisomerase II beta (TOP2B) gene, exons 16, 17, and 18
11554	24002	37074	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11554	24002	37075	2.05	6.4E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11931	24971		4.86	6.4E-02	AF107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
11986	24286	30983	2.86	6.4E-02	AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1791	14381	28928	3.03	6.3E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc701 gene, partial cds; smRNP, G7A, NG23.
3664	18266		2.41	6.3E-02	P37092	SWISSPROT	MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds; and unknown genes
6285	18893	31682	1.1	6.3E-02	BF210736.1	EST_HUMAN	HEAT SHOCK PROTEIN 70 HOMOLOG
7291	19819		1.05	6.3E-02	X97899.1	NT	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
9215	21732	34675	0.96	6.3E-02	AJ243918.1	NT	H. sapiens gene encoding Le autoantigen
9927	22423	35397	2.86	6.3E-02	AB010162.1	NT	Drosophila melanogaster Domina gene, exons 1-3
10172	22867		0.87	6.3E-02	AV698070.1	EST_HUMAN	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
10594	18893	31662	3.6	6.3E-02	BF210736.1	EST_HUMAN	AV698070 GKC Homo sapiens cDNA clone GKCAHE01 5'
4337	18924	28365	3.3	6.2E-02	AL161572.2	NT	601873316F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4097499 5'
4431	17017		1.04	6.2E-02	AF271235.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4692	17284		6.75	6.2E-02	Q62191	SWISSPROT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPI) mRNA, complete cds
6889	18624	32459	0.75	6.2E-02	D49530.1	NT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52)
7623	20136	33014	0.78	6.2E-02	U41453.1	NT	Spirulina platensis DNA for adenylate cyclase, complete cds
8877	25123	34742	0.51	6.2E-02	M61101.1	NT	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
9267	21793	34742	0.5	6.2E-02	AA778450.1	EST_HUMAN	Rattus norvegicus PKC binding protein and substrate mRNA, complete cds
9401	21910	34859	1.05	6.2E-02	6677898	NT	Porcine group C rotavirus (strain Cowden) outer membrane protein (VP7) mRNA, complete cds
11027	23541	36576	1.74	6.2E-02	AF217490.1	NT	af20e06.s1 Soares, total, fetus, NB2HF8_9w Homo sapiens cDNA clone IMAGE:1032178 3'
11226	23757	36814	1.89	6.2E-02	AJ242735.1	NT	Mus musculus stromal cell derived factor receptor 2 (Sdf2), mRNA
11770	25097		8.34	6.2E-02	AE000750.1	NT	Homo sapiens fragile 16D oddo reductase (FOR) gene, exons 8, 9, and partial cds
12200	24426	30951	3.56	6.2E-02	BF112039.1	EST_HUMAN	Metarhizium anisopliae mRNA for Chymotrypsin (chy1 gene)
277	12934	25420	4.8	6.1E-02	D16471.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
4063	16660		2.78	6.1E-02	U73325.1	NT	713708.x1 Soares, NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9Y4S8 Q9Y4S8 HYPOTHETICAL 30.3 KD PROTEIN, [1];
4759	17340	29786	1.09	6.1E-02	AF119413.1	NT	Human mRNA, Xq terminal portion
4759	17340	29787	1.09	6.1E-02	AF119413.1	NT	Arabidopsis thaliana K+ inward rectifying channel protein (AtKc1) gene, complete cds
6262	18870		1.42	6.1E-02	4507070	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
8207	20748	33661	3.31	6.1E-02	X99268.1	NT	Lupinus albus 1-aminocyclopropane-1-carboxylate synthase 3 (ACS3) gene, complete cds
8595	21134	34048	0.95	6.1E-02	BE971853.1	EST_HUMAN	Homo sapiens SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
8595	21134	34049	0.95	6.1E-02	BE971853.1	EST_HUMAN	H. sapiens mRNA for B-HLH DNA binding protein
10508	23142	36153	6.34	6.1E-02	BE179543.1	EST_HUMAN	601851086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
							601851086R1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:3934604 3'
							IL3-HT0618-110500-136-C06 HT0618 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11726	25009		23.38	6.1E-02	X70989.1	NT	S japonicum mRNA for serine-enzyme
12317	24880		1.39	6.1E-02	AI898811.1	EST_HUMAN	U5907 x1 NCL CGAP_Ov35 Homo sapiens cDNA clone IMAGE:2292801 3'
12464	24592		7.98	6.1E-02	AL16207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1305	13899	26419	1.01	6.0E-02	AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2700	15257	27825	1.16	6.0E-02	AW968848.1	EST_HUMAN	EST380924 MAGE resequences, MAGJ Homo sapiens cDNA
2801	15353		1.58	6.0E-02	AB031289.1	NT	Mesocricetus corti mitochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2963	12777	25259	1.09	6.0E-02	AA188730.1	EST_HUMAN	z78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
2963	12777	25260	1.09	6.0E-02	AA188730.1	EST_HUMAN	z78c04.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:626310 5'
3266	18878	28360	1.24	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Codon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3266	15878	28361	1.24	6.0E-02	AA372376.1	EST_HUMAN	EST84266 Codon adenocarcinoma IV Homo sapiens cDNA 5' and similar to tissue-specific protein
3697	18298		1.01	6.0E-02	BE964443.2	EST_HUMAN	601658150R1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3878060 3'
5104	17676	30118	0.95	6.0E-02	Z67739.2	NT	Streptococcus pneumoniae parC, parE and transposase genes and ORF DNA
5595	18225		1.69	6.0E-02	AW370211.1	EST_HUMAN	RC3-BT0253-011199-013-b04 BT0253 Homo sapiens cDNA
6364	18968	31746	1.43	6.0E-02	AI807537.1	EST_HUMAN	w48H05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358873 3' similar to contains L1.1 L1 repetitive element
7063	18082	30438	2.73	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7063	18082	30439	2.73	6.0E-02	5174698	NT	Homo sapiens stimulated trans-acting factor (50 kDa) (STAF50) mRNA
7239	19768	32624	2.17	6.0E-02	BF382349.1	EST_HUMAN	601815274F2 NIH_MGC 56 Homo sapiens cDNA clone IMAGE:4049226 5'
7672	20184	33072	1.94	6.0E-02	AI204275.1	EST_HUMAN	qf58b08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
8361	20901		0.57	6.0E-02	11466495	NT	Recidmonas americana mitochondrion, complete genome
9186	21713	34656	1.12	6.0E-02	AI623187.1	EST_HUMAN	ts78a06.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9186	21713	34657	1.12	6.0E-02	AI623187.1	EST_HUMAN	ts78a06.x1 NCL CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237362 3'
9327	21841	34792	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9327	21841	34793	2	6.0E-02	AJ245365.1	NT	Acipenser baeri partial IGLV gene for immunoglobulin light chain variable region, exons 1-2
9819	22317	35299	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' and similar to heat shock protein 1, 60 kDa-like
9819	22317	35300	0.51	6.0E-02	AA309797.1	EST_HUMAN	EST180654 Jurkat T-cells V Homo sapiens cDNA 5' and similar to heat shock protein 1, 60 kDa-like
11214	23717		2.13	6.0E-02	AA128386.1	EST_HUMAN	zn87c08.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:585166 5' similar to gb:X69181.60S RIBOSOMAL PROTEIN L31 (HUMAN);
11985	24295	30982	1.43	6.0E-02	11431702	NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
12394	24554		8.04	6.0E-02	AI809273.1	EST_HUMAN	wf69h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR-O60298 O60298 KIAA0551 PROTEIN;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
250	12910	25393	4.76	5.9E-02	AW034719.1	EST_HUMAN	RC1-DT0001-290100-012-e10 DT0001 Homo sapiens cDNA
3012	15628	28107	2.75	5.9E-02	AF190289.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4768	17349	29799	0.97	5.9E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4768	17349	29800	0.97	5.9E-02	AL161535.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 35
4852	17430		0.6	5.9E-02	AF168111.1	NT	Duck parvovirus strain 90-2193 capsid protein (VP3) gene, partial cds
4896	17570	30014	0.96	5.9E-02	AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
6973	24774	32374	0.87	5.9E-02	AF145680.1	NT	Drosophila melanogaster LD23107 sting (sting) mRNA, complete cds
8552	21091	34011	1.99	5.9E-02	9055249	NT	Mus musculus Iroquois related homeobox 5 (Drosophila) (Irx5), mRNA
9372	20311		0.82	5.9E-02	BF242748.1	EST_HUMAN	601877609F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105994 5'
10664	23196		3.41	5.9E-02	6678870	NT	Mus musculus follistatin-like (Fst), mRNA
10899	23419	36436	2.35	5.9E-02	11433356	NT	Homo sapiens ninein (LOC51198), mRNA
11429	23890		1.83	5.9E-02	AJ240733.1	NT	Gallus gallus HKC9 telomere junction
968	13579		5.2	5.8E-02	D90110.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
1700	14293	26828	1	5.8E-02	Q61768	SWISSPROT	KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC)
2868	15504		0.98	5.8E-02	AJ223621.1	NT	Populus trichocarpa GCoAOMT1 gene, exon 1 to exon 5
3725	16326	28793	1.35	5.8E-02	AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4446	17032	29473	5.29	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4446	17032	29474	5.29	5.8E-02	AW051927.1	EST_HUMAN	wx24c02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4645	17227	29682	5.04	5.8E-02	AJ247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to
4645	17227	29683	5.04	5.8E-02	AJ247505.1	EST_HUMAN	qh56f01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1848697 3' similar to
4674	17266		1.98	5.8E-02	AF096264.1	NT	gb.M13142 COAGULATION FACTOR XI PRECURSOR (HUMAN);
5294	17856	30282	0.57	5.6E-02	AF275366.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
5294	17856	30283	0.57	5.6E-02	AF275366.1	NT	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
6068	19685	31428	1.52	5.8E-02	AA190994.1	EST_HUMAN	Mus musculus epidermal growth factor receptor (Egfr) gene, exons 5 through 28, and complete cds, alternatively spliced
7670	20182	33069	2.73	5.8E-02	M99150.1	NT	z886t11.s1 Stratagene Hela cell s3 937216 Homo sapiens cDNA clone IMAGE:827068 3'
7670	20182	33070	2.73	5.8E-02	M99150.1	NT	Human polymorphic microsatellite DNA
8601	21140	34054	0.76	5.8E-02	AL163383.2	NT	Human polymorphic microsatellite DNA
11871	24223		2.86	5.8E-02	AF220177.1	NT	Homo sapiens chromosome 21 segment HS21C083
12177	25085		6.45	5.8E-02	AA604269.1	EST_HUMAN	Drosophila melanogaster male fruitless type-A (fru) mRNA, complete cds
							no75e11.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:1112684 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3083	15708	28179	1.13	5.7E-02	A1081644.1	EST_HUMAN	cu63b05.s1 NCL_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WP:C37A2.2
3107	15722	28183	1.8	5.7E-02	AF119117.1	NT	CE08811 ; Homo sapiens dopamine transporter (SLC6A3) gene, complete cds
3769	16370		0.98	5.7E-02	AF001292.1	NT	Chironomus thummi thummi globin VIIA.1 (ctt-9.1), globin II-beta (ctt-2beta), non-
3871	16469	28532	2.44	5.7E-02	AW988791.1	EST_HUMAN	functional globin XIII (ctt-13RT), globin XII (ctt-12) and globin XI (ctt-11) genes, complete cds
4795	17373		1.06	5.7E-02	M95099.1	NT	EST378885 IMAGE resequences, MAGI Homo sapiens cDNA
5334	17895	30310	0.89	5.7E-02	AJ251873.1	NT	Bos taurus lysozyme gene (cow 3), complete cds
6039	18858		0.8	5.7E-02	AF275948.1	NT	Homo sapiens partial stealin-1 gene
8096	20637	33548	1.46	5.7E-02	AJ296090.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
9764	22282	35245	0.65	5.7E-02	6681280	NT	Rattus norvegicus mRNA for potassium channel, alpha subunit (kv9.2 gene)
11087	23579	36617	4.17	5.7E-02	A1752685.1	EST_HUMAN	Mus musculus ect2 oncogene (Ect2), mRNA
11087	23579	36618	4.17	5.7E-02	A1752685.1	EST_HUMAN	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
11227	23768		1.56	5.7E-02	AL163303.2	NT	cn18b09.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn18b09 random
12085	24891		12.96	5.7E-02	D50320.1	NT	Homo sapiens chromosome 21 segment HS21C103
12257	24467		1.71	5.7E-02	AJ271735.1	NT	Pig DNA for SPAL-2, complete cds
12334	24965		3.31	5.7E-02	AF217490.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12483	25074		8.94	5.7E-02	AF261280.1	NT	Homo sapiens fragile 16D oxido reductase (FOR) gene, exons 8, 9, and partial cds
12622	24700	30863	1.58	5.7E-02	R48513.1	EST_HUMAN	Pan troglodytes epilipoprotein-E gene, complete cds
1574	14167	26698	1.2	5.8E-02	AF094455.1	NT	yf64d10.s1 Scores breast 2NbHBst Homo sapiens cDNA clone IMAGE:153523 3' similar to contains L1 repetitive element ;
4746	17327	29769	1.21	5.8E-02	AB013100.1	NT	Hydrocotyle rotundifolia ribosomal protein L16 (rp16) gene, intron; chloroplast gene for chloroplast product
4806	17384	29834	1.2	5.8E-02	AA280589.1	EST_HUMAN	Lycopodium obscurum LE-ACS6 mRNA for 1-aminocyclopropane-1-carboxylate synthase, complete cds
6766	18359	32168	5.98	5.8E-02	AW172708.1	EST_HUMAN	zs45c01.s1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:700418 3'
6971	19548	32372	0.9	5.8E-02	AA866182.1	EST_HUMAN	x02c10.x1 NCL_CGAP_U12 Homo sapiens cDNA clone IMAGE:2856050 3' similar to TR:084978 084979 KIAA0905 PROTEIN ;
7205	19736	32589	3.1	5.8E-02	BE080001.1	EST_HUMAN	cd47f12.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1371119 3' similar to contains Alu repetitive element ; contains element L1 repetitive element ;
8737	21276	34198	2.2	5.8E-02	BE542663.1	EST_HUMAN	QV0-ENQ147-260400-214-q07 BN0147 Homo sapiens cDNA
8737	21276	34199	2.2	5.8E-02	BE542663.1	EST_HUMAN	601087158F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453279 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9726	22224	35201	1.07	5.8E-02	AA482864.1	EST_HUMAN	n49d07.s1 NCI CGAP_A1V1 Homo sapiens cDNA clone IMAGE:923245 similar to TR:G769859 G769859
11439	23889		2.33	5.8E-02	AF260225.1	NT	LAMINA ASSOCIATED POLYPEPTIDE 1C.:
2679	15237	27804	6.14	5.8E-02	X97899.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
3251	15863	28345	3.83	5.8E-02	675550.1	NT	H. sapiens gene encoding La autantigen
4296	16882	29328	1.12	5.9E-02	L41591.1	NT	Mus musculus SH3 domain protein 1B (Sh3d1B), mRNA
5840	18464	31188	3.19	5.8E-02	Q01174	SWISSPROT	Gallid herpesvirus mRNA fragment
6176	18464	31188	3.86	5.8E-02	Q01174	SWISSPROT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
7412	19937	32802	1.77	5.8E-02	675590.2	NT	TROPOMYOSIN ALPHA CHAIN, NON MUSCLE
8063	20605	33516	0.77	5.9E-02	AF170911.1	NT	Mus musculus tufalin 1 (Tuf1), mRNA
8063	20605	33517	0.77	5.8E-02	AF170911.1	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9573	22073	35034	0.91	5.8E-02	10947034	NT	Homo sapiens sodium-dependent vitamin C transporter 1 (SVCT1) mRNA, complete cds
9573	22073	35035	0.61	5.8E-02	10947034	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
9664	22163	35136	1.28	5.8E-02	U89492.1	NT	Homo sapiens eIF4E-transporter (4E-T), mRNA
10598	23418	36435	11.52	5.5E-02	U09771.1	NT	Mus musculus second L11 receptor alpha chain (L11Ra2) gene, exons 1 and 2
3054	15670		0.95	5.4E-02	AJ277488.1	NT	Citrobacter freundii DSM 30040 cyclopropane fatty acid synthase (cfa) gene, partial cds, dihydroxyacetone kinase (dhak), glycerol dehydrogenase (dhaD), transcriptional activator (dhaR), 1,3-propanediol dehydrogenase (dhaT), glycerol dehydratase (dhaB), >
3469	18013		6.27	5.4E-02	BE073468.1	EST_HUMAN	Oryza sativa rbb3-1 gene for putative Bowman Birk trypsin inhibitor
3982	16580	28051	0.58	5.4E-02	U85808.1	NT	RC6-BT0559-140200-012-003 BT0559 Homo sapiens cDNA
5119	17691	30129	2.48	5.4E-02	U53528.1	NT	Hirudo medicinalis SNAP-25 homolog mRNA, complete cds
8067	20609		1.11	5.4E-02	Z99116.1	NT	Xenopus laevis homeobox protein (Vox-1) mRNA, complete cds
9001	21538	34467	0.61	5.4E-02	AF260225.1	NT	Bacillus subtilis complete genome (section 13 of 21): from 2395261 to 2613730
10578	23113	36126	1.88	5.4E-02	U20780.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
11058	23570	36808	1.56	5.4E-02	BF371289.1	EST_HUMAN	Neurospora crassa ubiquinol-cytochrome c oxidoreductase subunit VIII (QCR8) mRNA, complete cds
11058	23570	36807	1.56	5.4E-02	BF371289.1	EST_HUMAN	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
11968	24882		2.9	5.4E-02	U44894.1	NT	RC6-FN0112-190700-021-D06 FN0112 Homo sapiens cDNA
1091	13696	26205	1.58	5.3E-02	AW391248.1	EST_HUMAN	Rana catesbeiana heat shock protein 30 (HSP30) mRNA, complete cds
1091	13696	26206	1.58	5.3E-02	AW391248.1	EST_HUMAN	QV0-ST0213-021299-062-409 ST0213 Homo sapiens cDNA
1553	14145	26679	21.63	5.3E-02	T84759.1	EST_HUMAN	QV0-ST0213-021299-062-409 ST0213 Homo sapiens cDNA
2541	15105	27677	2.71	5.3E-02	AJ276408.1	NT	ye3712.1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:119951 5' similar to gb.K01506
2969	15585	28066	0.88	5.3E-02	M58417.1	NT	HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP(1) ALPHA CHAIN (HUMAN); Pseudomonas putida tfgS gene
						NT	Drosophila melanogaster laminin B2 gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2969	15585	28067	0.88	5.3E-02	M58417.1	NT	Drosophila melanogaster laminin B2 gene, complete cds
3187	15799	28271	4.52	5.3E-02	AJ276408.1	NT	Pseudomonas putida tfgS gene
5248	17811	30284	0.75	5.3E-02	AB051897.1	NT	Mus musculus Scya6, Scya8, Scya18-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scya16 pseudogene, small inducible cytokine A5 precursor, complete cds
5250	17813	30236	8.25	5.3E-02	M80463.1	NT	Mus musculus caudal type homeobox-1 (Cdx-1) gene, complete cds
5522	18154	30568	1.87	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
5522	18154	30569	1.97	5.3E-02	AE000527.1	NT	Helicobacter pylori 26695 section 5 of 134 of the complete genome
6251	18890	31632	0.71	5.3E-02	M85289.1	NT	Human heparan sulfate proteoglycan (HSPG2) mRNA, complete cds
6954	19541	32363	4.23	5.3E-02	9695413	NT	Lymphocystis disease virus 1, complete genome
7149	19682	32523	1.55	5.3E-02	U32882.1	NT	Haemophilus influenzae Rd section 147 of 163 of the complete genome
7396	19921	33189	2.05	5.3E-02	S78221.1	NT	nuclear protein TIF1 isoform [mouse, mRNA, 4053 nt]
7818	20290	33189	0.52	5.3E-02	P38742	SWISSPROT	HYPOTHEICAL 130.0 KD PROTEIN IN SNF6-SPO11 INTERGENIC REGION
8344	20865	34521	0.54	5.3E-02	U10098.1	NT	Mus musculus 129/Sv cystatin C (cst3) gene, complete cds
9053	21590	34521	1.83	5.3E-02	X03127.1	NT	Podospora anserina mitochondrial epsilon-sen DNA
10038	22533	35529	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10038	22533	35530	0.54	5.3E-02	AB022605.1	NT	Homo sapiens hCMT1b mRNA for mRNA (guanine-7-methyltransferase, complete cds)
10158	22851		0.62	5.3E-02	Y07907.1	NT	D. rerio mRNA for zc-23 POU gene, splice variant (neurula, 9-16 hpf and postsomitogenesis, 20-28 hpf)
10235	22730	35721	0.65	5.3E-02	X68432.1	NT	B. rerio pou3f mRNA for transcription factor
2324	14895		110.52	5.2E-02	5031908	NT	Homo sapiens meprin A, alpha (PABA peptide hydrolase) (MEP1A) mRNA
3148	15762	28228	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
3148	15762	28229	2.4	5.2E-02	AJ277661.1	NT	Homo sapiens partial LMO1 gene for LIM domain only 1 protein, exon 1
4013	16611	28084	0.7	5.2E-02	AF236101.1	NT	Arabidopsis thaliana putative dicarboxylate diiron protein (Crd1) mRNA, complete cds
4365	16952	28392	3.61	5.2E-02	U07132.1	NT	Human steroid hormone receptor Nco-1 mRNA, complete cds
4846	17424	29877	1.28	5.2E-02	L33246.1	NT	Drosophila melanogaster filament protein homolog (sepi) gene, complete cds
6076	18693	31439	0.89	5.2E-02	U14731.1	NT	Saccharomyces cerevisiae Cdc54p (CDC54) gene, complete cds
6255	18864		1.42	5.2E-02	A1830985.1	EST_HUMAN	w80504.x1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2409150 3' similar to contains MER15.b1
7318	19845	32706	1.19	5.2E-02	P36322	SWISSPROT	DNA POLYMERASE PROCESSIVITY FACTOR (POLYMERASE ACCESSORY PROTEIN) (PAP) (DNA-BINDING GENE 18 PROTEIN)
8136	20677		1.98	5.2E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9845	22145	35113	1.97	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds
9845	22145	35114	1.97	5.2E-02	D10927.1	NT	Turnip mosaic virus genomic RNA for Capsid protein, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12224	24445		1.84	5.2E-02	Q03030	SWISSPROT	OXALOACETATE DECARBOXYLASE ALPHA CHAIN
12327	24513		1.27	5.2E-02	D63382.1	NT	Mouse DNA for regII gamma protein, complete cds
2402	14970		1.14	5.1E-02	AL134071.1	EST_HUMAN	DKFZp547D073_1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D073 5'
4282	16868	26315	0.73	5.1E-02	AF001301.1	NT	Chlamydia trachomatis section 28 of 87 of the complete genome
4908	17493	28941	8.03	5.1E-02	AF085167.1	NT	Hardcore vulgaris receptor-like kinase ARK1AS gene, partial cds
5205	17770	30193	1.14	5.1E-02	BE957423.2	EST_HUMAN	601653565R2 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838361 3'
6777	19369	32182	0.76	5.1E-02	AF280369.1	NT	HIV-1 patient 96 from Italy protease (pol) gene, complete cds
6942	18050	30472	1.6	5.1E-02	BF378625.1	EST_HUMAN	QVO-UM0051-250800-350-508 UM0051 Homo sapiens cDNA
8195	20736	33646	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8195	20736	33647	0.82	5.1E-02	M26434.1	NT	Human hypoxanthine phosphoribosyltransferase (HPRT) gene, complete cds
8288	20829	33750	1.48	5.1E-02	AJ131968.1	NT	Spodoptera littoralis mRNA for 3-dehydrodysone 3beta-reductase
8818	21357	34282	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14)
8818	21357	34282	0.63	5.1E-02	P02533	SWISSPROT	KERATIN, TYPE I CYTOSKELETAL 14 (CYTOKERATIN 14) (K14) (OK 14)
9723	22221	35196	8.16	5.1E-02	AF012898.1	NT	Candida albicans protein phosphatase Ssd1 homolog (SSD1) gene, complete cds
10084	22579	35572	1.83	5.1E-02	P40603	SWISSPROT	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
10709	23237	36251	2.86	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
10709	23237	36250	2.86	5.1E-02	AF083930.1	NT	Homo sapiens ES18 mRNA, partial cds
12232	24448		1.51	5.1E-02	AF062467.1	NT	Cucumis melo polygalacturonase precursor (MPG3) mRNA, complete cds
508	13141	25626	1.76	5.0E-02	AF098004.1	NT	Mus musculus fatty acid amide hydrolase gene, exon 10
1246	13843	26360	6.63	5.0E-02	Z69104.1	NT	Bacillus subtilis complete genome (section 1 of 21); from 1 to 213080
2034	14616	27182	3.63	5.0E-02	P02810	SWISSPROT	4) (PIF-FPIF-S) (PROTEIN APROTEIN C) [CONTAINS: PEPTIDE P-C]
2045	13634	28150	1.78	5.0E-02	U72742.1	NT	Oryctolagus cuniculus UDP-glucuronosyltransferase (UGT2B13) mRNA, complete cds
3381	15990		1.42	5.0E-02	7305910	NT	Mus musculus Unc-51 like kinase 2 (C. elegans) (ULK2), mRNA
3655	16258		1.06	5.0E-02	U32782.1	NT	Haemophilus influenzae Rd section 97 of 163 of the complete genome
3747	16348	28816	5.6	5.0E-02	U12769.2	NT	Antheraea pernyi period clock protein homolog mRNA, complete cds
5102	17674	30114	1.11	5.0E-02	AF188530.1	NT	Homo sapiens ubiquitous tetrairicopeptide containing protein RoXan mRNA, partial cds
6279	18887	31656	0.74	5.0E-02	AF096264.1	NT	Gallus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds
6450	19051		1.23	5.0E-02	AJ242625.1	NT	Mus musculus Dmp-1 gene, exons 1-6
7544	20064	32938	10.74	5.0E-02	P35616	SWISSPROT	NEUROFILAMENT TRIPLET L PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NF-L)
10101	22696	35589	1.13	5.0E-02	AF305238.1	NT	Mus musculus Fas-interacting serine/threonine kinase 3 (Fist3) mRNA, complete cds
11384	23816	36877	2.87	5.0E-02	U67600.1	NT	Methanococcus jannaschii section 142 of 150 of the complete genome
11736	24924		7.22	5.0E-02	G04047	SWISSPROT	NO-ON-TRANSIENT A PROTEIN
242	12901		23.23	4.9E-02	M14230.1	NT	Chicken 28-kDa vitamin D-dependent calcium-binding protein (CaBP-28) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
392	13038	25528	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
392	13038	25529	3.62	4.9E-02	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
3328	15938	28414	1.58	4.9E-02	P54258	SWISSPROT	ATROPHIN-1 (DENTATORUBRAL-PALLIDOLYSIAN ATROPHY PROTEIN)
3628	16231		0.63	4.9E-02	AA189940.1	EST_HUMAN	z448a12.s1 Stralagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632926 3' similar to
3651	16254	28726	0.91	4.9E-02	AA400914.1	EST_HUMAN	contains Alu repetitive element/contains element MSR1 repetitive element ;
3651	16254	28727	0.91	4.9E-02	AA400914.1	EST_HUMAN	z448a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4966	17540	29982	1.59	4.9E-02	AW167821.1	EST_HUMAN	z448a12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728428 3'
4966	17540	29983	1.59	4.9E-02	AW167821.1	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5372	17931	30345	0.61	4.9E-02	7662616	EST_HUMAN	xg56g10.x1 NCL CGAP_U14 Homo sapiens cDNA clone IMAGE:2632386 3'
5408	17984		0.91	4.9E-02	AF135416.1	NT	Homo sapiens PRO1848 protein (PRO1848), mRNA
5425	17982		0.98	4.9E-02	AE001774.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
						NT	Thermotoga maritima section 86 of 136 of the complete genome
5437	17992	30398	1.03	4.9E-02	M94063.1	NT	Brucella ovis heat shock protein hsp70 (dnaK) gene, complete cds; heat shock protein hsp40 (dnaJ) gene, complete cds
5573	18204	30654	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
5573	18204	30655	1.95	4.9E-02	L00122.1	NT	Rat elastase II gene, exon 6
7196	18727	32578	0.99	4.9E-02	AE000980.1	NT	Archaeoglobus fulgidus section 127 of 172 of the complete genome
8551	21090		0.88	4.9E-02	AL161559.2	NT	Chlamydia muridarum, section 40 of 85 of the complete genome
8689	21228	34149	0.7	4.9E-02	AL161559.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
10183	22688	35681	0.54	4.9E-02	P19532	SWISSPROT	TRANSCRIPTION FACTOR E3
11280	23733	36788	3.67	4.9E-02	AF008303.1	NT	Homo sapiens prepro placental TGF-beta gene, complete cds
12148	24391		1.44	4.9E-02	8923880	NT	Homo sapiens CS box-containing WD protein (LOC55884), mRNA
12431	24573		2.92	4.9E-02	M19364.1	NT	Human gamma-B-crystallin (gamma 1-2) and gamma-C-crystallin (gamma 2-1) genes, complete cds
352	13002	25487	1.15	4.8E-02	D18471.1	NT	Human mRNA, Xq terminal portion
353	13002	25487	1.87	4.8E-02	D18471.1	NT	Human mRNA, Xq terminal portion
514	13147	25631	9.43	4.8E-02	AF003100.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.7 mRNA, partial cds
2312	14884	27459	1.96	4.8E-02	W51983.1	EST_HUMAN	z448a12.s1 Soares_sarcomer fibroblasts_NHHSF Homo sapiens cDNA clone IMAGE:325611 3' similar to
3244	15856	28339	2.34	4.8E-02	X17144.1	NT	gb:M30998 LUPUS KU AUTOANTIGEN PROTEIN P86 (HUMAN);
4778	17359		1.32	4.8E-02	Z54280.1	NT	Tetrahymena rostrata histone H3II and histone H4II intergenic DNA
6309	17871	30293	0.87	4.8E-02	U91914.1	NT	S. scrofa gene for skeletal muscle ryanodine receptor
5380	17939	30352	4.1	4.8E-02	AF199339.1	NT	Streptococcus constellatus D-alanine:D-alanine ligase gene, partial cds
5380	17939	30353	4.1	4.8E-02	AF199339.1	NT	Homo sapiens lens epithelium-derived growth factor gene, alternatively spliced, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8080	20622	33535	1.42	4.8E-02	AW388487.1	EST_HUMAN	MR2-ST0129-221089-012-b02 ST0129 Homo sapiens cDNA
9057	21594	34524	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
9057	21594	34525	1.3	4.8E-02	AJ001398.1	NT	Fugu rubripes rps24 gene
12018	24315		1.93	4.8E-02	9632893	NT	Streptococcus thermophilus bacteriophage Sf19, complete genome
6918	19577	32406	2.98	4.7E-02	W01153.1	EST_HUMAN	yz9709.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:281017 5' similar to contains Alu repetitive element
6965	19542	32384	0.78	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
6965	19542	32365	0.78	4.7E-02	BF68625.1	EST_HUMAN	602143554F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4304772 5'
6998	19496	32317	1.57	4.7E-02	M62752.1	NT	Rat statin-related protein (s1) gene, complete CDS
8193	20734	33644	8.55	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
8883	21421	34346	1.12	4.7E-02	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
8906	21444		2.29	4.7E-02	AB029678.1	NT	Gallus gallus Wpkci-8 gene, complete cds
9154	21689	34633	6.91	4.7E-02	X15543.1	NT	B. taurus mRNA for RF-36-DNA-binding protein
9565	22065	35024	0.55	4.7E-02	BF305237.1	EST_HUMAN	601892892F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4138414 5'
9650	22149		0.55	4.7E-02	A1873042.1	EST_HUMAN	we79c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347314 3'
10634	23166	36177	1.55	4.7E-02	6754565	NT	Mus musculus ligand of numb-protein X (Lnx), mRNA
11430	23881	36945	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11430	23881	36946	1.69	4.7E-02	U73621.1	NT	Bos taurus paired box protein (pax-6) gene, partial cds
11951	25087		6.94	4.7E-02	AV648521.1	EST_HUMAN	AV648521 GLC Homo sapiens cDNA clone GLCBK02 3'
12322	25089		1.47	4.7E-02	P52951	SWISSPROT	HOMEOBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEOBOX PROTEIN 2)
282	12948	25435	0.81	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
769	13388	25887	2.44	4.6E-02	AE000445.1	NT	Escherichia coli K-12 MG1685 section 335 of 400 of the complete genome
1335	13929		1.37	4.6E-02	A1014255.1	EST_HUMAN	am50d02.s1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1538979 3' similar to TR:P90533
1403	13996	26525	9	4.6E-02	AV727059.1	EST_HUMAN	P90533 LIMA :contains element L TR1 repetitive element ;
2530	15094	27066	2.77	4.6E-02	AW236023.1	EST_HUMAN	AV727059 HTG Homo sapiens cDNA clone HTCBWC01 5'
2834	12048	25435	1.83	4.6E-02	BE153583.1	EST_HUMAN	hm2403.x1 NCLCGAP_Kid11 Homo sapiens cDNA clone IMAGE:2694853 3' similar to SW:GRF1_HUMAN
3042	15658	28138	0.7	4.6E-02	BE153583.1	EST_HUMAN	Q12849 G-RICH SEQUENCE FACTOR-1 ;
3543	15658	28138	0.95	4.6E-02	BE153583.1	EST_HUMAN	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
4201	16780		0.97	4.6E-02	AF220365.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
5909	18531	31256	1.44	4.6E-02	AF076962.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
6377	18981	31760	3.77	4.6E-02	XG1624.1	NT	PM0-HT0339-251199-003-g05 HT0339 Homo sapiens cDNA
							Mus musculus nuclear RNA helicase I/Gu (ddx21) gene, complete cds
							Haplochromis burtoni gonadotropin-releasing hormone and GnRH-associated peptide precursor (GnRH2) gene, complete cds
							C.reinhardtii atp2 (atpB) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6377	18981	31761	3.77	4.8E-02	X61624.1	NT	C.reinhardtii alp2 (alpB) mRNA
6891	18925	32481	1.39	4.8E-02	A1149574.1	EST_HUMAN	qc60b08.x1 Soares_placenta_8to9weeks_2NblHP8ta9W Homo sapiens cDNA clone IMAGE:1713971 3'
8590	21129	34046	2.82	4.8E-02	BE154006.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element;
11281	23734	36789	4.26	4.8E-02	AA913328.1	EST_HUMAN	PMO-HT0339-090400-009-G12 HT0339 Homo sapiens cDNA
12541	24651		2.54	4.8E-02	X57808.1	NT	cd27h09.s1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1524737 3'
472	13105	25598	2.71	4.8E-02	P22448	SWISSPROT	Human germine immunoglobulin lambda light chain gene
1260	13857	26373	0.78	4.8E-02	AF005730.1	NT	RETINOIC ACID RECEPTOR BETA (RAR-BETA)
1260	13857	26374	0.78	4.8E-02	AF005730.1	NT	Marburg virus strain M/S.Africa/Johannesburg/1975/Oxalin VP35 gene, complete cds
1840	14428	26980	3.54	4.8E-02	P32182	SWISSPROT	Marburg virus strain M/S.Africa/Johannesburg/1975/Oxalin VP35 gene, complete cds
2156	14733	27308	3.65	4.8E-02	AE003964.1	NT	HEPATOCYTE NUCLEAR FACTOR 3-BETA (HNF-3B)
3786	16386	28652	3.84	4.8E-02	AL163276.2	NT	Xylella fastidiosa, section 110 of 228 of the complete genome
6378	18982	31762	1.68	4.8E-02	AJ400877.1	NT	Homo sapiens chromosome 21 segment HS21C078
6631	19227	32032	0.89	4.8E-02	AL163280.2	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8332	20873	33785	1.8	4.8E-02	AF036684.1	NT	Homo sapiens chromosome 21 segment HS21C080
9680	22357	35337	5.91	4.8E-02	AA325216.1	EST_HUMAN	Arabidopsis thaliana CCAAT-box binding factor HAP3 homolog gene, complete cds
10117	22612	35602	0.77	4.8E-02	AB000470.1	NT	EST28187 Cerebellum II Homo sapiens cDNA 5' end similar to neuro-D4 protein
11947	24276	31018	2.92	4.8E-02	11418013	NT	Gallus gallus mRNA for alpha1 integrin, complete cds
12367	24973	30636	6.27	4.8E-02	AA191097.1	EST_HUMAN	Homo sapiens ref finger protein-like 3 (RFPL3), mRNA
237	12897		3.08	4.8E-02	BE972733.1	EST_HUMAN	Zg4311.1 Strabagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632493 5'
2144	14722		6.8	4.8E-02	P31568	SWISSPROT	601652154F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935388 5'
2532	15098	27668	2.82	4.8E-02	AW875475.1	EST_HUMAN	HYPOTHETICAL PROTEIN (ORF 2280)
3702	16303	28771	1.5	4.8E-02	AF159160.1	NT	QV2-PT0012-010300-070-g02 PT0012 Homo sapiens cDNA
4733	17314	29756	1.23	4.4E-02	AF109907.1	NT	Mycoplasma xanthus serine/threonine kinase Pkn10 (pkn10) gene, complete cds
4733	17314	29757	1.23	4.4E-02	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32551	1.56	4.4E-02	AF095824.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
7172	19704	32552	1.56	4.4E-02	AF095824.1	NT	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
8687	21226	34146	2.04	4.4E-02	AA736969.1	EST_HUMAN	Canis familiaris matrix metalloproteinase 9 (MMP-9) mRNA, partial cds
10951	23466	36489	4.58	4.4E-02	AF060869.1	NT	nm13003.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1239221 3'
11080	23592	36628	2.63	4.4E-02	AA496739.1	EST_HUMAN	Hepatitis E virus strain HEV-US2 polyprotein (ORF1), (ORF3), and capsid protein (ORF2) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11664	24088		3.26	4.4E-02	AB040926.1	NT	Homo sapiens mRNA for KIAA1493 protein, partial cds
813	13431	25936	8.91	4.3E-02	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
2603	15185	27732	1.16	4.3E-02	AV704878.1	EST_HUMAN	AV704878 ADB Homo sapiens cDNA clone ADBA0408 5'
3477	16083	28557	8.12	4.3E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3720	16321		1.12	4.3E-02	AF060583.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
6822	19219	32023	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6822	19219	32024	5.71	4.3E-02	P30427	SWISSPROT	PLECTIN
6830	19420	32236	0.68	4.3E-02	AA652268.1	EST_HUMAN	ns69c12 s1 NCL CGAP_P12 Homo sapiens cDNA clone IMAGE:1188986
8450	20960	33908	0.74	4.3E-02	AF283359.1	NT	Homo sapiens desmocollin 3 (DSC3) gene, complete cds, alternatively spliced
8736	21275	34198	0.98	4.3E-02	AF283322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
8736	21275	34197	0.98	4.3E-02	X55322.1	NT	H. sapiens NCAM mRNA for neural cell adhesion molecule
855	13471	25982	1.57	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
899	13513		2.24	4.2E-02	AU123327.1	EST_HUMAN	AU123327 NT2RM2 Homo sapiens cDNA clone NT2RM2000020 5'
929	13542	28060	0.89	4.2E-02	AW003845.1	EST_HUMAN	wk34g01.x1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:2545584 3' similar to TR:Q63291 Q63291
1758	14348		1.32	4.2E-02	AL445066.1	NT	L1 REI TROPOSON, ORF2 MRNA ; contains L1 L3 L1 L1 repetitive element ; Thermoplasma acidophilum complete genome; segment 4/5
3180	15902	28274	0.88	4.2E-02	AI493472.1	EST_HUMAN	q195f10.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2019787 3' similar to gb:M35718
3726	16327	28784	1.36	4.2E-02	P23091	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR BFR-2 PRECURSOR (HUMAN); TRANSFORMING PROTEIN MAF
4410	16995	28437	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4410	16995	28438	1.03	4.2E-02	U26674.1	NT	Saccharomyces cerevisiae general sporulation (GSG1) gene, complete cds
4854	17432	29883	0.68	4.2E-02	BF342965.1	EST_HUMAN	602017105FT NCL CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4152672 5'
5802	18427	31145	1.49	4.2E-02	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5802	18427	31146	1.49	4.2E-02	AF280107.1	NT	4 (CYP3A4) and cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7534	20054	32927	5.29	4.2E-02	AF276752.1	NT	Legionella pneumophila catalase-peroxidase (katA) gene, complete cds
8745	21284	34206	3.5	4.2E-02	P05095	SWISSPROT	ALPHA-ACTININ 3, NON MUSCULAR (F-ACTIN CROSS LINKING PROTEIN)
10068	22564	35559	1.17	4.2E-02	Q16650	SWISSPROT	T-BRAIN-1 PROTEIN (T-BOX BRAIN PROTEIN 1) (TBR-1) (TES-56)
10919	23438	36459	3.12	4.2E-02	AA976118.1	EST_HUMAN	gn33b11.at NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558461 3' similar to gb:M65290
11187	23692	36739	2.3	4.2E-02	BE815822.1	EST_HUMAN	INTERLEUKIN-12 BETA CHAIN PRECURSOR (HUMAN); PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11187	23692	38740	2.3	4.2E-02	BE815822.1	EST_HUMAN	PM3-BN0174-250500-009-d10 BN0174 Homo sapiens cDNA
11379	23831	38894	2.06	4.2E-02	AF179498.1	NT	PRRS isolate PRRSV36 envelope glycoprotein gene, complete cds
12226	25023		3.4	4.2E-02	A1983494.1	EST_HUMAN	w49g10.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2510850 3'
536	13167	25648	0.7	4.1E-02	AF200628.1	NT	Homo sapiens HPS1 gene, intron 5
2701	15258	27826	2.87	4.1E-02	AE002330.2	NT	Chlamydia muridarum, section 60 of 65 of the complete genome
4571	17154		8.95	4.1E-02	AW893484.1	EST_HUMAN	QV1-NN0012-180400-184-R66 NN0012 Homo sapiens cDNA
5295	17857		0.69	4.1E-02	X85880.1	NT	L.monocytogenes type 3 partial lap gene (strain 443)
5824	18448	31170	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
5824	18448	31171	0.98	4.1E-02	BE251894.1	EST_HUMAN	601107535F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343856 5'
6962	19539		0.97	4.1E-02	X75881.1	NT	A.thaliana mRNA for plasma membrane intrinsic protein 1a
7156	19688	32532	1.92	4.1E-02	AE002132.1	NT	Ureaplasma urealyticum section 33 of 59 of the complete genome
7522	20042	32811	1.76	4.1E-02	7662347	NT	Homo sapiens KIAA0867 protein (KIAA0867), mRNA
							Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1) gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds; and calcium channel alpha-1 subunit>
7742	20250	33143	3.14	4.1E-02	AF026188.1	NT	CUTICLE COLLAGEN 34
8577	21116	34036	0.56	4.1E-02	P34687	SWISSPROT	EST84291 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
8081	21617	34552	0.85	4.1E-02	AA372398.1	EST_HUMAN	Brassica napus gln gene for plastid glutamine synthetase, exons 1-12
12572	25024	30618	24.9	4.1E-02	AJ271909.1	NT	Homo sapiens mRNA for KIAA1471 protein, partial cds
3281	18892	28371	3.71	4.0E-02	AB040904.1	NT	Human retinoblastoma susceptibility gene exons 1-27, complete cds
3868	18466	28929	0.98	4.0E-02	L11970.1	NT	Homo sapiens PTS gene for 6-pyruvoyltetrahydropterin synthase, complete cds
5296	17858	30284	0.58	4.0E-02	AB042297.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
5581	18212	30661	5.51	4.0E-02	AF280107.1	NT	7n52h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3568380 3' similar to TR:O75296 O75298
6362	18966	31744	1.66	4.0E-02	BF110434.1	EST_HUMAN	R29124_1.; Strongylocentrotus purpuratus homolog of human bone morphogenetic protein 1 (submp) mRNA, complete cds
7678	20189	33078	5.8	4.0E-02	L23888.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33144	0.87	4.0E-02	AB000381.1	NT	Homo sapiens DNA for GPI-anchored molecule-like protein, complete cds
7743	20251	33145	0.87	4.0E-02	AB000381.1	NT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
8651	21180	34108	2.94	4.0E-02	P08640	SWISSPROT	GLUCOHYDROLASE
9562	22062		0.84	4.0E-02	BF679376.1	EST_HUMAN	602153884F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294724 5'
9586	22086	35051	3.35	4.0E-02	AJ000941.1	NT	Methanobacterium thermoautotrophicum strain Marburg, Thioflavin reductase subunit A

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9895	22392		1.28	4.0E-02	D43949.1	NT	Human mRNA for KIAA0082 gene, partial cds
11608	24051		1.82	4.0E-02	AJ001018.1	NT	Kluyveromyces fragilis gene for Ca++ ATPase
11841	24834	30796	18.69	4.0E-02	AJ001056.1	NT	Ovis aries mRNA for acetyl-coA carboxylase
1159	13762	26273	3.8	3.9E-02	BF516149.1	EST_HUMAN	UI-HBW-1-ant-h-08-0-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084134 3'
1390	13984	26510	1.88	3.9E-02	P41047	SWISSPROT	FAS ANTIGEN LIGAND
2004	14586	27145	2.67	3.9E-02	AJ403386.1	NT	Minimusculus DNA for desmin-binding fragment DesD7
2728	15283		1.85	3.9E-02	4506862	NT	Homo sapiens succinate dehydrogenase complex, subunit C, integral membrane protein, 15kD (SDHC) mRNA
5325	17887	30303	0.6	3.9E-02	AW392417.1	EST_HUMAN	RC8-ST0258-171199-021-C09 ST0258 Homo sapiens cDNA
5344	17905	30320	1.14	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5344	17905	30321	1.14	3.9E-02	8924019	NT	Homo sapiens hypothetical protein PRO1163 (PRO1163), mRNA
5687	18313	30810	0.73	3.9E-02	D50608.1	NT	Rat gene for cholecystikinin type-A receptor (CCKAR), complete cds
5687	18313	30811	0.73	3.9E-02	D50608.1	NT	Rat gene for cholecystikinin type-A receptor (CCKAR), complete cds
5806	18528	31254	1.24	3.9E-02	BE968841.1	EST_HUMAN	601649874F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933642 5'
6018	18637	31377	0.68	3.9E-02	BF675203.1	EST_HUMAN	602138132F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274910 5'
7118	19458	32273	1.01	3.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7781	20324	33229	0.93	3.9E-02	BF239613.1	EST_HUMAN	601906848F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4134779 5'
8004	20546	33449	0.56	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
8004	20546	33450	0.56	3.9E-02	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11287	20289	33188	1.6	3.9E-02	P48778	SWISSPROT	ANTIGEN GOR
11691	24981		7.19	3.9E-02	AB042553.1	NT	Felis catus G-CSF gene for granulocyte colony-stimulating factor, complete cds
12373	24543		1.73	3.9E-02	U68061.1	NT	Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV19S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBJ1S1, TCRBJ1S2>
12503	24902		64.84	3.9E-02	AL049866.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, nmox28orf
1995	14577	27137	1.24	3.9E-02	BE885137.1	EST_HUMAN	601510891F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912215 5'
4897	17571	30015	0.99	3.9E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
4997	17571	30016	0.99	3.9E-02	BE393275.1	EST_HUMAN	601308488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626757 5'
5062	17635	30078	0.93	3.9E-02	AU124122.1	EST_HUMAN	AU124122 NT2RM2 Homo sapiens cDNA clone NT2RM2001698 5'
5632	18261	30733	1.07	3.9E-02	M11228.1	NT	Human protein C gene, complete cds
6237	18846	31617	1.07	3.9E-02	P10284	SWISSPROT	HOMEOBOX PROTEIN HOX-B4 (HOX-2.6)
7359	19885	32748	1.43	3.9E-02	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA

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8598	21137		1.3	3.8E-02	M60675.1	NT	Human von Willebrand factor gene, exons 23 through 34
10508	23000		0.47	3.8E-02	AE001329.1	NT	Chlamydia trachomatis section 56 of 87 of the complete genome
10532	23069	36082	2.17	3.8E-02	AF143952.2	NT	Homo sapiens PELOTA (PELOTA) gene, complete cds
1029	13639	26154	3.69	3.7E-02	P18137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
1432	14025	26553	1.15	3.7E-02	L14591.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
2278	14852	27430	4.49	3.7E-02	A184806.1	EST_HUMAN	w85c08.s1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494502 3'
2613	15175	27743	0.93	3.7E-02	AB018261.1	NT	Homo sapiens mRNA for KIAA0718 protein, partial cds
3086	15701	28174	0.97	3.7E-02	P79944	SWISSPROT	EOMESODERMIN
3088	15703	28175	4.74	3.7E-02	BF312963.1	EST_HUMAN	601896233F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125584 5'
7138	25118		0.73	3.7E-02	AP000083.1	NT	Aeropyrum pernix genomic DNA, section 617
8828	22424		0.89	3.7E-02	AA782516.1	EST_HUMAN	ai55c09.s1 Soares parathyroid tumor_Nb-HPA Homo sapiens cDNA clone 1360912 3'
11735	24139	37156	7.89	3.7E-02	BF124974.1	EST_HUMAN	601762117F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4024973 5'
12435	24866	30707	3.02	3.7E-02	11418392	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1 (SLC22A1), mRNA
3715	16316	28784	0.82	3.8E-02	X73221.1	NT	H. vulgare Sst1 gene for sucrose synthase
3723	16324	28791	0.87	3.8E-02	AL068806.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 10[10q26.3] of Homo sapiens
5620	18249	30701	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
5620	18249	30717	0.77	3.6E-02	X59403.1	NT	C. glutamicum gap, pgk and tpi genes for glyceraldehyde-3-phosphate, phosphoglycerate kinase and triosephosphate isomerase
6808	19399	32213	5.32	3.6E-02	AW945516.1	EST_HUMAN	GM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
6808	19399	32214	5.32	3.6E-02	AW945516.1	EST_HUMAN	GM2-EN0013-110500-192-b10 EN0013 Homo sapiens cDNA
7143	19676	32516	1.88	3.6E-02	AF025952.1	NT	Chromatium thiosulfatophilum sulfur globule protein Cy2 precursor (sgp2) gene, complete cds
7347	19873	32739	3.52	3.6E-02	AA714521.1	EST_HUMAN	rw20e05.s1 NCI CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241024 3' similar to gb:J00314_rna2
7629	20141	33020	0.86	3.6E-02	BE143078.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
9313	21827	34776	1.87	3.6E-02	U20608.1	NT	MRO-H1T0158-030200-003-b08 HT0158 Homo sapiens cDNA
9313	21827	34777	1.87	3.6E-02	U20608.1	NT	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
9530	22030	34989	0.72	3.6E-02	BF37586.1	EST_HUMAN	Dictyostelium discoideum unknown spore germination-specific protein-like protein, orf1, orf2 and orf3 genes, complete cds
928	13541	26059	1.57	3.5E-02	U09506.1	NT	Drosophila melanogaster tigrin mRNA, complete cds
1046	13654	26166	2.29	3.5E-02	AF263417.1	NT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds

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1610	14203	26736	1.49	3.5E-02	BF676085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
1610	14203	26737	1.49	3.5E-02	BF676085.1	EST_HUMAN	602085136F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249377 5'
4293	16879	29326	1.91	3.5E-02	AE001773.1	NT	Thermidoga maritima section 85 of 136 of the complete genome
4406	16891	29435	1.16	3.5E-02	P53780	SWISSPROT	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE)
6370	18974	31752	2.11	3.5E-02	J01238.1	NT	Maize actin 1 gene (MAct1), complete cds
7918	20460		0.82	3.5E-02	H29951.1	EST_HUMAN	y44405.f1 Soares retina N265HR Homo sapiens cDNA clone IMAGE:190256 5' similar to contains Alu repetitive element;
8558	21097	34018	3.5	3.5E-02	BE958970.1	EST_HUMAN	60164701R2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3928737 3'
9931	22427	35401	2.44	3.5E-02	X76642.1	NT	Lactis MG1363 grpE and dnaK genes
9977	22472	35455	0.49	3.5E-02	BE861042.1	EST_HUMAN	601344681F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677654 5'
11367	23819	36880	1.92	3.5E-02	AW861041.1	EST_HUMAN	PM1-CT0326-291299-002-h03 CT0326 Homo sapiens cDNA
11387	23819	36881	1.92	3.5E-02	AW861041.1	EST_HUMAN	Homo sapiens T cell receptor beta locus, TCRBV8SP to TCRBV21S2A2 region
12357	24534		1.39	3.5E-02	AF009663.1	NT	601178765F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3543833 5'
12429	24913		4.38	3.5E-02	BE276948.1	EST_HUMAN	Homo sapiens mRNA for FLJ00013 protein, partial cds
604	13233	25706	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
604	13233	25707	1.18	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
605	13233	25707	3.27	3.4E-02	AK024424.1	NT	Homo sapiens mRNA for FLJ00013 protein, partial cds
1089	13694	26203	3.22	3.4E-02	AW274020.1	EST_HUMAN	xv28d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814253 3' similar to SW:0211_HUMAN P53801 PUTATIVE SURFACE GLYCOPROTEIN C21ORF1 PRECURSOR ;
1248	13845		6.54	3.4E-02	11345459	NT	Homo sapiens hypothetical protein FLJ13220 (FLJ13220), mRNA
2435	15002	27574	1.92	3.4E-02	T57160.1	EST_HUMAN	yc20a06.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81250 5' similar to contains MER29 repetitive element
3478	16084	28558	1.11	3.4E-02	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
3943	16442	28503	0.88	3.4E-02	BE839514.1	EST_HUMAN	RC3-FN0155-060700-011-d10 FN0155 Homo sapiens cDNA
3963	16991	29063	4.29	3.4E-02	AW794952.1	EST_HUMAN	RC8-UM0015-210200-021-A10 UM0015 Homo sapiens cDNA
4703	17285	29730	3.17	3.4E-02	X59799.1	NT	M.musculus S-antigen gene promoter region
5217	17782		2.61	3.4E-02	Q26457	SWISSPROT	LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)
5237	17801	30220	1.47	3.4E-02	AJ012469.1	NT	Caenorhabditis elegans mRNA for DYS-1 protein, partial
6353	18958		0.88	3.4E-02	BF131628.1	EST_HUMAN	601820445F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052434 5'
6938	18046	30468	4.63	3.4E-02	U24393.1	NT	Human lysyl oxidase-like protein gene, exon 3
8204	20745		3.76	3.4E-02	AI866629.1	EST_HUMAN	wf69404.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2433031 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8682	21221	34141	1.64	3.4E-02	AA684888.1	EST_HUMAN	nu70708.s1 NCL_CGAP_Alv1 Homo sapiens cDNA clone IMAGE:1216071 similar to contains Alu repetitive element/contains element MER25 MER25 repetitive element:
8848	21387						zq04f11.s1 Strabagene muscle 937209 Homo sapiens cDNA clone IMAGE:628749 3' similar to TR:G1017425 G1017425
9693	22192		5.71	3.4E-02	AA194306.1	EST_HUMAN	IPISGKPLPKVTLSDRGVPLKATMRFNTEITAENL TINLKESVTADAGRYEITAANSSGTTKAFINIVLDRPG
395	13041		0.53	3.4E-02	A102719.1	EST_HUMAN	PPT GPVVISDITEESVTLKWEPPKDGSGVNTYLLKRETSATVTSATVARTMMKVMKL ...
1209	13809	26322	11.74	3.3E-02	AA398735.1	EST_HUMAN	oz89h08.x1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1683519 3'
1681	14273	26806	18.12	3.3E-02	AB035667.1	NT	z75e08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728198 3'
1775	14365		1.28	3.3E-02	AF110763.1	NT	Oricellulus griseus CYP2A17 mRNA for cytochrome P450 2A17, complete cds
2131	14709		1.28	3.3E-02	AE007700.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3406	16015	28404	2.05	3.3E-02	R09112.1	EST_HUMAN	Aquifex acidicus section 32 of 109 of the complete genome
4256	14273	26806	0.85	3.3E-02	H02389.1	EST_HUMAN	y25c08.r1 Soares_fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:127888 5'
4566	17149	29598	2.91	3.3E-02	AF110763.1	NT	y35h02.r1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:150771 5'
6561	19159	31956	2.15	3.3E-02	6755862	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
6561	19159	31957	26.84	3.3E-02	BF245995.1	EST_HUMAN	Mus musculus tumor rejection antigen gp98 (Tra1), mRNA
9246	21772	34721	26.84	3.3E-02	BF245995.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9246	21772	34722	0.73	3.3E-02	BF115621.1	EST_HUMAN	601853910F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073787 5'
9345	21859	34807	0.73	3.3E-02	BF115621.1	EST_HUMAN	7m92d04.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
9345	21859	34808	0.59	3.3E-02	AA488202.1	EST_HUMAN	7m92d04.x1 NCL_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:3562423 3'
10491	22985		0.59	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
11000	23514	36548	0.59	3.3E-02	AA488202.1	EST_HUMAN	ad08f09.s1 Soares_NbHFB Homo sapiens cDNA clone IMAGE:877673 3' similar to gb:X70944_cds1
11932	24266		0.5	3.3E-02	H38109.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
12089	24358		3.5	3.3E-02	BF691107.1	EST_HUMAN	MYOBLAST CELL SURFACE ANTIGEN 24.1D5 (HUMAN);
137	12802	25291	2.14	3.3E-02	T96545.1	EST_HUMAN	yp51f11.s1 Soares_refina N2b4HR Homo sapiens cDNA clone IMAGE:190989 3'
1165	13767	26277	2.05	3.3E-02	M81890.1	NT	602247171F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332497 5'
1165	13767	26277	1.87	3.2E-02	AJ002005.1	NT	yp49f11.1 Soares_fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:121101 5'
1808	14398	26943	19.04	3.2E-02	AF096275.1	NT	Human Interleukin 11 (IL11) gene, complete mRNA
2164	14741		19.04	3.2E-02	AF096275.1	NT	Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
2865	12802	25291	1.36	3.2E-02	AF128894.1	NT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
3168	15782	28253	1.35	3.2E-02	P28955	SWISSPROT	Drosophila melanogaster heat shock protein 68 (hsp68) gene, hsp68d allele, complete cds
			0.59	3.2E-02	AJ002005.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
			12.01	3.2E-02	BE867353.1	EST_HUMAN	LARGE TEGUMENT PROTEIN
							Oryctolagus cuniculus gene encoding ileal sodium-dependent bile acid transporter
							601442431F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846727 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3776	16376	28842	1.3	3.2E-02	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4299	16885		20.05	3.2E-02	X94788.1	NT	H. sapiens RP3 gene (XLRP gene 3)
4882	17457	29909	3.35	3.2E-02	AF114182.1	NT	Saxifraga nidifica maturase (matK) gene, chloroplast gene encoding chloroplast protein, partial cds
5726	18352	31055	1.45	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
5726	18352	31058	1.45	3.2E-02	X68709.1	NT	S. griseocarneum whiG-Stv gene
6646	19242	32045	2.59	3.2E-02	M32437.1	NT	Rat/polyomavirus left junction in cell line W98.14
6647	19243		27.51	3.2E-02	T89367.1	EST_HUMAN	y433h12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:110087 3' similar to contains
6722	19316	32119	3.78	3.2E-02	AF173845.1	NT	Alu repetitive element; contains LTR1 repetitive element;
7739	20247	33140	0.85	3.2E-02	11424049	NT	Seguinus oedipus tissue kallikrein gene, complete cds
8242	20783	33702	13.06	3.2E-02	6680565	NT	Homo sapiens cytochrome P450, subfamily 1B (phenobarbital-inducible) (CYP2B), mRNA
8871	21410		0.69	3.2E-02	AF109718.1	NT	Mus musculus kinesin family member 3c (Kif3c), mRNA
9152	21687	34630	1.06	3.2E-02	A1278971.1	EST_HUMAN	Homo sapiens chromosome 3 subtelomeric region
9152	21687	34631	1.06	3.2E-02	A1278971.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
9969	22464		4.05	3.2E-02	AA719795.1	EST_HUMAN	qm17b04.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1882063 3'
10260	22755	35743	0.95	3.2E-02	U98762.1	NT	zq54b12.s1 Soares pineal gland_N3HPG Homo sapiens cDNA clone IMAGE:397151 3' similar to
1303	13897		1.8	3.1E-02	4503418	NT	gb108441 CYTOCHROME C OXIDASE POLYPEPTIDE III (HUMAN);
1348	13943	26466	1.26	3.1E-02	P18845	SWISSPROT	Macaca mulatta chemokine receptor CCR5 mRNA, complete cds
1936	14520	27078	1.52	3.1E-02	6871564	NT	Homo sapiens dual specificity phosphatase 4 (DUSP4) mRNA
2017	14599		1.14	3.1E-02	Z50097.1	NT	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-3 CHAIN PRECURSOR (GF-ALPHA-3)
5207	17772		0.87	3.1E-02	BE091869.1	EST_HUMAN	Mus musculus adaptor-related protein complex AP-3, delta subunit (Ap3d), mRNA
5331	17892		3.09	3.1E-02	AL161550.2	NT	Drosophila melanogaster mRNA for headcase protein
5371	16916		0.86	3.1E-02	AU119006.1	EST_HUMAN	IL2-BT0733-130400-067-A06 BT0733 Homo sapiens cDNA
5468	18102	30421	1.13	3.1E-02	AU119006.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5963	18194		2.32	3.1E-02	AA278478.1	EST_HUMAN	AU119006 HEMBA1 Homo sapiens cDNA clone HEMBA1004842 5'
5829	18453	31176	0.8	3.1E-02	BF687742.1	EST_HUMAN	Human leukemia inhibitory factor receptor (LIFR) gene, promoter and partial exon 1
9944	22439	35417	3.63	3.1E-02	AF034779.1	NT	zs81a06.t1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703858 5'
12667	24737		2.24	3.1E-02	AW468414.1	EST_HUMAN	602068783F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4065789 5'
1664	14257		2.3	3.0E-02	AF187125.1	NT	Enterococcus faecalis surface protein precursor, gene, complete cds
2621	15183	27749	0.9	3.0E-02	AA402242.1	EST_HUMAN	he3767.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2921221 3'
3623	16226	28704	1.24	3.0E-02	MB94176.1	NT	Ptykites minus cytochrome oxidase I gene, partial cds; mitochondrial gene for mitochondrial product
							z65f03.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727263 5'
							Saccharomyces cerevisiae stem-loop mutation suppressor SSL2 gene, complete cds

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3714	16315	28763	3.07	3.0E-02	AF247844.1	NT	Pseudomonas fluorescens family II aminotransferase gene, complete cds
3808	16407		0.79	3.0E-02	AW820223.1	EST_HUMAN	QV2-ST0296-150200-040-e09 ST0296 Homo sapiens cDNA
4021	16619		0.74	3.0E-02	AA364003.1	EST_HUMAN	EST74530 Pineal gland II Homo sapiens cDNA 5' end
5000	17573	30017	1.04	3.0E-02	BE782830.1	EST_HUMAN	601472331F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3875603 5'
5208	17773	30195	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5208	17773	30196	7.49	3.0E-02	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
5303	17865	30289	1.1	3.0E-02	BE689917.1	EST_HUMAN	601649872R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933928 3'
5590	18221		3.62	3.0E-02	AB046793.1	NT	Homo sapiens mRNA for KIAA1573 protein, partial cds
6402	19005	31784	0.76	3.0E-02	N99615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ;
6402	19005	31785	0.76	3.0E-02	N99615.1	EST_HUMAN	za39a10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:294906 5' similar to contains element TAR1 repetitive element ;
6884	19619	32453	2.93	3.0E-02	AJ242906.1	NT	Cyprinus carpio mRNA for inducible nitric oxide synthase (iNOS) gene
6987	19485	32306	3.15	3.0E-02	BE889848.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
6987	19485	32307	3.15	3.0E-02	BE889848.1	EST_HUMAN	601512206F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913848 5'
7131	19471	32290	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7131	19471	32291	1.93	3.0E-02	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
7282	19810	32666	1.32	3.0E-02	M86524.1	NT	Human dystrophin gene
7583	20098		0.76	3.0E-02	BF246361.1	EST_HUMAN	601854981F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4074548 5'
8575	21114	34033	0.79	3.0E-02	BF353889.1	EST_HUMAN	IL5-HT0704-290800-108-c04 HT0704 Homo sapiens cDNA
8728	21287		1.77	3.0E-02	AF275654.1	NT	Ornithorhynchus anatinus coagulation factor X mRNA, complete cds
10357	22851	35845	1.46	3.0E-02	AE001787.1	NT	Thermotoga maritima section 109 of 136 of the complete genome
10441	22935	35944	0.46	3.0E-02	Z21211.1	EST_HUMAN	HSAADITHS TEST1, Human adult Testis tissue Homo sapiens cDNA clone cam test244 (b)
11111	23621	36662	4.11	3.0E-02	M81357.1	NT	Human coagulation factor VII (F7) gene exon 1 and factor X (F10) gene, exon 1
11538	23986	37057	8.47	3.0E-02	AA483216.1	EST_HUMAN	ne87f04.s1 NCI_CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911263
12043	25076	30515	2.56	3.0E-02	R32019.1	EST_HUMAN	yn63d04.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:134407 3'
12417	24670		18.42	3.0E-02	AW895565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
12460	25089		3.53	3.0E-02	AF048687.1	NT	Rattus norvegicus UDP-Gal-glucosyltransferase beta-1.4-galactosyltransferase mRNA, complete cds
2479	15467	27614	1.05	2.9E-02	AF228703.1	NT	Homo sapiens mitochondrial glutathione reductase and cytosolic glutathione reductase (GRD1) gene, complete cds, alternatively spliced
3021	15637	28114	1.11	2.9E-02	BE565944.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680895 5'

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3021	15637	28115	1.11	2.9E-02	BE585644.1	EST_HUMAN	601338428F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680695 5'
3616	16219	28698	0.64	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
4003	16601	29075	0.69	2.9E-02	H72805.1	EST_HUMAN	y07e10.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:233130 5'
5272	18016		62.36	2.9E-02	R09112.1	EST_HUMAN	y25c09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127888 5'
6213	18823	31594	1.31	2.9E-02	AF060221.1	NT	Sus scrofa deoxyribonuclease II mRNA, complete cds
6434	19037	31824	6.5	2.9E-02	BF032233.1	EST_HUMAN	601452861F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3856598 5'
7298	19824	32683	10.37	2.9E-02	BE271437.1	EST_HUMAN	601140729F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049830 5'
7455	19979	32845	0.67	2.9E-02	D29214.1	EST_HUMAN	HUMNK262 Human epidermal keratinocyte Homo sapiens cDNA clone 262
7940	20482	33393	0.91	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
7940	20482	33394	0.91	2.9E-02	AF129279.1	NT	Buchnera aphidicola natural-host Schlechtendalia chinensis gluconate-6-phosphate dehydrogenase (gnd) gene, partial cds
9577	22077	35040	2.16	2.9E-02	AW875979.1	EST_HUMAN	GM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9577	22077	35041	2.18	2.9E-02	AW875979.1	EST_HUMAN	GM3-PT0014-071299-051-c04 PT0014 Homo sapiens cDNA
9788	22286		0.59	2.9E-02	AW976597.1	EST_HUMAN	EST388706 MAGE resequences, MAGN Homo sapiens cDNA
10247	22742	35732	0.94	2.9E-02	AP000064.1	NT	Aeropyrum pernix genomic DNA, section 7/7
10925	16219	28698	1.73	2.9E-02	X55294.1	NT	Sheep gene for ultra high-sulphur keratin protein
12045	24979		1.88	2.9E-02	AU135817.1	EST_HUMAN	AU135817 PLACE1 Homo sapiens cDNA clone PLACE1002862 5'
591	13221		0.99	2.9E-02	AW970153.1	EST_HUMAN	EST382234 MAGE resequences, MAGK Homo sapiens cDNA
3414	16022	28502	1.62	2.9E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
3414	16022	28503	1.62	2.9E-02	AF066063.1	NT	Homo sapiens retinal fascic (FSCN2) gene, exon 2
4401	16986		0.71	2.9E-02	8393751	NT	Rattus norvegicus microtubule-associated protein tau (Mapt), mRNA
5337	17898	30313	0.92	2.9E-02	N87073.1	EST_HUMAN	L2083F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone L2083 5' similar to tRNA-GUANINE TRANSGLYCOSYLASE
5679	18306	30802	11.28	2.9E-02	BE741083.1	EST_HUMAN	601594078F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948087 5'
6900	19634	32472	1.14	2.9E-02	T78960.1	EST_HUMAN	y421508.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109855 5'
8270	20811	33732	1.6	2.9E-02	AJ005820.1	NT	Craterostigma plantagineum mRNA for homeodomain leucine zipper protein (hb-1)
8947	21485	34407	0.74	2.9E-02	AA280762.1	EST_HUMAN	zs96c08.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711468 5'
9135	21670	34612	0.91	2.9E-02	AF187872.1	NT	Cavia porcellus inwardly-rectifying potassium channel Kir2.1 (KCNJ2) gene, complete cds
9237	21763	34709	0.64	2.9E-02	AE001092.1	NT	Archaeoglobus fulgidus section 15 of 172 of the complete genome
10498	22992	36002	1.81	2.9E-02	BF527244.1	EST_HUMAN	602039477F2 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:417267 5'
3479	16085	28559	4.18	2.7E-02	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
4280	16966	29312	1.91	2.7E-02	N47258.1	EST_HUMAN	y966h12.r1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'
4280	16966	29313	1.91	2.7E-02	N47258.1	EST_HUMAN	y966h12.r1 Soares_multiple_sclerosis_2NBHMSP Homo sapiens cDNA clone IMAGE:280487 5'

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5633	19262	30734	1.11	2.7E-02	R12245.1	EST_HUMAN	yf33d09.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:128657 5' similar to
6061	18878	31420	0.7	2.7E-02	X61670.1	NT	SP:JC2264 JC2264 TISSUE FACTOR PATHWAY INHIBITOR - RHESUS ;
6713	19307		0.9	2.7E-02	X97580.1	NT	T.aestivum p1TH20 mRNA for wheat type V thionin
7127	19467	32285	2.06	2.7E-02	AA993571.1	EST_HUMAN	A.bisporus ptkA gene
8295	20836		1.21	2.7E-02	AI377036.1	EST_HUMAN	ab09h03.s1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1624661 3'
597	13228	25700	1.52	2.8E-02	AL163282.2	NT	tc28q08.x1 Soares total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:2065982 3' similar to
2404	14972	27544	2.78	2.8E-02	AA490021.1	EST_HUMAN	contains Alu repetitive element
2406	14974	27546	7.33	2.8E-02	6754241	NT	Homo sapiens chromosome 21 segment HS21C082
2406	14974	27547	7.33	2.8E-02	6754241	NT	ab02b02.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839595 3'
2840	15556		1.17	2.8E-02	AF109806.1	NT	Mus musculus histidine rich calcium binding protein (Hrc), mRNA
5031	17605	30049	4.74	2.8E-02	L12032.1	NT	Mus musculus MHC class III region RD gene, partial cds; Bf C2 G9A, NG22, G9, HSP70, HSP70, HSC70,
5224	17789	30208	1.58	2.8E-02	AE002014.1	NT	and smRNP genes, complete cds; G7A gene, partial cds, and unknown genes
5254	17817	30241	2.34	2.8E-02	AW241154.1	EST_HUMAN	Chicken dorsalis-1 mRNA, complete cds
6368	18972		6.32	2.8E-02	AI209030.1	EST_HUMAN	Deinococcus radiodurans R1 section 151 of 228 of the complete chromosome 1
6556	19154	31950	2.29	2.8E-02	BE621748.1	EST_HUMAN	xa52b04.x1 NCI CGAP_Sar4 Homo sapiens cDNA clone IMAGE:2570383 3' similar to SW:Y069_HUMAN
6915	19374	32402	0.75	2.8E-02	Z99064.1	NT	Q15041 HYPOTHETICAL PROTEIN KIAA0089
6915	19574	32403	0.75	2.8E-02	Z99064.1	NT	q927f11.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1762317 3'
6990	19488	32310	8.45	2.8E-02	AA860946.1	EST_HUMAN	601493473T1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895578 3'
8442	20982	33897	0.77	2.8E-02	AA860946.1	EST_HUMAN	Vaccinia virus ORF1L, strain Wyeth
9282	21882	34827	1.41	2.8E-02	11432020	NT	Vaccinia virus ORF1L, strain Wyeth
9630	22130	35094	0.6	2.8E-02	AF114952.1	NT	Rattus norvegicus Nerve growth factor receptor, fast (Ngfr), mRNA
9630	22130	35095	0.6	2.8E-02	AF114952.1	NT	ak22f04.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1406719 3'
10302	22796	35787	4.1	2.8E-02	AL163303.2	NT	Homo sapiens KIAA1070 protein (KIAA1070), mRNA
11265	23783		2.44	2.8E-02	AA279861.1	EST_HUMAN	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
11437	23887	36955	1.63	2.8E-02	AW500547.1	EST_HUMAN	encoding mitochondrial protein, complete cds
11965	25060	30512	1.26	2.8E-02	BF343827.1	EST_HUMAN	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene
12083	24354		1.26	2.8E-02	11422938	NT	encoding mitochondrial protein, complete cds
557	13188	25666	1.76	2.5E-02	AI783130.1	EST_HUMAN	Saccharomyces dairenensis NRRL Y-12639(T) ATP synthase subunit 9 (ATP9) gene, mitochondrial gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
557	13188	25687	1.76	2.5E-02	AI703130.1	EST_HUMAN	on26f08.v5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1557827 5'
842	13458	25967	19.68	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
902	13516	26034	4.46	2.5E-02	BE974314.1	EST_HUMAN	601680305R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950865 3'
2791	15344		2.84	2.5E-02	U12571.1	NT	Rattus norvegicus rabphilin-3A mRNA, complete cds
2983	15599	28078	3.52	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
2983	15599	28079	3.52	2.5E-02	X99697.1	NT	H. carterae mRNA for fucoxanthin chlorophyll a/c binding protein, Fcp1
4119	18005	29167	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4119	18005	29168	0.77	2.5E-02	BE701165.1	EST_HUMAN	PM2-NN0128-080700-001-a12 NN0128 Homo sapiens cDNA
4284	18870	29318	5.25	2.5E-02	AW592114.1	EST_HUMAN	h36h08.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2934015 3'
5889	18512	31238	0.7	2.5E-02	AI732776.1	EST_HUMAN	z683c10.x5 Soares ovary tumor NBHOT Homo sapiens cDNA clone IMAGE:810354 3'
6340	18946		4.9	2.5E-02	BE970128.1	EST_HUMAN	7a30a09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284008 3' similar to contains L1.1 L1
6357	18961		4.3	2.5E-02	BE746888.1	EST_HUMAN	repetitive element 1
6478	19079	31862	0.72	2.5E-02	L29029.1	NT	601578393F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928054 5'
7660	20172	33058	1.52	2.5E-02	BF626722.1	EST_HUMAN	Chlamydomonas reinhardtii VSP-3 mRNA, complete cds
7660	20172	33059	1.52	2.5E-02	BF626722.1	EST_HUMAN	602070562F1 NCI_CGAP_Brt64 Homo sapiens cDNA clone IMAGE:4213406 5'
7920	20462	33068	0.48	2.5E-02	BE252469.1	EST_HUMAN	602070562F1 NCI_CGAP_Brt64 Homo sapiens cDNA clone IMAGE:4213406 5'
8759	21298	34219	0.93	2.5E-02	Q91713	SWISSPROT	601108291F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3344278 5'
8894	21432	34355	0.45	2.5E-02	AW025821.1	EST_HUMAN	CHORDIN PRECURSOR (ORGANIZER-SPECIFIC SECRETED DORSALIZING FACTOR)
8978	22473		0.6	2.5E-02	X71303.1	NT	wu08c10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2516370 3'
10475	22969	35978	0.73	2.5E-02	AI147615.1	EST_HUMAN	D.radicum 28S ribosomal RNA, D2 domain
10889	23219	36231	2.04	2.5E-02	Q10335	SWISSPROT	qb22a08.x1 Soares_pregnant_uterus_NbrHPU Homo sapiens cDNA clone IMAGE:1696982 3'
10889	23219	36232	2.04	2.5E-02	Q10335	SWISSPROT	HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							HYPOTHETICAL 46.7 KD PROTEIN C19G10.05 IN CHROMOSOME I
							Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds;
10761	23285		4.04	2.5E-02	AF050157.1	NT	butyrophilin-like (NG9), butyrophilin-lp
11602	24045		1.73	2.5E-02	AB007546.1	NT	Homo sapiens gene for LECT2, complete cds
11922	24993		3.33	2.5E-02	11420078	NT	Homo sapiens similar to ALEX3 protein (H. sapiens) (LOC63634), mRNA
12115	24955		1.53	2.5E-02	11433220	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
12215	24438		2.17	2.5E-02	U60169.1	NT	Homo sapiens putative protein kinase MkaA (mkaA) gene, complete cds
12242	24454	30957	1.31	2.5E-02	BE973327.1	EST_HUMAN	Dicotyledon discoidium putative protein kinase MkaA (mkaA) gene, complete cds
185	12846	25332	0.75	2.4E-02	AI378592.1	EST_HUMAN	601652365R2 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3935513 3'
1842	14234	26768	2.09	2.4E-02	H65884.1	EST_HUMAN	tc72c07.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2070156 3'
2088	15457	27239	2.02	2.4E-02	P01901	SWISSPROT	y7511.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211149 5'
							H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2088	15457	27240	2.02	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4458	17044	28487	1.89	2.4E-02	J05110.1	NT	T. thermophila calcium-binding 25 kDa (TCBP 25) protein mRNA, complete cds
4619	17202	28650	1.63	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
4619	17202	28651	1.63	2.4E-02	P01901	SWISSPROT	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B ALPHA CHAIN PRECURSOR (H-2K(B))
6363	18967	31745	0.94	2.4E-02	W86680.1	EST_HUMAN	zh63h04.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416791 3'
7273	19801	32658	1.06	2.4E-02	Z20573.1	EST_HUMAN	HSAALOKVXT, Human adult Rhabdomyosarcoma cell-line Homo sapiens cDNA
7287	19815	32672	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7287	19815	32673	0.95	2.4E-02	X12925.1	NT	Rat gene for uncoupling protein (UCP)
7831	20373	32673	0.69	2.4E-02	AW813007.1	EST_HUMAN	RC3-ST0186-230300-019-h06 ST0186 Homo sapiens cDNA
7884	20426		0.6	2.4E-02	M18780.1	NT	Human retrotransposon 3' long terminal repeat
8379	20919		0.86	2.4E-02	H78376.1	EST_HUMAN	WJ12c05.s1 Soares_fetal_liver_spleen_INFLS Homo sapiens cDNA clone IMAGE:233576 3' similar to contains
8468	21008	33925	10.74	2.4E-02	N69442.1	EST_HUMAN	Alu repetitive element; contains A3R repetitive element;
8917	21455	34375	0.54	2.4E-02	AE001125.1	NT	gb K02909 RATSR7K Rat (RNA); contains A3R.b1 A3R repetitive element;
							Borrelia burgdorferi (section 11 of 70) of the complete genome
8939	21477	34398	0.75	2.4E-02	AA625680.1	EST_HUMAN	zu91c06.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745354 3' similar to gb:J04422 ISLET
9720	22218	35193	2.76	2.4E-02	AV692954.1	EST_HUMAN	AMYLOID POLYPEPTIDE PRECURSOR (HUMAN); contains Alu repetitive element; contains element XTR
9891	22388	35366	2.9	2.4E-02	AA493894.1	EST_HUMAN	AV692954 GKC Homo sapiens cDNA clone GKCDSC03 5'
							rh07b12.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943583 similar to contains Alu repetitive element; contains element PTRS repetitive element;
11447	23897	36962	1.9	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
11447	23897	36963	1.9	2.4E-02	AF109905.1	NT	Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds; smRNP, G7A, NG23, MuS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds, and unknown genes
11718	24127		3.56	2.4E-02	9627909	NT	Bacteriophage bIL87, complete genome
11868	24222	31044	2.48	2.4E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
11924	24259	31013	1.36	2.4E-02	BE926889.1	EST_HUMAN	MRO-FT0175-310800-202-a06 FT0175 Homo sapiens cDNA
11984	24294	30981	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
11984	24294	31025	1.38	2.4E-02	U78167.1	NT	Rattus norvegicus cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12164	24404		8.87	2.4E-02	AB008569.1	NT	Caenorhabditis elegans mRNA for iron-sulfur subunit of mitochondrial succinate dehydrogenase, complete cds
12191	24422		2.11	2.4E-02	N42980.1	EST_HUMAN	Y03a08.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:270810 5'
12197	24425		1.55	2.4E-02	BF679477.1	EST_HUMAN	602153281F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294173 5'
12362	24827	30795	1.48	2.4E-02	AA179693.1	EST_HUMAN	zp13h01.r1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609361 5'
1913	14498		5.46	2.3E-02	W05340.1	EST_HUMAN	z884g08.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299294 5'
1931	14515		21.68	2.3E-02	U94165.1	NT	4 Homo sapiens mammary tumor-associated protein INT6 (INT6) gene, exon 4
2053	14634	27205	0.96	2.3E-02	AW797355.1	EST_HUMAN	CM2-UM0038-290400-172-b11 UM0038 Homo sapiens cDNA
2389	14957	27529	2.31	2.3E-02	Z74293.1	NT	S.oerevisiae chromosome IV reading frame ORF YDL245c
3745	16346	28814	6.21	2.3E-02	Z20377.1	EST_HUMAN	H5AAGACADH P. Human foetal Brain Whale tissue Homo sapiens cDNA
3777	16377		0.82	2.3E-02	L23429.1	NT	Canis beta-galactosides-binding lectin (LGALS3) mRNA, 3'end
4230	16818	29266	0.75	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4230	16818	29267	0.75	2.3E-02	L24799.1	NT	Gallus gallus connexin 45.6 (Cx45.6) gene, complete cds
4511	17095	29542	1.21	2.3E-02	AW899107.1	EST_HUMAN	CM4-NN0080-290400-160-b04 NN0080 Homo sapiens cDNA
4546	17130	29574	0.91	2.3E-02	BE93225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4546	17130	29575	0.91	2.3E-02	BE93225.1	EST_HUMAN	CM3-MT0118-010900-318-g07 MT0118 Homo sapiens cDNA
4547	18006	29576	1.05	2.3E-02	AW563693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4547	18006	29577	1.05	2.3E-02	AW563693.1	EST_HUMAN	xs25d08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2770871 3'
4698	17280	29726	2.96	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
4698	17280	29727	2.96	2.3E-02	BF026487.1	EST_HUMAN	601672279F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955386 5'
5182	17748	30177	0.93	2.3E-02	AW844307.1	EST_HUMAN	RC2-CN0051-280100-011-a07 CN0051 Homo sapiens cDNA
5368	17928	30342	2.72	2.3E-02	A1038076.1	EST_HUMAN	ox21c10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656978 3' similar to gb:X69908_ma1 ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (HUMAN);
5578	18209	30659	3.34	2.3E-02	U86303.1	NT	Caulobacter crescentus topoisomerase IV ParE subunit (parE) gene, complete cds, and propionyl-CoA carboxylase beta chain (pcdB) homolog gene, partial cds
6733	19327	32132	4.43	2.3E-02	AL161505.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 17
7056	18075	30428	0.88	2.3E-02	BE141475.1	EST_HUMAN	MR0-HIT0080-011099-002-c08 HT0080 Homo sapiens cDNA
7817	20360	33266	6	2.3E-02	U63910.1	NT	Human plectin (PLECT) gene, exons 3-32, and complete cds
8407	20947	33867	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8407	20947	33868	0.74	2.3E-02	AJ298105.1	NT	Homo sapiens PDX1 gene for lipoyl-containing component X, exons 1-11
8630	21169	34085	0.83	2.3E-02	A1885380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
8630	21169	34086	0.83	2.3E-02	A1885380.1	EST_HUMAN	wa78h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302147 3'
9085	21602	34532	0.81	2.3E-02	P41898	SWISSPROT	HYPOPHETICAL 55.6 KD PROTEIN B0280.5 IN CHROMOSOME III PRECURSOR
9773	22271	35256	0.72	2.3E-02	P50532	SWISSPROT	CHROMOSOME ASSEMBLY PROTEIN XCAP-C

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9843	22438	35415	1.4	2.3E-02	AE000199.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
9843	22438	35416	1.4	2.3E-02	AE000198.1	NT	Escherichia coli K-12 MG1655 section 89 of 400 of the complete genome
10661	23183	36208	2.37	2.3E-02	P08640	SWISSPROT	GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)
11628	24070		1.67	2.3E-02	AF159132.1	NT	Melanococcus ensis fushi larazu-factor 1 mRNA, complete cds
11846	24843		5.2	2.3E-02	BE278331.1	EST_HUMAN	601178958F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3546587 5'
12282	24485	30840	1.59	2.3E-02	BF528482.1	EST_HUMAN	602043829F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12282	24485	30941	1.59	2.3E-02	BF528482.1	EST_HUMAN	602043829F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4181454 5'
12392	24552	30907	2.2	2.3E-02	U39394.1	NT	Streptomyces sp. alpha-1,3/4-fucosidase precursor gene, complete cds
12447	25100		3.04	2.3E-02	U11077.1	NT	Dictyostellium discoideum extracellular signal-regulated protein kinase (ERK1) mRNA, complete cds
12660	24940		1.73	2.3E-02	11426388	NT	Homo sapiens dead ringer (Drosophila)-like 1 (DRIL1), mRNA
767	13386	25885	3	2.2E-02	AF018287.1	NT	Columbia liva nucleoside diphosphate kinase (NDPK) gene, nuclear gene encoding mitochondrial protein, complete cds
1783	14373		1.03	2.2E-02	4557448	NT	Homo sapiens chromodomain helicase DNA binding protein 2 (CHD2) mRNA
2059	14639	27212	1.33	2.2E-02	Z82001.1	NT	S. pneumoniae pcpA gene and open reading frames
3482	16088		2.1	2.2E-02	AA577785.1	EST_HUMAN	nm24a04.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084782 3'
3708	16309		3.58	2.2E-02	AF083094.1	NT	Infectious bursal disease virus segment B strain IL4 VP1 gene, complete cds
3920	16518	28684	1.11	2.2E-02	AW601317.1	EST_HUMAN	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
3992	16590	29062	0.85	2.2E-02	Z74283.1	NT	PMO-BT0340-170100-004-b03 BT0340 Homo sapiens cDNA
5225	17780	30209	0.92	2.2E-02	Z73597.1	NT	S. cerevisiae chromosome IV reading frame ORF YDL245c
7294	19822	32681	3.52	2.2E-02	AV699721.1	EST_HUMAN	S. cerevisiae chromosome XVI reading frame ORF YPL241c
8312	20853	33778	2.58	2.2E-02	AL161515.2	NT	AV699721 GKB Homo sapiens cDNA clone GKBAND03 3'
8312	20853	33779	2.56	2.2E-02	AL161515.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
8744	21283	34205	0.75	2.2E-02	X79468.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 27
9574	22074	35036	0.57	2.2E-02	AJ243025.1	NT	P. vulgaris alpha tub 2 mRNA
9574	22074	35037	0.57	2.2E-02	AJ243025.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9804	22104	35066	1.88	2.2E-02	AB026898.1	NT	Mus musculus partial FBPase 2 gene for Fructose-1,6-bisphosphatase, exon 5 and intron 5
9804	22104	35067	1.88	2.2E-02	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10106	22601		0.86	2.2E-02	6678140	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12120	24379		3.95	2.2E-02	AA503553.1	EST_HUMAN	Mus musculus Sjogren syndrome antigen A1 (Ssa1), mRNA ne47n07.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:900541 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
444	13077		4.45	2.1E-02	AV781502.1	EST_HUMAN	AV781502 MDS Homo sapiens cDNA clone MDSADG01 5'
474	13107		5.21	2.1E-02	AF029728.1	NT	Dicystotellum discoideum histidine kinase C (dhkC) mRNA, complete cds
1308	13900	26420	8.15	2.1E-02	U72073.1	NT	Bacillus subtilis cotKLM cluster, CotK (cotK), CdtL (cotL), and spore coat protein CotM (cotM) genes, complete cds
1430	14022	26550	1.46	2.1E-02	AF204396.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
1430	14022	26551	1.46	2.1E-02	AF204396.1	NT	Mus musculus macrophage migration inhibitory factor (MIF) gene, 5' flanking region and partial cds
2842	13429	25934	3.37	2.1E-02	N28286.1	EST_HUMAN	y43h07.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:264541 5'
3184	14660	27231	0.83	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3184	14660	27232	0.83	2.1E-02	BE072546.1	EST_HUMAN	PM2-BT0546-120100-001-f11 BT0546 Homo sapiens cDNA
3643	18248	28721	1.47	2.1E-02	AA461271.1	EST_HUMAN	z63b09.r1 Soares total fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786121 5'
4211	18800	29249	0.77	2.1E-02	Z74283.1	NT	S cerevisiae chromosome IV reading frame ORF YDL245c
4398	18983	29428	0.83	2.1E-02	BF343655.1	EST_HUMAN	602015308F1 NCL CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4151161 5'
4540	17124	29569	1.64	2.1E-02	U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, erpC and erpD genes, complete cds; and unknown genes
4552	17135	29583	1.3	2.1E-02	A1768127.1	EST_HUMAN	wg61d1.1.x1 Soares NSF_F8_9w_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2371509 3'
4820	17398	29852	5.95	2.1E-02	Y08501.1	NT	A.thaliana mitochondrial genome, part A
4836	17414	29867	0.57	2.1E-02	AA665737.1	EST_HUMAN	ag55g12.s1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1126918 3'
4944	17519	29861	0.63	2.1E-02	A1823432.1	EST_HUMAN	wt54a05.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384528 3'
5321	17883		1.52	2.1E-02	S82470.1	NT	BB1-malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]
5821	18445	31167	0.8	2.1E-02	AW379529.1	EST_HUMAN	CM4-HT0244-111199-040-R05 HT0244 Homo sapiens cDNA
7126	19468	32284	0.74	2.1E-02	BF086199.1	EST_HUMAN	QV3-GN0058-120800-328-a12 GN0058 Homo sapiens cDNA
8456	20908	33914	0.66	2.1E-02		NT	Mus musculus sorting nexin 1 (Snx1), mRNA
9422	21931	34879	0.56	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element
9549	22049	35010	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9549	22049	35011	2.41	2.1E-02	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
9894	22391	35369	1.22	2.1E-02	L28324.1	NT	Streptococcus pneumoniae integrase, excisionase, repressor protein, relaxase, UmuC MucB homolog, and UmuD MucA homolog genes, complete cds; and unknown genes
9973	22468	35452	0.57	2.1E-02	AA984288.1	EST_HUMAN	am83e07.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629732 3' similar to contains Alu repetitive element; contains element MER11 repetitive element
12098	18030		11.53	2.1E-02	Y19213.1	NT	Homo sapiens putative pshHBA pseudogene for hair keratin, exons 2 to 7
12141	24839	30798	1.31	2.1E-02	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
12552	24555	30871	16.83	2.1E-02	AF183913.1	NT	Azospirillum brasilense major outer membrane protein OmaA precursor (omaA) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
20	12699	25155	1.34	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13 MER1 repetitive element;
21	12700	25156	9.6	2.0E-02	AF85565.1	EST_HUMAN	QV4-NN0038-270400-187-h05 NN0038 Homo sapiens cDNA
280	12837	25422	2.31	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
317	12971	25460	2.42	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
831	13448	25955	1.2	2.0E-02	6753635	NT	Mus musculus DinB homolog 1 (E. coli) (Dinb1), mRNA
1128	13729	26240	1.32	2.0E-02	AL096805.1	NT	Homo sapiens genomic region containing hypervariable minisatellites chromosome 1 [p36.33] of Homo sapiens
1241	13839	26356	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1241	13839	26357	0.79	2.0E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
1914	14499	27053	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
1914	14499	27054	2.3	2.0E-02	8922453	NT	Homo sapiens hypothetical protein FLJ10486 (FLJ10486), mRNA
2824	15376		3.19	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
3115	12699	25155	1.84	2.0E-02	BF002832.1	EST_HUMAN	7g51c08.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3309998 3' similar to contains MER1.13 MER1 repetitive element;
3178	15791		1.38	2.0E-02	7305474	NT	Mus musculus sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorm) 6B (Sema6b), mRNA
3264	15876		1.57	2.0E-02	AF095588.1	NT	Arabidopsis thaliana C2H2 zinc finger protein ZF7 mRNA, complete cds
4078	16874	29135	1.54	2.0E-02	M18095.1	NT	P. vulgaris hydroxyproline-rich glycoprotein (HRGP) mRNA, 3' end
5268	17830	30255	1.12	2.0E-02	AF189368.1	NT	Ajellomyces capsulatus catalase isozyme A (CATA) mRNA, complete cds
6056	18873	31414	0.87	2.0E-02	L36321.2	NT	Dictyostelium discoideum class VII unconventional myosin (myoI) gene, complete cds
7553	20072	32947	1.26	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
7553	20072	32948	1.26	2.0E-02	AP000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position (417)
9791	22289		2.5	2.0E-02	U70408.1	NT	Japanese encephalitis virus envelope protein mRNA, partial cds
10264	22759	35746	1.63	2.0E-02	A1640342.1	EST_HUMAN	wa17b02.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2298315 3'
10522	23060	36070	2.05	2.0E-02	Z73968.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 69/162
11250	23780	36836	2.85	2.0E-02	D88184.1	NT	Equus caballus DNA for 17alpha-hydroxylase/17,20-lyase, complete cds
11530	23978	37047	1.96	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11530	23978	37048	1.96	2.0E-02	10947055	NT	Homo sapiens ankyrin 3, node of Ranvier (ankyrin G) (ANK3), transcript variant 1, mRNA
11654	18034	30484	1.91	2.0E-02	AA456538.1	EST_HUMAN	aa15b10.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813307 5'
12138	15376		1.94	2.0E-02	AL161532.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 32
12635	24711		8.4	2.0E-02	T80037.1	EST_HUMAN	yc04c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:24675 5'
722	13342	25832	1.93	1.9E-02	AA572764.1	EST_HUMAN	mf19a07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914196 similar to contains L1.11 L1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1658	14251	26785	0.96	1.9E-02	P18488	SWISSPROT	EMPTY SPIRACLES HOMEOTIC PROTEIN
2083	14684	27234	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2083	14684	27235	1.96	1.9E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2549	15113	27683	0.9	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
2930	15546	28021	8.7	1.9E-02	AA113858.1	EST_HUMAN	nm04105.s1 NCI CGAP_S51 Homo sapiens cDNA clone IMAGE:1238337 3'
2980	15596	28076	1.56	1.9E-02	AV048669.1	EST_HUMAN	AV048669 GLC Homo sapiens cDNA clone GLCBLH07 3'
3268	15609		0.75	1.9E-02	AB033611.1	NT	Utrichus talpoides mitochondrial gene for cytochrome b, complete cds
3671	16272		1.08	1.9E-02	N52250.1	EST_HUMAN	y28b02.s1 Soares_multiple_sclerosis_2Nbl-MSP Homo sapiens cDNA clone IMAGE:284331 3'
3766	16307		6.81	1.9E-02	BE738088.1	EST_HUMAN	601572682F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839564 5'
4121	16714	29170	1.48	1.9E-02	AF141940.1	NT	Mycoplasma imitans Vha1 precursor (vha1) and Vha2 precursor (vha2) genes, partial cds
4271	16857	29305	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4271	16857	29306	1.57	1.9E-02	P09081	SWISSPROT	HOMEOTIC BICOID PROTEIN (PRD-4)
4639	17221	29875	3.21	1.9E-02	AI452899.1	EST_HUMAN	tf46d04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144551 3' similar to contains Alu repetitive element;
5157	15113	27683	2.73	1.9E-02	AL161550.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 50
5519	18151	30565	0.83	1.9E-02	AF037352.1	NT	Mus musculus T cell receptor gamma locus, TCR gamma 1 and gamma 3 gene clusters
5660	18287	30765	1.38	1.9E-02	L47572.1	NT	Meleagris gallopavo paraoxonase-2 (PON2) mRNA, complete cds
5959	18581		0.81	1.9E-02	AB018507.1	NT	Drosophila kanekoi gene for glycerol-3-phosphate dehydrogenase, complete cds
7158	19690	32534	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
7158	19690	32535	1.41	1.9E-02	U19241.1	NT	Homo sapiens interferon-gamma receptor alpha chain gene, exon 1
8506	21045		1.06	1.9E-02	AL162754.2	NT	Neisseria meningitidis serogroup A strain Z2491 complete genome; segment 3/7
9254	21780	34732	0.94	1.9E-02	BF316129.1	EST_HUMAN	601896130F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125462 5'
9629	22129	35093	0.66	1.9E-02	L10114.1	NT	Nicotiana tabacum type II phytochrome (phyB) gene, complete cds
9958	22453	35435	1.04	1.9E-02	BF695832.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10054	22549	35543	0.49	1.9E-02	N39160.1	EST_HUMAN	601852385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4076253 5'
10151	22848	35639	0.96	1.9E-02	D84001.1	NT	Synechocystis sp. PCC6803 complete genome, 20/27, 2539000-2644794
11878	24847	30801	4.29	1.9E-02	AF101065.1	NT	Hirudo medicinalis intermediate filament gillrin mRNA, complete cds
12477	24818		1.27	1.9E-02	L11068.1	NT	Candida albicans lambda Cas3B fragment
12587	24980	30879	1.7	1.9E-02	X68271.1	NT	Hi.sapiens MUC18 gene exon 16
368	13017	25500	1.84	1.8E-02	AW771104.1	EST_HUMAN	hm52c06.x1 NCI CGAP_Co17 Homo sapiens cDNA clone IMAGE:3027274 3' similar to contains element MER29 repetitive element;
714	13335	25821	2.26	1.8E-02	BF308122.1	EST_HUMAN	601894329F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139983 5'
1202	13802	26315	1.51	1.8E-02	X17664.1	NT	H.francisci mRNA for myelin basic protein (MBP)
1484	14077	26615	2.3	1.8E-02	AF243382.1	NT	Drosophila melanogaster cytoplasmic protein encore (enc) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2704	15261	27828	1.22	1.8E-02	AE004544.1	NT	Pseudomonas aeruginosa PA01, section 105 of 529 of the complete genome
3247	15859		0.72	1.8E-02	AI805828.1	EST_HUMAN	hs2a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090296 3'
3956	16554	29023	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
3956	16554	29024	1.07	1.8E-02	AW879122.1	EST_HUMAN	MR1-OT0011-280300-009-g04 OT0011 Homo sapiens cDNA
4160	16752		1.41	1.8E-02	AA861448.1	EST_HUMAN	ak24h04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1406935 3'
4521	17105	29551	1.67	1.8E-02	AW936383.1	EST_HUMAN	QV4-DT0021-301288-071-b11 DT0021 Homo sapiens cDNA
5090	17683	30103	1.08	1.8E-02	O60810	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.2
6901	19635	32473	4.27	1.8E-02	P14310	SWISSPROT	HYPOTHETICAL 7.9 KD PROTEIN IN FIXW 5 REGION
8071	20613	33527	0.81	1.8E-02	U37091.1	NT	Mus musculus carbonic anhydrase IV gene, complete cds
8404	20944	33666	0.91	1.8E-02	AW905327.1	EST_HUMAN	QV2-NN1073-220400-159-h09 NN1073 Homo sapiens cDNA
8449	20989	33907	0.75	1.8E-02	667894.3	NT	Mus musculus microtubule-associated protein 2 (Map2), mRNA
9413	21922	34870	0.45	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9413	21922	34871	0.45	1.8E-02	BF241924.1	EST_HUMAN	601877026F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4105303 5'
9560	22060		2.41	1.8E-02	AA897543.1	EST_HUMAN	aj6209.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394921 3' similar to gb.L11672 ZINC FINGER PROTEIN 91 (HUMAN);
9875	22470	35453	1.72	1.8E-02	BE778274.1	EST_HUMAN	601463545F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866963 5'
10126	22621	35611	1.12	1.8E-02	X98933.1	NT	L. stagnalis mRNA for myomodulin neuro peptide precursor
11313	23011	36019	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11313	23011	36020	1.79	1.8E-02	AB002337.2	NT	Homo sapiens mRNA for KIAA0339 protein, partial cds
11480	23930	37001	1.73	1.8E-02	AP000006.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1168001-1485000 nt. position (817)
11489	23938	37008	3.88	1.8E-02	U62749.1	NT	Zea mays acidic ribosomal protein P2a-3 (rpp2a-3) mRNA, partial cds
839	13552	28068	0.77	1.7E-02	BE394869.1	EST_HUMAN	601310626F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632190 5'
1827	14416	26963	1.89	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1827	14416	26964	1.89	1.7E-02	AW573183.1	EST_HUMAN	h34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933740 3' similar to contains L1.11 L1 repetitive element;
1912	14497		3.27	1.7E-02	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2159	14736		12.81	1.7E-02	AB004816.1	NT	Oryctolagus cuniculus mRNA for mitsugumin29, complete cds
2332	14903	27474	4.64	1.7E-02	S74186.1	NT	[mitochondrial INRA41] [Ovis aries=sheep, Genomic, 361 nt, segment 1 of 2]
3028	15644	28123	0.84	1.7E-02	AI147615.1	EST_HUMAN	qb22a08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1696982 3'
3562	16166		4.33	1.7E-02	AW827368.1	EST_HUMAN	hm45a04.x1 NCI CGAP RDF1 Homo sapiens cDNA clone IMAGE:3015534 3' similar to contains MER19 b1 MER19 repetitive element;
3687	16268		0.65	1.7E-02	P04929	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4248	16836		1.08	1.7E-02	AA669618.1	EST_HUMAN	ac19f04.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856927 3' similar to contains Alu repetitive element; contains element MER24 repetitive element
4278	18864		2.52	1.7E-02	R02508.1	EST_HUMAN	ye86f08.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:124647 5'
4551	17134	29582	0.61	1.7E-02	A1305279.1	EST_HUMAN	qm08g07.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881276 3' similar to gb:X52359 ZINC FINGER PROTEIN 30 (HUMAN);
4626	17209	29859	1.44	1.7E-02	AW573183.1	EST_HUMAN	hf34a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2833740 3' similar to contains L1.11 L1 repetitive element
4824	17402	29855	1.78	1.7E-02	V00841.1	NT	Messenger RNA for anglerfish (Lophius americanus) somatostatin II
4938	17511		5.59	1.7E-02	A1015076.1	EST_HUMAN	ov51e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640858 3'
6274	18882	31650	1.8	1.7E-02	A1769247.1	EST_HUMAN	wg35f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367113 3' similar to contains Alu repetitive element
6693	19289	32091	1.98	1.7E-02	A1038280.1	EST_HUMAN	oy85f03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672661 3'
7112	19452	32268	1.05	1.7E-02	AF180930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
7255	19783	32639	1.96	1.7E-02		NT	Homo sapiens nebulin (NEB), mRNA
7394	19919	32783	1.07	1.7E-02	L07899.1	NT	Human apolipoprotein (a) gene, exon 1
7394	19919	32784	1.07	1.7E-02	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7724	20232		1.7	1.7E-02	U21854.1	NT	Caenorhabditis elegans cCAF1 protein gene, complete cds
9357	20296	33195	0.97	1.7E-02	U21854.1	NT	DKFZp434i0314_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434i0314 5'
9615	22115	35079	1.31	1.7E-02	AL040554.1	EST_HUMAN	CM4-NN1030-040400-130-06 NN1030 Homo sapiens cDNA
12462	25025	30619	3.35	1.7E-02	AW903482.1	EST_HUMAN	Mycobacterium tuberculosis H37Rv complete genome, segment 13/162
537	13168		3.38	1.8E-02	AL021928.1	NT	Treponema maltophilum flaB2, flaB3 and flid genes for flagellin subunit proteins and CAP protein homologue
1696	14289	26825	1.05	1.8E-02	Y18889.1	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2290	14864	27438	2.13	1.8E-02	Q84176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2280	14864	27439	2.13	1.8E-02	Q84176	SWISSPROT	Homo sapiens KVLQ1 gene
2600	15162	27730	0.98	1.8E-02	AJ008345.1	NT	ne81406.s1 NCI CGAP_Ew1 Homo sapiens cDNA clone IMAGE:910687
2669	15227	27789	1.82	1.8E-02	AA494872.1	EST_HUMAN	Homo sapiens mRNA for KIAA0634 protein, partial cds
2718	15275		1.14	1.8E-02	AB014534.1	NT	Lasaea sp. isolate 1Bd cytochrome oxidase III gene, partial cds; mitochondrial gene for mitochondrial product
3052	15668	28146	0.73	1.8E-02	AF112282.1	NT	IL3-CT0219-160200-063-C07 CT0219 Homo sapiens cDNA
3378	16182	28664	5.61	1.8E-02	AW850652.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
3914	16512	28974	0.82	1.8E-02	AL183301.2	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4254	16842		1.77	1.6E-02	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG28, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
4388	16974	29424	1.26	1.6E-02	AW875407.1	EST_HUMAN	QV2P.T0012-140100-030-07 PT0012 Homo sapiens cDNA
4901	17476	29932	3.99	1.6E-02	AI769132.1	EST_HUMAN	wg34b09.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2366969 3'
5308	17868		0.61	1.6E-02	N80158.1	EST_HUMAN	z665607.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:287444 3'
5807	18432	31153	1.26	1.6E-02	687171.5	NT	Mus musculus CD5 antigen (Cd5), mRNA
6752	19345	32152	2	1.6E-02	AB015281.1	NT	Candida albicans GaGCR3 gene, complete cds
7011	19509	32329	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7011	19509	32330	1.22	1.6E-02	AB027571.1	NT	Saccharomyces cerevisiae CAD2 gene for cadmium resistance protein, complete cds
7696	20205	33092	0.9	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
8064	20606	33518	0.78	1.6E-02	AJ277662.1	NT	Homo sapiens partial TUB gene for tubby (mouse) homolog and LMO1 gene for LIM domain only 1 protein
8119	20660		1.55	1.6E-02	X05151.1	NT	Human apoC-II gene for preproapolipoprotein C-II
9953	22448		2.32	1.6E-02	AF079784.1	NT	Drosophila melanogaster enhancer of polycomb (E(P-c)) mRNA, complete cds
10317	22811	35805	1.17	1.6E-02	AA572818.1	EST_HUMAN	nf19g03.s1 NCI CGAP_P1 Homo sapiens cDNA clone IMAGE:914260 similar to SW:TELO_RABIT
10317	22811	35806	1.17	1.6E-02	AA572818.1	EST_HUMAN	P29294 TELOKIN. [1]:
10788	24800	36319	2.38	1.6E-02	Z94828.1	NT	P29294 TELOKIN. [1]:
11090	23602	36602	2.5	1.6E-02	AL161508.2	NT	G. gallus microsatellite DNA (LE10260 (=T1811E11))
11090	23602	36641	2.5	1.6E-02	AL161508.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11385	23837	36899	2.38	1.6E-02	A1373558.1	EST_HUMAN	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 20
11855	14864	27438	3.63	1.6E-02	Q64176	SWISSPROT	q26610.x1 Soares_pregnant_uterus_NibHPU Homo sapiens cDNA clone IMAGE:2042442 3'
11855	14864	27439	3.63	1.6E-02	Q64176	SWISSPROT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
781	13400		51.07	1.5E-02	8923734	NT	LIVER CARBOXYLESTERASE 22 PRECURSOR (EGASYN) (ESTERASE-22)
2187	14763	27332	4.36	1.5E-02	N39521.1	EST_HUMAN	Homo sapiens transcription factor (HSA130894), mRNA
2219	14794	27367	1.76	1.5E-02	AL161594.2	NT	y27b07.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:243925 3'
3097	15712	28184	0.99	1.5E-02	AJ006216.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
3787	16387	28853	0.96	1.5E-02	BF092842.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
4222	16810	29257	0.86	1.5E-02	AA160967.1	EST_HUMAN	Homo sapiens CACNA1F gene, exons 1 to 48
5160	17729		0.78	1.5E-02	M13879.1	NT	MR4-TN0115-080900-201-b12 TN0115 Homo sapiens cDNA
5405	17863	30374	1.14	1.5E-02	AW770341.1	EST_HUMAN	zq40g10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632226 5'
							Human interleukin 2 gene, exons 1 and 2
							h76h11.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3007173 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6436	19039	31826	1.31	1.5E-02	Q09711	SWISSPROT	HYPOTHETICAL CALCIUM-BINDING PROTEIN C18B11.04 IN CHROMOSOME 1
7360	19886		1.62	1.5E-02	11467282	NT	Cyanophora paradoxa cyanelle, complete genome
7432	19956	32821	1.36	1.5E-02	11418713	NT	Homo sapiens KIAA1009 protein (KIAA1009), mRNA
7815	20358	33265	1.44	1.5E-02	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7822	20384	33273	4.16	1.5E-02	11417739	NT	Homo sapiens vally-rRNA synthetase 2 (VARS2), mRNA
8764	21303	34224	1.62	1.5E-02	BF345564.1	EST_HUMAN	602019135F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4154504 5'
9389	21812		0.51	1.5E-02	AF098774.1	NT	Homo sapiens kinase-related protein isoform 1 mRNA, complete cds
9490	21949	34895	1.64	1.5E-02	D44606.1	NT	Saccharomyces cerevisiae chromosome VI plasmid GapC
9725	22223	35199	1.08	1.5E-02	R32687.1	EST_HUMAN	yH54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
9725	22223	35200	1.08	1.5E-02	R32687.1	EST_HUMAN	yH54b10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133531 5'
10697	23227		1.71	1.5E-02	D26547.1	NT	Rice gene for thiredoxin h, complete cds
11047	23560	36597	2.32	1.5E-02	L40609.1	NT	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's
12076	24892		2.26	1.5E-02	AW750834.1	EST_HUMAN	RC4-CN0049-140100-011-c11 CN0049 Homo sapiens cDNA
12636	24712		1.55	1.5E-02	AI783127.1	EST_HUMAN	w06h03.x1 NCI_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:2389483 3' similar to contains Alu repetitive element; contains element MER26 MSR1 repetitive element
442	13075		1.41	1.4E-02	AE002230.2	NT	Chlamydia pneumoniae AR39, section 58 of 94 of the complete genome
1157	13760	26270	4.22	1.4E-02	7705980	NT	Homo sapiens NESH protein (LOC51225), mRNA
1299	13893		1.29	1.4E-02	U32800.1	NT	Haemophilus influenzae Rd section 115 of 163 of the complete genome
1341	13936		3.36	1.4E-02	U67779.1	NT	Xenopus laevis neurogenin related 1b (XNGNR-1b) mRNA, complete cds
1584	14166		1.09	1.4E-02	AV723785.1	EST_HUMAN	AV723785 HTB Homo sapiens cDNA clone HTBA-h11 5'
3249	15861	28342	1.91	1.4E-02	AF160669.2	NT	Bifidobacterium longum Ncr+/H+ antiporter (nhaB), cytosine deaminase, and alpha-galactosidase (egl) genes, complete cds; and N-acetylglucosaminexylose repressor protein (nagCxyR) gene, partial cds
3445	16053	28530	0.98	1.4E-02	AW074212.1	EST_HUMAN	xb06d09.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575793 3'
3531	16136	28616	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3531	16136	28617	5.67	1.4E-02	AL161586.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 82
3571	16175	28657	0.88	1.4E-02	4503628	NT	Homo sapiens coagulation factor XII (Hageman factor) (F12), mRNA
3717	16318	28786	6.27	1.4E-02	6966918	NT	Mus musculus histocompatibility 2, complement component factor B (H2-Bf), mRNA
4587	17170	29614	8.86	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG resequences, MAGG Homo sapiens cDNA
4587	17170	29615	8.86	1.4E-02	AW962688.1	EST_HUMAN	EST374761 MAGG resequences, MAGG Homo sapiens cDNA
4767	17348	29797	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4767	17348	29798	1.2	1.4E-02	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
5003	17576	30020	6.64	1.4E-02	BE733142.1	EST_HUMAN	601587403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5003	17576	30021	6.64	1.4E-02	BE733142.1	EST_HUMAN	601567403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842280 5'
6547	19145	31941	4.61	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
6547	19145	31942	4.61	1.4E-02	AA559030.1	EST_HUMAN	nt11c04.s1 NCI_CGAP_B12 Homo sapiens cDNA clone IMAGE:1029990 3' similar to contains Alu repetitive element;
8081	20623		1.97	1.4E-02	AL022073.1	NT	Mycobacterium tuberculosis H37Rv complete genome; segment 88/162
8829	21368	34292	1.24	1.4E-02	M81702.1	NT	Candida boidinii methanol oxidase (AOD1) gene, complete cds
9082	21618	34553	0.99	1.4E-02	AJ27285.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-3
9321	21835	34786	2.48	1.4E-02	BE544561.1	EST_HUMAN	601078239F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484241 5'
10451	22945		0.81	1.4E-02	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
11765	24156	36772	12.78	1.4E-02	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
12134	24387		3.62	1.4E-02	AF324985.1	NT	Arabidopsis thaliana F21J9.2 mRNA, complete cds
12433	24574		2.32	1.4E-02	11426998	NT	Homo sapiens sperm associated antigen 7 (SPAG7), mRNA
1905	14490	27138	1.18	1.3E-02	BE739263.1	EST_HUMAN	601556462F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3828335 5'
1998	14580	27138	2.55	1.3E-02	AL169201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3250	15862	28343	1.91	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
3250	15862	28344	1.91	1.3E-02	BF697081.1	EST_HUMAN	602129475F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286203 5'
4041	16639		1.66	1.3E-02	AF169288.1	NT	Mus musculus beta-sarcoglycan gene, complete cds
5455	18090	30447	1.46	1.3E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
5455	18090	30448	1.46	1.3E-02	AL049868.2	NT	Mus musculus chromosome X contigB; X-linked lymphocyte regulated 5 gene, Zinc finger protein 275, Zinc finger protein 92, mnxq28orf
6312	18919	31694	1.4	1.3E-02	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nrip) and survival motor neuron protein (smn) genes, complete cds
6345	18951	31729	0.86	1.3E-02	M62962.1	NT	C. reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
7041	18061	30449	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7041	18061	30450	1.25	1.3E-02	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
7578	20094	32971	4.79	1.3E-02	A031593.1	EST_HUMAN	ox06g05.x1 Soares_parathyroid_tumor_NB-HPA Homo sapiens cDNA clone IMAGE:1646072 3' similar to contains Alu repetitive element;
8418	20958	33876	1.63	1.3E-02	AF159961.1	NT	Homo sapiens human endogenous retrovirus W gagC3.37 G gag (gag) gene, complete cds
10108	22603	35593	1.71	1.3E-02	M63707.1	NT	Mouse kidney androgen-regulated protein (KAP) gene, complete cds
10178	22673	35665	0.77	1.3E-02	AE001304.1	NT	Chlamydia trachomatis section 31 of 87 of the complete genome
10871	23392	36406	4.07	1.3E-02	AW288563.1	EST_HUMAN	x34603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'
10871	23392	36407	4.07	1.3E-02	AW288563.1	EST_HUMAN	x34603.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2815036 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11742	25051		2.12	1.3E-02	X51780.1	NT	Yeast ABP1 gene for actin binding protein
12139	25039		2	1.3E-02	Z89117.1	NT	Bacillus subtilis complete genome (section 14 of 21): from 2589451 to 2812870
12246	24457		2.77	1.3E-02	8633069	NT	Human herpesvirus 68, complete genome
12438	24813		47.13	1.3E-02	AF152238.1	NT	Homo sapiens V1b vasopressin receptor (VPR3) gene, complete cds
228	12888		20.25	1.2E-02	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
377	13025	25511	3.79	1.2E-02	AA059298.1	EST_HUMAN	zf85g01.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381840 5' similar to contains element L1 repetitive element
478	13111	25601	1.71	1.2E-02	P38898	SWISSPROT	HYPOTHETICAL 17.1 KD PROTEIN IN PUR5 3'REGION
788	13387	25886	8.37	1.2E-02	AI183522.1	EST_HUMAN	q686e12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1734670 3' similar to contains L1.H1.L1 repetitive element
2221	14796	27389	1.85	1.2E-02	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2223	14798	27371	1.15	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
2487	15052	27624	1	1.2E-02	AW172950.1	EST_HUMAN	X37609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659432 3'
2542	15106	27678	1.05	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
2542	15106	27679	1.05	1.2E-02	BE538310.1	EST_HUMAN	601068406F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454608 5'
3135	15749		7.56	1.2E-02	AA075418.1	EST_HUMAN	zrn88e03.r1 Strategene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:545020 5'
3327	15937	28413	2.02	1.2E-02	R62805.1	EST_HUMAN	y11b08.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:138903 3'
4938	17513	29959	0.61	1.2E-02	AL161593.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 89
5040	17613	30057	2.65	1.2E-02	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NP T3) gene, complete cds
5194	17759		1.61	1.2E-02	AB019786.1	NT	Cynops pyrrhogaster CpUbiq1 mRNA, partial cds
5244	17808	30230	2.01	1.2E-02	AV731704.1	EST_HUMAN	AV731704 HTF Homo sapiens cDNA clone HTFBHG11 5'
5927	18549	31275	1.76	1.2E-02	D76589.1	NT	Rana rugosa mRNA for calreticulin, complete cds
7078	19650	32489	5.21	1.2E-02	AF175412.1	NT	Mus musculus DNA methyltransferase (Dnmt1) gene, exons 2, 3, 4, and 5
7334	19861	32725	1.06	1.2E-02	H02197.1	EST_HUMAN	y34h12.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150695 3'
7353	19879	32744	19.46	1.2E-02	AV732093.1	EST_HUMAN	AV732093 HTF Homo sapiens cDNA clone HTFBUC09 5'
7939	20481	33382	2.3	1.2E-02	Q11205	SWISSPROT	GMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ALPHA 2,3-ST) (GAL-NAC6S) (GAL-BETA-1,3-GALNAc-ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL4.2) (SIAT4-B)
8133	20874	33585	1.2	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8133	20874	33586	1.2	1.2E-02	AF193612.1	NT	Homo sapiens fringe protein mRNA, partial cds
8822	21361		1.08	1.2E-02	T76987.1	EST_HUMAN	y472c08.s1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:113774 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9557	22057	35018	2.7	1.2E-02	AB031013.1	NT	Norwalk-like virus genogroup 2 gene for capsid protein, complete cds
9589	22089	35053	1.74	1.2E-02	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
12446	24582		4.73	1.2E-02	C18119.1	EST_HUMAN	C18119 Human placenta cDNA (Tfujiwara) Homo sapiens cDNA clone GEN:557G06 5'
1312	13906	26426	1.49	1.1E-02	AA070364.1	EST_HUMAN	zn69s11.s1 Stralagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:530924 3'
1744	14334	26880	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
1744	14334	26881	1.91	1.1E-02	X75491.1	NT	H. sapiens LIPA gene, exon 4
2082	14693	27233	5.42	1.1E-02	BF345263.1	EST_HUMAN	602018037F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4153808 5'
2902	15518		4.2	1.1E-02	N99523.1	EST_HUMAN	za40e05.r1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:2216539 3' similar to SW:XP_F_HUMAN
3575	16179	28662	2.88	1.1E-02	A1653508.1	EST_HUMAN	Q92889 DNA-REPAIR PROTEIN COMPLEMENTING XP-F CELL ;
4094	16689		2.1	1.1E-02	BE144637.1	EST_HUMAN	PM3-HT0175-120200-015-g11 ST0197 Homo sapiens cDNA
4183	16773		0.61	1.1E-02	AW813786.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
4956	17531	29973	2.09	1.1E-02	AL048383.2	EST_HUMAN	DKFZp588E0924_s1 588 (synonym: huts1) Homo sapiens cDNA clone DKFZp588E0924
6298	18906	31677	1.03	1.1E-02	U66480.1	NT	Bacillus subtilis SpoVK (spoVK), YnaB (ybaA), YnaB (ybaB), GhrR (ghrR), glutamine synthetase (ghnA), YnaA (ybaA), YnaB (ybaB), YnaC (ybaC), YnaD (ybaD), YnaE (ybaE), YnaF (ybaF), YnaG (ybaG), YnaH (ybaH), YnaI (ybaI), YnaJ (ybaJ), YnaK (ybaK), YnaL (ybaL), YnaM (ybaM), YnaN (ybaN), YnaO (ybaO), YnaP (ybaP), YnaQ (ybaQ), YnaR (ybaR), YnaS (ybaS), YnaT (ybaT), YnaU (ybaU), YnaV (ybaV), YnaW (ybaW), YnaX (ybaX), YnaY (ybaY), YnaZ (ybaZ), YnaA (ybaA), YnaB (ybaB), YnaC (ybaC), YnaD (ybaD), YnaE (ybaE), YnaF (ybaF), YnaG (ybaG), YnaH (ybaH), YnaI (ybaI), YnaJ (ybaJ), YnaK (ybaK), YnaL (ybaL), YnaM (ybaM), YnaN (ybaN), YnaO (ybaO), YnaP (ybaP), YnaQ (ybaQ), YnaR (ybaR), YnaS (ybaS), YnaT (ybaT), YnaU (ybaU), YnaV (ybaV), YnaW (ybaW), YnaX (ybaX), YnaY (ybaY), YnaZ (ybaZ)
7594	20108	32983	2.55	1.1E-02	BE149611.1	EST_HUMAN	RC1-HT0256-100300-016-h07 HT0256 Homo sapiens cDNA
8189	20740	33652	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8189	20740	33653	0.49	1.1E-02	P80394	SWISSPROT	METALLOTHIONEIN (MT-1/MT-2)
8574	21113	34032	0.64	1.1E-02	AW996160.1	EST_HUMAN	QV3-BN0045-220300-128-h02 BN0045 Homo sapiens cDNA
8756	21295	34215	0.69	1.1E-02	C04803.1	EST_HUMAN	C04803 Human heart cDNA (Ynakamura) Homo sapiens cDNA clone 3NHC40 40
8833	21372	34287	7.39	1.1E-02	Q61982	SWISSPROT	NEUROGENIC LOCUS NOTCH 3 PROTEIN
9842	22340	35322	2.07	1.1E-02	AA082578.1	EST_HUMAN	zn24e01.r1 Stralagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548328 5'
10006	22501	35492	3.79	1.1E-02	AA314665.1	EST_HUMAN	EST186494 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end
10658	23379	36398	3.88	1.1E-02	11435505	NT	Homo sapiens T-box 5 (TBX5), mRNA
11702	24116		2.57	1.1E-02	AA688239.1	EST_HUMAN	ab77f11.s1 Stralagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:853005 3' similar to contains
12512	16773		1.87	1.1E-02	AW813796.1	EST_HUMAN	Alu repetitive element
7	12686	25144	6.97	1.0E-02	AW846120.1	EST_HUMAN	RC3-ST0197-120200-015-g11 ST0197 Homo sapiens cDNA
1570	14163	26694	2.33	1.0E-02	AW368128.1	EST_HUMAN	MR3-CT0176-111089-003-e10 CT0176 Homo sapiens cDNA
2606	15168		1.9	1.0E-02	AA806389.1	EST_HUMAN	CM2-HT0177-041099-017-h12 HT0177 Homo sapiens cDNA
3126	15740	28209	3.7	1.0E-02	BE835556.1	EST_HUMAN	cc22h08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1350495 3'
3302	15913	28391	1.41	1.0E-02	BE968999.1	EST_HUMAN	RC0-FN0025-250500-021-d02 FN0025 Homo sapiens cDNA
							601649687R1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933689 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3556	16182		0.83	1.0E-02	AW845621.1	EST_HUMAN	MR0-CT0060-081089-003-h10 CT0060 Homo sapiens cDNA
3950	16548	28016	0.88	1.0E-02	AI065086.1	EST_HUMAN	HA0921 Human fetal liver cDNA library Homo sapiens cDNA
4891	17466	29921	5.12	1.0E-02	6753521	NT	Mus musculus corticotropin releasing hormone receptor 2 (Chr2), mRNA
4870	17544	29986	5.03	1.0E-02	R66567.1	EST_HUMAN	y454h01.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:199633 5'
5221	17786	30204	1.01	1.0E-02	AF218910.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 25 and complete cds, alternatively spliced
5317	17879	30298	0.98	1.0E-02	P06599	SWISSPROT	EXTENSIN PREGURSOR
5394	17952		16.85	1.0E-02	AV723678.1	EST_HUMAN	AV723678 HTB Homo sapiens cDNA clone HTBAPF08 5'
5445	18000		3.87	1.0E-02	D34632.1	NT	Arabidopsis thaliana ecc2 gene for acetyl-CoA carboxylase, partial cds
5610	18239	30688	0.8	1.0E-02	H52081.1	EST_HUMAN	y436h11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:235941 5'
5921	18543	31269	0.7	1.0E-02	AF309388.1	NT	Mus musculus transcription complex subunit NF-ATc4 (Nfatc4) gene, exons 1 and 2
6264	18872	31642	0.99	1.0E-02	AF257303.1	NT	Mus musculus synaptotagmin II (Syx2) gene, complete cds
6328	18934	31709	2.67	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6328	18934	31710	2.67	1.0E-02	AW577113.1	EST_HUMAN	MR4-BT0356-070100-201-h01 BT0356 Homo sapiens cDNA
6859	19593	32425	2.22	1.0E-02	Z28642.1	NT	Z.mays U3snRNA pseudogene
8240	20781		0.46	1.0E-02	Z28107.1	NT	S.cerevisiae chromosome XI reading frame ORF YKL107w
9314	21828	34778	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
9314	21828	34779	4.29	1.0E-02	BF036331.1	EST_HUMAN	601459570F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3863177 5'
11143	23651		2.17	1.0E-02	AF157559.1	NT	Citridia fasciculata 27 kDa guide RNA-binding protein mRNA, complete cds; mitochondrial gene for mitochondrial product
11246	23778	36833	2.02	1.0E-02	AV780016.1	EST_HUMAN	AV780016 MDS Homo sapiens cDNA clone MDSBDC10 5'
11785	25110		2.16	1.0E-02	Q62203	SWISSPROT	SPICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
11847	24862	30705	4.64	1.0E-02	AW695521.1	EST_HUMAN	RC2-DT0007-120200-016-h02 DT0007 Homo sapiens cDNA
11861	24922		6.07	1.0E-02	S70330.1	NT	Homo sapiens renal dipeptidase (RDP) gene, complete cds
12254	24896		1.53	1.0E-02	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
12422	24982		4.42	1.0E-02	X62654.1	NT	H. sapiens gene for Me491/CD63 antigen
926	13539	26057	3.16	9.0E-03	A1796126.1	EST_HUMAN	wp42f09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2383433 3' similar to contains element
1307	13901		1.26	9.0E-03	BE781889.1	EST_HUMAN	MER22 MER22 repetitive element
2439	15006	27578	3.82	9.0E-03	AL161559.2	NT	601470242F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873346 5'
2449	15016	27588	0.87	9.0E-03	AF099934.1	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 59
2931	15472	28022	0.61	9.0E-03	AJ251744.1	EST_HUMAN	Mus musculus MHC class III protein RP1 (Rp1) mRNA, partial cds
2931	15472	28023	0.61	9.0E-03	AJ251744.1	EST_HUMAN	q190f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
3731	16332	28788	0.8	9.0E-03	J05184.1	NT	q190f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854281 3'
5978	18598		1.17	9.0E-03	AI809792.1	EST_HUMAN	S.acidocalcarian thermopsis gene, complete cds
							w177f04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2361631 3'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6741	19335		4.24	9.0E-03	BE745988.1	EST_HUMAN	601573438F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3834752 5'
7487	20010	32876	0.73	9.0E-03	8922570	NT	Homo sapiens hypothetical protein FLJ10650 (FLJ10650), mRNA
7816	20359		0.83	9.0E-03	AL039991.1	EST_HUMAN	DKFZp434L0412_r1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZp434L0412 5'
8191	20732		0.56	9.0E-03	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
9759	22257	35240	0.5	9.0E-03	P26011	SWISSPROT	INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P) (M280 IEL ANTIGEN)
9776	22274	35259	1.28	9.0E-03	P20908	SWISSPROT	COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
10865	23386		1.8	9.0E-03	Y18000.1	NT	Homo sapiens NF2 gene
10891	23412	36431	1.71	9.0E-03	BE395380.1	EST_HUMAN	601310881F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632181 5'
11505	23954	37022	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
11505	23954	37023	1.58	9.0E-03	L11144.1	NT	Homo sapiens preprogalactin (GAL1) gene, exons 1, 2, and 3
12001	25111		1.79	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA
12221	25105		36.8	9.0E-03	BE348385.1	EST_HUMAN	hw17b09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183161 3'
12319	24509	30843	1.38	9.0E-03	AL163287.2	NT	Homo sapiens chromosome 21 segment HS21C067
12539	24649		31.67	9.0E-03	BF351141.1	EST_HUMAN	PM1-HT0452-291289-001-e09 HT0452 Homo sapiens cDNA
527	13159		2.87	8.0E-03	AA723007.1	EST_HUMAN	zh30e03.e1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:413598 3' similar to contains Alu repetitive element;
1026	13637	26152	35.57	8.0E-03	AF106656.1	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
2203	14779	27351	1.28	8.0E-03	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3351	15959	28436	0.99	8.0E-03	BE171225.1	EST_HUMAN	RC1-HT0545-120200-011-b09 HT0545 Homo sapiens cDNA
3404	16013	28492	0.89	8.0E-03	A131016.1	NT	Homo sapiens SCL gene locus
3738	16339	28805	1.77	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
3738	16339	28808	1.77	8.0E-03	P32844	SWISSPROT	HYPOTHETICAL 127.0 KD PROTEIN IN RAD24-BMH1 INTERGENIC REGION
4343	16930	29371	1.19	8.0E-03	BE840048.1	EST_HUMAN	QV0-FN0181-140700-304-g10 FN0181 Homo sapiens cDNA
4472	17058	29505	6.36	8.0E-03	BF369327.1	EST_HUMAN	CMA-NN0119-300600-223-b05 NN0119 Homo sapiens cDNA
5378	17937	30350	1.02	8.0E-03	U02970.1	NT	Prototheca wickerhamii 263-11 complete mitochondrial DNA
5410	17987	30376	0.88	8.0E-03	P01871	SWISSPROT	IG MU CHAIN C REGION
5714	18340	30846	2.89	8.0E-03	AF110520.1	NT	Mus musculus major histocompatibility complex region NG27, NG28, RPS28, NADH oxidoreductase, NG29, KIFC1, Fas-binding protein, BING1, tapasin, RalGDS-like, KE2, BING4, beta 1,3-galactosyl transferase, and RPS18 genes, complete cds; Sacm21 gene, partial>
6346	24762	31730	1.34	8.0E-03	AF000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (27)
6846	19436	32251	4.45	8.0E-03	P55577	SWISSPROT	PROBABLE PEPTIDASE Y4NA
6999	19497		1.72	8.0E-03	V01109.1	NT	Human BK virus (strain MM) genome. (Closely related to SV40.)
7259	19787	32643	1.8	8.0E-03	M17197.1	NT	A. californica (marine gastropod mollusc) neuropeptide gene (bag cell), exon 1, 5' end

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7547	20067		1.84	8.0E-03	AB038287.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
8816	21355	34279	0.62	8.0E-03	P98160	SWISSPROT	BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN
8841	21380	34304	3.73	8.0E-03	AW608692.1	EST_HUMAN	PRECURSOR (HSPG) (PERLECAN) (PLC)
8910	21448	34370	0.68	8.0E-03	9789956	NT	MR1-ST0111-111199-011-h06 ST0111 Homo sapiens cDNA
8959	22356		4.76	8.0E-03	BE086509.1	EST_HUMAN	Mus musculus fusion 2 (human) (Fus2), mRNA
10864	23385		3.01	8.0E-03	Z49652.1	NT	QV1-BT0677-040400-131-g03 BT0677 Homo sapiens cDNA
11259	23789	36845	1.97	8.0E-03	AA828817.1	EST_HUMAN	S.cerevisiae chromosome X reading frame ORF YJR152w
11259	23789	36846	1.97	8.0E-03	AA828817.1	EST_HUMAN	cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11562	24009	37079	4.96	8.0E-03	AF084589.1	NT	cd80a09.s1 NCL_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1374232
11713	24123		2.81	8.0E-03	M69035.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
11761	24154		5.99	8.0E-03	AB038161.1	NT	Oryctolagus cuniculus eIF-2a kinase mRNA, complete cds
723	13343	25833	14.03	7.0E-03	AF097183.1	NT	Homo sapiens ABCG1 gene for ABC transporter (ATP-binding cassette, sub-family G (WHITE), member 1), complete cds
723	13343	25834	14.03	7.0E-03	AF097183.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1012	13822	26137	5.78	7.0E-03	AF243376.1	NT	Cryptosporidium parvum HC-10 gene, complete cds
1155	13758	26268	3.21	7.0E-03	AV731712.1	EST_HUMAN	Glycine max glutathione S-transferase GST 21 mRNA, partial cds
1408	14001		1.26	7.0E-03	Q61060	SWISSPROT	AV731712 HTF Homo sapiens cDNA clone HTFAZF10 5'
1439	14032	26560	4.09	7.0E-03	AA668298.1	EST_HUMAN	FORKHEAD BOX PROTEIN D3 (HNF3/FH TRANSCRIPTION FACTOR GENESIS) (HEPATOCYTE
1550	14142	26675	3.14	7.0E-03	AW303599.1	EST_HUMAN	NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 2 (HNF-2)
2297	15482	27447	2.12	7.0E-03	P04929	SWISSPROT	ab79k09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:853145 3'
3614	16217	28696	0.58	7.0E-03	A1150273.1	EST_HUMAN	xt21b02.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813739 3'
3830	16430	28892	0.91	7.0E-03	AW444463.1	EST_HUMAN	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3885	16483	28945	1.01	7.0E-03	AF196344.1	NT	qt34h02.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1751955 3'
4091	16430	28892	0.63	7.0E-03	AW444463.1	EST_HUMAN	UI-H-BI3-akb-c-10-0-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
4704	17286		1.1	7.0E-03	AW630888.1	EST_HUMAN	Rattus norvegicus neuronal nicotinic acetylcholine receptor subunit (Alpha10) mRNA, complete cds
5125	17697		2.08	7.0E-03	AL163278.2	NT	UI-H-BI3-akb-c-10-0-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733691 3'
5985	18605		0.79	7.0E-03	H71106.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS27C078
6280	24760		5.32	7.0E-03	AW861059.1	EST_HUMAN	y82g01.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:211824 5' similar to
6456	19057	31842	1.45	7.0E-03	W68251.1	EST_HUMAN	gb:X174723 CLUSTERIN PRECURSOR (HUMAN);
6658	19254	32056	2.98	7.0E-03	AA327129.1	EST_HUMAN	RC1-C10286-050400-018-c08 C10286 Homo sapiens cDNA
							z433110.r1 Soares fetal_heart_NHH19W Homo sapiens cDNA clone IMAGE:342475 5'
							EST30674 Colon I Homo sapiens cDNA 5' end

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8881	19277	32080	0.82	7.0E-03	BE657385.1	EST_HUMAN	7g34b10.x1 NCL CGAP_Bm23 Homo sapiens cDNA clone IMAGE:3308347 3' similar to TR:Q13387
7139	19519	32341	2.12	7.0E-03	BE928133.1	EST_HUMAN	Q13387 HYPOTHETICAL PROTEIN 384D8_2; contains TAR1.12 TAR1 TAR1 repetitive element;
7529	20049	32921	5.78	7.0E-03	Z35838.1	NT	GM2-CT0478-230800-347-b11 CT0478 Homo sapiens cDNA
7529	20049	32922	5.78	7.0E-03	Z35838.1	NT	S cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33238	0.54	7.0E-03	AJ229043.1	NT	S cerevisiae chromosome II reading frame ORF YBL077w
7789	20332	33239	0.54	7.0E-03	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
8055	20597	33504	2.38	7.0E-03	BE175687.1	EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
9318	21832		0.6	7.0E-03	AF111168.2	NT	RGS-HT0582-160300-011-002 HT0582 Homo sapiens cDNA
9513	22013	34972	0.87	7.0E-03	N52378.1	EST_HUMAN	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
9636	22136	35101	2.48	7.0E-03	P48982	SWISSPROT	yy49c10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248066 3' similar to contains
9636	22136	35102	2.48	7.0E-03	P48982	SWISSPROT	Alu repetitive element;
10207	22702		0.99	7.0E-03	AV687379.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10381	22875		0.93	7.0E-03	AI799734.1	EST_HUMAN	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
10706	23235	36248	3.48	7.0E-03	AB008852.1	NT	AV687379 GKc Homo sapiens cDNA clone GKCAFC07 5'
10780	23304	36311	1.61	7.0E-03	AJ004862.1	NT	wc37609.x1 NCL CGAP_P128 Homo sapiens cDNA clone IMAGE:2320840 3'
10780	23304	36312	1.61	7.0E-03	AJ004862.1	NT	Bos taurus mRNA for NDP52, complete cds
10930	23448		1.66	7.0E-03	AJ242804.1	NT	Homo sapiens partial MUC5B gene, exon 1-29
12273	25095		1.83	7.0E-03	H94095.1	EST_HUMAN	Homo sapiens partial MUC5B gene, exon 1-29
12281	24484		1.58	7.0E-03	BE263253.1	EST_HUMAN	Sporobolus stipticus mRNA for putative glycine and proline-rich protein
12382	24549		1.86	7.0E-03	Y17455.1	NT	yy15h01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:242833 3' similar to contains
12527	25092		1.38	7.0E-03	AL163300.2	EST_HUMAN	Alu repetitive element;
12664	24734		3.18	7.0E-03	AW868110.1	EST_HUMAN	601145154F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160476 5'
1283	13879	28400	10.8	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens LSFR2 gene, penultimate exon
1283	13879	28401	10.8	6.0E-03	AW511148.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
2800	15362	27921	1.82	6.0E-03	AF112374.1	NT	RCD-SN0052-110400-021-a04 SN0052 Homo sapiens cDNA
2916	15533	28004	3.54	6.0E-03	AA759135.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
2916	15533	28005	3.54	6.0E-03	AA759135.1	EST_HUMAN	SW:PXH HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXH
3283	15894		2.17	6.0E-03	H75690.1	EST_HUMAN	hd22a05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910224 3' similar to
							SW:PXH HUMAN 075469 ORPHAN NUCLEAR RECEPTOR PXH
							Danio rerio odorant receptor gene cluster
							ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							ah78e11.s1 Soares_testis_NHT Homo sapiens cDNA clone 1321772 3'
							yy77h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:211351 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3344	15954		0.79	6.0E-03	AF190338.1	NT	Notoncus sp. cytochrome c oxidase subunit II gene, partial cds; mitochondrial gene for mitochondrial product
3429	16037	28518	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3429	16037	28519	1.14	6.0E-03	U90880.1	NT	Fugu rubripes zinc finger protein, isotocin, fatty acid binding protein, sepiapterin reductase and vasotocin genes, complete cds
3600	16204		1.13	6.0E-03	W37985.1	EST_HUMAN	zc13a11.1 Soares parathyroid tumor NbhHPA Homo sapiens cDNA clone IMAGE:322172 5'
3721	16322	28789	2.6	6.0E-03	BF510986.1	EST_HUMAN	UI-H-B14-4pm-c-08-0-UI.s1 NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3087754 3'
3757	16358	28828	1.53	6.0E-03	BE077356.1	EST_HUMAN	RC1-BT0606-260400-014-a07 BT0606 Homo sapiens cDNA
3845	16444	28905	1.14	6.0E-03	6754029	NT	Mus musculus glucosamine-6-phosphate deaminase (Gnpi), mRNA
3995	16593	29068	0.83	6.0E-03	AW847284.1	EST_HUMAN	RCO-CT0204-240999-021-b10 CT0204 Homo sapiens cDNA
4030	16628		0.92	6.0E-03	BE250108.1	EST_HUMAN	600942304F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:2859513 5'
4419	17004		1.1	6.0E-03	N58946.1	EST_HUMAN	Y62H10.s1 Soares multiple sclerosis 2NbrHMSF Homo sapiens cDNA clone IMAGE:278179 3'
4454	17040		1.58	6.0E-03	A016833.1	EST_HUMAN	ov33c11.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1639124 3'
4805	17383	29833	8.21	6.0E-03	AA324242.1	EST_HUMAN	EST27118 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing Alu repeat
5290	17852		0.92	6.0E-03	L34170.1	NT	Human germline UBE1L gene similar to the gene for ubiquitin-activating enzyme, exons 1-22
6301	24761	31680	0.72	6.0E-03	9627521	NT	Varidla virus, complete genome
6906	19640	32476	0.73	6.0E-03	O14994	SWISSPROT	SYNAPSIN III
6939	18047	30469	0.72	6.0E-03	BE253748.1	EST_HUMAN	601112353F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3353172 5'
7642	20154	33040	0.76	6.0E-03	AF128694.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 7-16 and complete cds
7774	20283	33180	24.22	6.0E-03	AJ243211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7799	20342	33251	6.91	6.0E-03	A103980.1	EST_HUMAN	ow13a04.x1 Soares parathyroid tumor NbhHPA Homo sapiens cDNA clone IMAGE:1646670 3' similar to contains MER10.b1 MER10 repetitive element
7915	20457	33363	2.45	6.0E-03	AW798337.1	EST_HUMAN	RCO-UM0051-210300-032-g02 UM0051 Homo sapiens cDNA
7990	20532		1.59	6.0E-03	BF038198.1	EST_HUMAN	601454915F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3858028 5'
9473	21872	34821	8.46	6.0E-03	D10548.1	NT	Subacute sclerosing panencephalitis (SSPE) virus mRNA for fusion protein
9956	22451		2.15	6.0E-03	A1432661.1	EST_HUMAN	h22c02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2131202 3' similar to SW:R13A_HUMAN
10067	22582	35557	0.73	6.0E-03	AJ011849.1	NT	P40429 60S RIBOSOMAL PROTEIN L13A
10197	22692		0.91	6.0E-03	AF084555.1	NT	Bacillus subtilis fndD gene
10303	22787	35788	0.63	6.0E-03	X68366.1	NT	Homo sapiens okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP-19) mRNA, complete cds
10623	23155	36168	2.04	6.0E-03	AW962164.1	EST_HUMAN	M.thermoformicicum complete plasmid pFV1 DNA
10690	23220		2.23	6.0E-03	11545814	NT	EST1374237 MAGE sequences, MAGG Homo sapiens cDNA
							Homo sapiens hypothetical zinc finger protein FLJ14011 (FLJ14011), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10726	23252	36269	2.16	6.0E-03	A1420786.1	EST_HUMAN	te91c12.x1 NOI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
10726	23252	36270	2.16	6.0E-03	A1420786.1	EST_HUMAN	te91c12.x1 NOI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE.
10861	23382	36401	2.08	6.0E-03	U14556.1	NT	Mus musculus zinc-finger protein mRNA, complete cds
10862	23383	36401	2.4	6.0E-03	BE737895.1	EST_HUMAN	601572748F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:3839747 5'
11630	24072	37134	1.57	6.0E-03	H70296.1	EST_HUMAN	y9501.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213049 5' similar to SP:SPGD_PIG P14332 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING.
11829	24195		3.52	6.0E-03	AF010498.1	NT	Rhodobacter capsulatus strain SB1003, partial genome
11956	24848		5.1	6.0E-03	AE000833.1	NT	Methanobacterium thermoautotrophicum from bases 420182 to 450298 (section 39 of 148) of the complete genome
12039	24914		3.02	6.0E-03	U30790.1	NT	Pneumocystis carinii f. sp. ratti guanine nucleotide binding protein alpha subunit (pcg1) gene, complete cds
12098	24357		1.61	6.0E-03	Q62209	SWISSPROT	SYNAPTOMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN)
12402	24501		1.49	6.0E-03	BE788019.1	EST_HUMAN	601482621F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885388 5'
12418	24571		1.52	6.0E-03	AJ245480.1	NT	Brassica napus sig gene for S-locus glycoprotein, cultivar T2
12556	24942		1.6	6.0E-03	X74807.1	NT	R. norvegicus VEGP2 gene
229	12889	25375	5.16	5.0E-03	X67344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
697	13320	25806	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
697	13320	25807	1.73	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
698	13320	25806	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
698	13320	25807	2.74	5.0E-03	L25105.1	NT	Chlamydia trachomatis partial ORF8; aminoacyl-tRNA synthase, complete cds; complete ORFA, and grpE- like protein, complete cds
1151	13754	26264	0.91	5.0E-03	AJ010457.1	NT	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH3
2706	15293	27830	2.77	5.0E-03	AB033006.1	NT	Homo sapiens mRNA for KIAA1180 protein, partial cds
2982	15579	28057	0.66	5.0E-03	BE266057.1	EST_HUMAN	601194798F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538799 5'
3170	15784	28256	4.54	5.0E-03	T67623.1	EST_HUMAN	y81f09.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22395 3'
3189	15801		2.22	5.0E-03	AL161491.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 3
3202	15814	28289	1.15	5.0E-03	R71794.1	EST_HUMAN	y86g02.s1 Soares breast 2NBH8t Homo sapiens cDNA clone IMAGE:155666 3'
3316	15926		0.86	5.0E-03	AJ297357.1	NT	Homo sapiens partial LIMD1 gene for LIM domains containing protein 1 and KIAA0851 gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3728	16328	28795	5.04	5.0E-03	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
3762	16363	28831	4.88	5.0E-03	AF147449.2	NT	Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 1B (ponB) gene, complete cds
3822	16422	28884	0.68	5.0E-03	U388914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4043	16841		1.78	5.0E-03	AA286675.1	EST_HUMAN	EST12218 Uterus tumor 1 Homo sapiens cDNA 5' end
4204	16793	28239	0.57	5.0E-03	AJ002125.1	NT	Natrix domestica Zfx type gene
4302	16978	28425	0.88	5.0E-03	H78355.1	EST_HUMAN	yu79g10.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:240086 5'
4394	16422	28884	0.71	5.0E-03	U388914.1	NT	Citrus sinensis seed storage protein citrin mRNA, complete cds
4570	17252	28704	0.68	5.0E-03	U46691.1	NT	Human putative chromatin structure regulator (SUPT6H) mRNA, complete cds
4714	17295	28739	0.8	5.0E-03	AJ131016.1	NT	Homo sapiens SCL gene locus
4828	17406	28860	1.72	5.0E-03	AJ752387.1	EST_HUMAN	en15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en15c02 random
5087	17840	30083	1.02	5.0E-03	P15285	SWISSPROT	SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS)
5391	17949	30362	0.95	5.0E-03	AF171686.1	NT	Bos taurus acidic alpha-glucosidase gene, exons 2 through 20 and complete cds
5664	18586	31320	7.68	5.0E-03	P35500	SWISSPROT	SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN)
6195	18805	31574	2.33	5.0E-03	Q00507	SWISSPROT	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF-Y (UBIQUITIN THIOLESTERASE FAF-Y) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE FAF-Y) (DEUBIQUITINATING ENZYME FAF-Y) (FAT FACETS PROTEIN RELATED, Y-LINKED) (UBIQUITIN-SPECIFIC PROTEASE 9, Y CHROMOSOME)
6230	18839		0.91	5.0E-03	AE002234.2	NT	Gliemysophila pneumoniae AR39, section 62 of 94 of the complete genome
6708	18302		10.88	5.0E-03	BE300091.1	EST_HUMAN	600944564T1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960871 3'
6832	18040	30483	6.39	5.0E-03	AB025024.1	NT	Mus musculus AMD1 gene for S-adenosylmethionine decarboxylase, complete cds
7106	19448		0.85	5.0E-03	AB038267.1	NT	Tursiops truncatus mRNA for p40-phox, complete cds
7595	20109		1.16	5.0E-03	AW854327.1	EST_HUMAN	RC3-CT0255-031099-011-f07 CT0255 Homo sapiens cDNA
7744	20252	33146	7.43	5.0E-03	AB016818.1	NT	Homo sapiens MASL1 mRNA, complete cds
8162	20703	33618	1	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8162	20703	33619	1	5.0E-03	AW855907.1	EST_HUMAN	RC8-CT0281-081199-011-A05 CT0281 Homo sapiens cDNA
8181	20722	33636	2.28	5.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
8548	21087		6.35	5.0E-03	M61132.1	NT	Mouse complement receptor (CR2) mRNA, 3' end
8742	21281	34204	1.47	5.0E-03	D90723.1	NT	Escherichia coli genomic DNA. (19.1 - 19.4 min)
8870	21409	34333	0.69	5.0E-03	M25080.1	NT	Rabbit uteroglobin (UGL) gene, exon 1
9503	22003	34960	0.45	5.0E-03	P33750	SWISSPROT	SOF1 PROTEIN
9753	22251	35234	0.82	5.0E-03	L21710.1	NT	Plasmodium berghei 58 kDa phosphoprotein mRNA, partial cds
9881	22378	35354	0.77	5.0E-03	AW821888.1	EST_HUMAN	RC0-S10379-210100-032-c02 ST0379 Homo sapiens cDNA
10062	22557	35552	0.49	5.0E-03	AA533143.1	EST_HUMAN	nj48h10.s1 NCI_CGAP_P19 Homo sapiens cDNA clone IMAGE:985587

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10238	22731	35722	0.92	5.0E-03	7662557	NT	Homo sapiens PRO0471 protein (PRO0471), mRNA
10598	23133		10.33	5.0E-03	T19586.1	EST_HUMAN	894F Heart Homo sapiens cDNA clone 694
10631	23163	36175	2.28	5.0E-03	D28273.1	NT	Unknown nitrogen-fixing bacteria nifD gene encoding alpha subunit of dinitrogenase (MoFe protein)
10819	23340	36354	2.94	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCC_cervical tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element
10819	23340	36355	2.94	5.0E-03	AW170334.1	EST_HUMAN	xn59g05.x1 Soares_NHCC_cervical tumor Homo sapiens cDNA clone IMAGE:2698040 3' similar to contains L1 L2 L1 repetitive element
10920	23439	36460	2.02	5.0E-03	T49163.1	EST_HUMAN	y099a04.r1 Stratagene placenta (#937225) Homo sapiens cDNA clone IMAGE:70686 5'
11212	23715		3.91	5.0E-03	BE048055.1	EST_HUMAN	tz46a04.y1 NCI_CGAP_Brm52 Homo sapiens cDNA clone IMAGE:2291822 5'
11972	25054		8.12	5.0E-03	AF047874.1	NT	Gallus gallus glyceraldehyde-3-phosphate dehydrogenase mRNA, complete cds
12111	24372		21.73	5.0E-03	AF067253.1	NT	Brugia malayi Y chromosome marker
12217	24440		1.81	5.0E-03	L10347.1	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
12250	24461		1.78	5.0E-03	AA456597.1	EST_HUMAN	zx75a03.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809548 3' similar to
12283	24856		5.46	5.0E-03	BF572332.1	EST_HUMAN	SW:DXA2 MOUSE P14885 PROBABLE DIAPHENOL OXIDASE A2 COMPONENT
12473	24598	30883	2.21	5.0E-03	AW449109.1	EST_HUMAN	UIH-B13-akf-08-0-UI.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2734215 3'
12498	24932		1.42	5.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
253	12913	25397	2.58	4.0E-03	AW500196.1	EST_HUMAN	UIHF-BNO-ako-h-04-0-UI.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076831 5'
343	12995	25480	1.77	4.0E-03	R46482.1	EST_HUMAN	y651a04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
468	13101	25594	0.89	4.0E-03	P54675	SWISSPROT	PHOSPHATIDYLINOSITOL 3-KINASE 3 (P13-KINASE) (PI3K)
629	13256	25730	3.12	4.0E-03	AA939339.1	EST_HUMAN	cn75g12.s1 Soares_NFL_T_GBC_ST Homo sapiens cDNA clone IMAGE:1562566 3'
910	13523	26043	1.75	4.0E-03	R46482.1	EST_HUMAN	y651a04.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35988 3'
944	13557		3.19	4.0E-03	AW749101.1	EST_HUMAN	RC3-BT03333-110100-012-101 BT0333 Homo sapiens cDNA
1190	13791	26302	25.91	4.0E-03	AA099777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
1211	13811	26325	1.71	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA
1346	13941	26463	1.4	4.0E-03	AA284374.1	EST_HUMAN	zs59a01.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701736 5'
1630	14222		1.06	4.0E-03	AV708305.1	EST_HUMAN	AV708305 ADC Homo sapiens cDNA clone ADCAKB06 5'
1779	14369	26913	2.74	4.0E-03	U33472.1	NT	Rattus norvegicus type 1 astrocyte and olfactory-limbic associated protein AT1-48 mRNA, complete cds
2062	14642	27217	14.12	4.0E-03	AA099777.1	EST_HUMAN	z81a08.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:510998 5'
2289	14863		1.82	4.0E-03	BE410556.1	EST_HUMAN	601304181F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638510 5'
2317	14889	27464	2.63	4.0E-03	AW794740.1	EST_HUMAN	RC6-UM0014-170400-023-G01 UM0014 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2608	15170	27737	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein >
2608	15170	27738	1.6	4.0E-03	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenergic dystrophy protein >
2715	15272	27838	3.14	4.0E-03	AJ277365.1	NT	CDM protein (CDM), adrenergic dystrophy protein >
2715	15272	27839	3.14	4.0E-03	AJ277365.1	NT	Homo sapiens polyglutamine-containing C14ORF4 gene
2721	15277	27842	1.25	4.0E-03	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
3262	15874	28355	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151298-003-H08 HT0340 Homo sapiens cDNA
3262	15874	28356	1.07	4.0E-03	BE154134.1	EST_HUMAN	PM1-HT0340-151298-003-H08 HT0340 Homo sapiens cDNA
3583	16187	28669	0.85	4.0E-03	AW188426.1	EST_HUMAN	xp8804.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3583	16187	28670	0.85	4.0E-03	AW188426.1	EST_HUMAN	xp8804.x1 NCL CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2665279 3'
3685	16286	28755	0.63	4.0E-03	Q13606	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
3698	16297	28767	0.63	4.0E-03	AV646253.1	EST_HUMAN	AV646253 GLC Homo sapiens cDNA clone GLCADO2 3'
4067	16863		1.93	4.0E-03	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
4323	16909	29350	1.88	4.0E-03	A1766727.1	EST_HUMAN	w187a06.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2614469 3' similar to contains L1.11 L1
5307	17869	30291	2.1	4.0E-03	AW103719.1	EST_HUMAN	x883d03.x1 NCL CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2400274 3'
5354	17914	30329	1.17	4.0E-03	AA699895.1	EST_HUMAN	L1 repetitive element
5433	17989	30395	1.19	4.0E-03	AL163284.2	NT	269b01.s1 Soares_fetal_liver_spleen_1NELS_S1 Homo sapiens cDNA clone IMAGE:436009 3'
5480	18114	30523	1.36	4.0E-03	AF005859.1	NT	Homo sapiens chromosome 21 segment HS21C084
5596	18228	30873	21.16	4.0E-03	AF189825.1	NT	Drosophila melanogaster anon2D7 (anon2D7) mRNA, complete cds
5963	18585	31319	3.31	4.0E-03	P04196	SWISSPROT	Rattus norvegicus beta-catenin binding protein mRNA, complete cds
5965	18587	31321	1.56	4.0E-03	P21849	SWISSPROT	(HPRG)
6042	18661	31400	0.97	4.0E-03	AL133871.1	EST_HUMAN	MAJOR SURFACE-LABELED TROPHOZOITE ANTIGEN PRECURSOR
6235	18844		3.41	4.0E-03	U22180.1	NT	DKFZp7611014_f1 761 (synonym: hemy2) Homo sapiens cDNA clone DKFZp7611014 5'
6381	18985	31765	0.98	4.0E-03	AW680572.1	EST_HUMAN	Rattus norvegicus opsin gene, complete cds
6451	19052	31837	1.95	4.0E-03	BE548453.1	EST_HUMAN	hg48c07.x1 NCL CGAP_G06 Homo sapiens cDNA clone IMAGE:2948652 3'
6775	19367	32179	1.04	4.0E-03	AA813222.1	EST_HUMAN	601076016F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
6872	19606	32440	1.51	4.0E-03	U76408.1	NT	601076016F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
7130	19470	32288	1.13	4.0E-03	AL163278.2	NT	601076016F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
7130	19470	32289	1.13	4.0E-03	AL163278.2	NT	601076016F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3461954 5'
7249	19778	32633	5.45	4.0E-03	Q02817	SWISSPROT	Lycopodium obscurum knotted 3 protein (TKn3) mRNA, complete cds
							Homo sapiens chromosome 21 segment HS21C078
							Homo sapiens chromosome 21 segment HS21C078
							MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2)

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7459	19982	32847	1.14	4.0E-03	AI681483.1	EST_HUMAN	bc37g12.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2271814 3'
7461	19984	32849	0.95	4.0E-03	BE670170.1	EST_HUMAN	7c31b02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284043 3'
7883	20425	33334	0.63	4.0E-03	Q9T192	SWISSPROT	ADAM-TS 5(A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 5)
7992	20534	33438	4.22	4.0E-03	AF111944.1	NT	(ADAMTS-5) (ADAM-TS5) (AGGRECANASE-2) (ADMP-2) (ADAM-TS 11)
8145	20686	33598	1.94	4.0E-03	7682067	NT	Dictyostellium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds
8648	21187	34105	6.89	4.0E-03	AI553983.1	EST_HUMAN	Homo sapiens KIA0345 gene product (KIA0345), mRNA
8821	21360		4.46	4.0E-03	AL163209.2	NT	te49b11.x1 Soares_NFL_T_GBC_31 Homo sapiens cDNA clone IMAGE:2090013 3' similar to contains Alu repetitive element
8830	21369	34293	3.12	4.0E-03	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C009
9840	22338	35319	0.78	4.0E-03	H30664.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
10278	22773	35762	0.7	4.0E-03	AL161555.2	NT	yp42g12.1 Soares retina N265HR Homo sapiens cDNA clone IMAGE:190150 5'
11009	23523	36557	6.06	4.0E-03	AL163206.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 55
11393	23845	36909	1.69	4.0E-03	AI208703.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C008
11393	23845	36910	1.69	4.0E-03	AI208703.1	EST_HUMAN	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11607	24050	37116	1.62	4.0E-03	AE002102.1	NT	qg56c05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1839178 3'
11938	25071		10.45	4.0E-03	BE815173.1	EST_HUMAN	Ureaplasma urealyticum section 3 of 59 of the complete genome
11982	24284		1.62	4.0E-03	BE288290.1	EST_HUMAN	PM4-BN0138-180600-002-b08 BN0138 Homo sapiens cDNA
12047	24331		2.71	4.0E-03	AW504273.1	EST_HUMAN	601118164F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028095 5'
12294	24493		3.86	4.0E-03	BF224125.1	EST_HUMAN	UIHF-BN0-alp-g-04-0-UIr1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080622 5'
12341	24975		2.24	4.0E-03	AW614598.1	EST_HUMAN	7q74c09.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains Alu repetitive element; contains element MER31 repetitive element;
12352	24532		3.01	4.0E-03	AW819141.1	EST_HUMAN	hh02c07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953932 3' similar to contains element LTR5 repetitive element;
394	13040	25531	1.73	3.0E-03	AF011920.1	NT	RC3-ST0281-240400-015-f03 ST0281 Homo sapiens cDNA
912	13525	26044	5.57	3.0E-03	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
1701	14294	26829	2.85	3.0E-03	AA468110.1	EST_HUMAN	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
2298	14871		1.76	3.0E-03	AF055066.1	NT	nc73c05.s1 NCI CGAP_P22 Homo sapiens cDNA clone IMAGE:762984 similar to contains Alu repetitive element;
2333	14904		4.14	3.0E-03	Z32521.1	NT	Homo sapiens MHC class 1 region
2334	14905	27475	1.03	3.0E-03	U46858.1	NT	S.cereale (cv. Halo) mRNA for triosephosphate isomerase
2334	14805	27476	1.03	3.0E-03	U46858.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
2448	15015	27587	1.13	3.0E-03	AF240789.1	NT	Mus musculus intestinal trefoil factor gene, partial cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3022	15638		0.68	3.0E-03	Y08006.1	NT	Arabidopsis thaliana rpoMt gene
3119	15733	28203	3.25	3.0E-03	BE379296.1	EST_HUMAN	601237882.F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3809933 5'
3186	15768	28270	3.21	3.0E-03	AW802887.1	EST_HUMAN	IL2-UM0076-240300-058-D03 UM0076 Homo sapiens cDNA
3464	16071	28544	2.13	3.0E-03	U34606.1	NT	Mus musculus alpha-1(XVII) collagen (COL18A1) gene, exon 1 and 2
3473	16079		7.31	3.0E-03	Y12500.1	NT	C. elegans samdc gene
4049	16846	28114	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4049	16846	28115	7.57	3.0E-03	AV762392.1	EST_HUMAN	AV762392 MDS Homo sapiens cDNA clone MDSBSG01 5'
4109	16703	28158	1.75	3.0E-03	AI792278.1	EST_HUMAN	ah04109.y6 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1155689 5'
4485	17070	28520	6.2	3.0E-03	AJ011432.1	NT	Rattus norvegicus gdnf gene
4560	17143		0.71	3.0E-03	BE348739.1	EST_HUMAN	h168g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151934 3'
4616	17169	28647	5.73	3.0E-03	AI536141.1	EST_HUMAN	ab18a08.x5 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:841142 3' similar to contains Alu repetitive element
4960	17535	29977	2.45	3.0E-03	AI732754.1	EST_HUMAN	
4979	17553	29695	6.1	3.0E-03	BE787945.1	EST_HUMAN	601482715F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3885483 5'
5069	17642	30084	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus cuniculus sod gene
5069	17642	30085	1.01	3.0E-03	AJ007044.1	NT	Oryctolagus cuniculus sod gene
5470	18104	30423	3.56	3.0E-03	8922499	NT	Homo sapiens hypothetical protein FLJ10539 (FLJ10539), mRNA
5744	18370	31078	1.18	3.0E-03	AJ249681.1	NT	Mus musculus mRNA for hypothetical protein (ORF2 ortholog)
5809	18434	31155	13.97	3.0E-03	U35323.1	NT	Mb1) gene, low molecular weight protein 2 Lmp2 (Lmp2) gene, complete cds
6670	19268	32070	10.41	3.0E-03	AA456701.1	EST_HUMAN	601310.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:813163 5'
7256	19784	32640	1.45	3.0E-03	AJ011419.1	NT	Kluyveromyces fragilis pcp3 gene for purine-cytosine permease
7531	20051	32624	3.37	3.0E-03	AB021736.1	NT	Oryza sativa gene for bZIP protein, complete cds
7879	20421	33329	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
7879	20421	33330	0.91	3.0E-03	BF333058.1	EST_HUMAN	RC0-BT0812-250900-032-e07 BT0812 Homo sapiens cDNA
8097	20638	33549	4.71	3.0E-03	N92580.1	EST_HUMAN	z527804.s1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:304783 3'
8257	20708		0.55	3.0E-03	M63408.1	NT	S. cerevisiae UGA35 gene, complete cds
8397	20937	33660	1.11	3.0E-03	P57689	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
8419	20959	33877	1.31	3.0E-03	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
8522	21061		1.37	3.0E-03	QBQM81	SWISSPROT	NONSTRUCTURAL PROTEIN V
8922	21460		12.62	3.0E-03	AW613774.1	EST_HUMAN	h180710.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2869131 3' similar to contains L1.t1 L1 repetitive element
8975	21513	34436	4.44	3.0E-03	AL161589.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 85

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8999	21536	34468	0.98	3.0E-03	AI016731.1	EST_HUMAN	ov03d12.x1 NCI CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1636247 3' similar to gb:X57138_mna1
9008	21545	34474	0.92	3.0E-03	BF338078.1	EST_HUMAN	HISTONE H2B.2 (HUMAN);
9330	21844		1	3.0E-03	D90901.1	NT	602035980F1 NCI CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4183938 5'
9368	20307	33210	0.66	3.0E-03	BE154670.1	EST_HUMAN	Synechocystis sp. PCC6803 complete genome, 3/27, 271600-402289
9554	22054		0.67	3.0E-03	P03355	SWISSPROT	PM3-HT0344-071-289-003-007 HT0344 Homo sapiens cDNA
9623	22123		5.92	3.0E-03	P08672	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
							CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
							RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE;
							ENDONUCLEASE]
9809	22307	35291	1.58	3.0E-03	P11389	SWISSPROT	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2 HOMOLOG 1 (HNRNP A2(A))
9907	22404	35379	1.3	3.0E-03	P51989	SWISSPROT	Homo sapiens chromosome 21 segment HS21C103
10046	22541	35538	3.96	3.0E-03	AL163303.2	NT	Homo sapiens ATP/GTP-binding protein (HEAB), mRNA
10728	23254		4.26	3.0E-03	5803028	NT	Homo sapiens ATPI/GTP-binding protein (HEAB), mRNA
11257	23787	36843	2.21	3.0E-03	AF009222.1	NT	Pneumocystis carinii kexin-like serine endoprotease mRNA, partial cds
11321	23019	36028	1.99	3.0E-03	AF266285.1	NT	Homo sapiens gadin-like protein (GLP) gene, complete cds
11354	23808	36867	3.96	3.0E-03	AF094491.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11354	23808	36868	3.96	3.0E-03	AF094491.1	NT	Homo sapiens trinucleotide repeat DNA binding protein p20-CGGBP (CGGBP) gene, complete cds
11707	24869		2.32	3.0E-03	AI525056.1	EST_HUMAN	promRNA-5.E07.r bvtumor Homo sapiens cDNA 5'
							at77b10.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622779 3' similar to
							contains L1.t3 MER26 repetitive element:
11743	24142	36763	1.31	3.0E-03	AA983154.1	EST_HUMAN	Homo sapiens gene for GMP-N-acetylneuraminic acid hydroxylase, partial cds
11804	25007		1.81	3.0E-03	AB009688.1	NT	Rattus norvegicus mRNA for connexin36 (cx36 gene)
11988	24288	30884	2.67	3.0E-03	AJ296282.1	NT	RING CANAL PROTEIN (KELCH PROTEIN)
541	13172	25651	0.8	2.0E-03	Q04652	SWISSPROT	RING CANAL PROTEIN (KELCH PROTEIN)
541	13172	25652	0.8	2.0E-03	Q04652	SWISSPROT	yd15h03.t1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:108341 5'.
818	15426		11.05	2.0E-03	T70874.1	EST_HUMAN	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1407	14000	26529	2.25	2.0E-03	M20783.1	NT	Human alpha-2-plasmin inhibitor gene, exons 6 and 7
1410	14003	26531	1.35	2.0E-03	AJ4661605.1	EST_HUMAN	nu8601.s1 NCI CGAP_AVI1 Homo sapiens cDNA clone IMAGE:1217563
1418	14011	26540	20.96	2.0E-03	AF284446.1	NT	Homo sapiens tumor-related protein DRC2 (DRC2) gene, complete cds
							PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN
							SFA-1) (CD151 ANTIGEN)
1536	14128	26664	1.04	2.0E-03	P48509	SWISSPROT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
							type VI) (PLOD) mRNA
1563	14155	26686	2.05	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
							type VI) (PLOD) mRNA
1563	14155	26687	2.05	2.0E-03	4557836	NT	Homo sapiens procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome
1635	14227		5.58	2.0E-03	P28400	SWISSPROT	COLLAGEN ALPHA 5(V) CHAIN PRECURSOR

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1807	14397	26942	1.01	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares, total, fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
1922	14507		0.89	2.0E-03	BE144808.1	EST_HUMAN	CM2-HT0183-061099-018-d03 HT0183 Homo sapiens cDNA
2038	14620	27188	1.25	2.0E-03	AF302691.1	NT	Mus musculus myelin expression factor-3-like protein gene, partial cds
2281	14865	27440	0.97	2.0E-03	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
2615	15177		4.13	2.0E-03	AW137782.1	EST_HUMAN	UI-H-B11-adi-g-10-Q-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717010 3'
3463	16070	28543	4.95	2.0E-03	AA450138.1	EST_HUMAN	z42a10.r1 Soares, total, fetus Nb2HF8_9w Homo sapiens cDNA clone IMAGE:789114 5'
3470	16076	28549	0.76	2.0E-03	BF568955.1	EST_HUMAN	602183960T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300070 3'
3729	16330	28766	5.87	2.0E-03	X67344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
4024	16622	29094	0.89	2.0E-03	AB040802.1	NT	Rattus norvegicus mRNA for SREB1, complete cds
4191	16780	29228	2.48	2.0E-03	P03374	SWISSPROT	ENV POLYPEPTIDE [CONTAINS: COAT PROTEIN GP52; COAT PROTEIN GP36]
4302	16888		12.85	2.0E-03	U68491.1	NT	Rattus norvegicus 5-hydroxytryptamine7 receptor gene, partial cds
4502	17086		1.09	2.0E-03	L35079.1	NT	Porcine rotavirus major outer capsid protein (VP7) mRNA, complete cds
4518	17102		1.34	2.0E-03	AW297380.1	EST_HUMAN	UI-H-BW0-air-g-03-Q-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2730413 3'
4523	17107	29553	0.98	2.0E-03	AI064746.1	EST_HUMAN	HA0507 Human fetal liver cDNA library Homo sapiens cDNA
4644	17226	29680	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shorttailed class 2 (shs) mRNA, complete cds
4644	17226	29681	1.82	2.0E-03	L42512.1	NT	Drosophila melanogaster shorttailed class 2 (shs) mRNA, complete cds
4821	17369		1.92	2.0E-03	R87773.1	EST_HUMAN	y045a02.s1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:180890 3'
4848	17426	29678	5.2	2.0E-03	AA909466.1	EST_HUMAN	at1405.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1523457 3'
5187	17736	30163	0.81	2.0E-03	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5428	17985		0.9	2.0E-03	AF205067.1	NT	Desulfotribio desulfuricans cytochrome c3 precursor (cycA) gene, complete cds
5678	18305	30787	1.16	2.0E-03	BF241410.1	EST_HUMAN	601876385F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4104692 5'
5810	24749	31156	2.28	2.0E-03	AB014593.1	NT	Homo sapiens mRNA for KIAA0693 protein, partial cds
5887	18510	31238	2.11	2.0E-03	U63711.1	NT	Xenopus laevis xefillin mRNA, complete cds
6258	18867	31637	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6258	18867	31637	4.06	2.0E-03	P23477	SWISSPROT	ATP-DEPENDENT NUCLEASE SUBUNIT B
6483	19087	31869	2.38	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6488	19087	31870	2.38	2.0E-03	Q95203	SWISSPROT	CARBONIC ANHYDRASE-RELATED PROTEIN 2 PRECURSOR (CARP 2) (CA-XP II) (CA-XI)
6488	19089	31872	7	2.0E-03	BF308187.1	EST_HUMAN	601887434F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4121408 5'
6521	19121	31912	2.17	2.0E-03	Q8UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
6546	19144	31940	1.46	2.0E-03	X94451.1	NT	L. esculentum mRNA for lysyl-tRNA synthetase (LysRS)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6715	19309		2.03	2.0E-03	AB91089.1	EST_HUMAN	wu36h09.x1 Soares Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522177 3' similar to SW:RL29 HUMAN P47914 60S RIBOSOMAL PROTEIN L29; contains element MSR1 repetitive element ;
7038	18058	30480	0.99	2.0E-03	AB038502.1	NT	Caenorhabditis elegans mRNA for galectin LEC-11, complete cds
7104	19674	32513	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
7104	19674	32514	1.54	2.0E-03	5031864	NT	Homo sapiens lipoma HMGIC fusion partner (LHFP) mRNA
7141	19521	32343	3.59	2.0E-03	BE067986.1	EST_HUMAN	OM4-BT0366-061299-054-d01 BT0366 Homo sapiens cDNA
7188	19729	32580	0.7	2.0E-03	A1298883.1	EST_HUMAN	gm99d11.x1 NCI_OGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896885 3'
7335	19862	32728	0.87	2.0E-03	T86569.1	EST_HUMAN	yd77g10.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:114306 5'
7613	20126	33003	1.49	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
7985	20537	33440	2.47	2.0E-03	AW592004.1	EST_HUMAN	h37b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2834035 3' similar to TR:Q60976 Q60976 JERKY. ;
8159	20700	33614	5.96	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8159	20700	33615	5.96	2.0E-03	N20287.1	EST_HUMAN	yx42g08.s1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:264442 3' similar to contains L1.b2 L1 repetitive element ;
8208	20749	33662	0.52	2.0E-03	Q92350	SWISSPROT	HYPOTHETICAL 328 KD PROTEIN O8G9.05 IN CHROMOSOME I
8228	20769	33668	0.94	2.0E-03	P19137	SWISSPROT	LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN)
8282	20823	33743	0.82	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8282	20823	33744	0.82	2.0E-03	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
8307	20848	33771	0.8	2.0E-03	AU136879.1	EST_HUMAN	AU136879 PLACE1 Homo sapiens cDNA clone PLACE1004839 5'
8358	20898		2.04	2.0E-03	AJ400877.1	NT	Homo sapiens ASC1.3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
8123	18508	31233	0.69	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
8123	18508	31234	0.69	2.0E-03	AW798111.1	EST_HUMAN	MR2-UM0025-300300-102-f02 UM0025 Homo sapiens cDNA
9164	21699	34843	0.85	2.0E-03	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9445	21871	34920	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194296 3'
9445	21871	34921	0.99	2.0E-03	H50832.1	EST_HUMAN	yp86a09.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:194296 3'
							TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (GMEW) (JI) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C) (TN-C)
9477	21876	34823	2.57	2.0E-03	P24821	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35049	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)
9585	22085	35050	1.03	2.0E-03	P48982	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE)

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9639	22139	35105	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9639	22139	35108	0.54	2.0E-03	AF097732.1	NT	Homo sapiens caspase recruitment domain-containing protein (BCL10) gene, complete cds
9829	22327	35308	0.99	2.0E-03	AW884288.1	EST_HUMAN	QV3-OT0084-060400-144-601 OT0084 Homo sapiens cDNA
9855	22450		4.55	2.0E-03	AA251378.1	EST_HUMAN	Zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3'
10894	23415		3.24	2.0E-03	M89524.1	NT	Human dystrophin gene
11361	20126	33003	2.13	2.0E-03	P07354	SWISSPROT	PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP)
11417	23868		2.25	2.0E-03	BF330909.1	EST_HUMAN	RC3-BT0333-310800-115-g04 BT0333 Homo sapiens cDNA
11424	23875	36939	13.97	2.0E-03	Z11740.1	NT	H. sapiens variable number tandem repeat (VNTR) locus DNA
11687	24103		3.17	2.0E-03	A625745.1	EST_HUMAN	Y65H03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283989 3' similar to SW:VATG_MANSE
11705	24118	37151	4.77	2.0E-03	AF157516.2	NT	Q25532 VACUOLAR ATP SYNTHASE SUBUNIT G ; Homo sapiens SEL1L (SEL1L) gene, partial cds
11730	24135	37155	1.94	2.0E-03	A084325.1	EST_HUMAN	043g06.s1 Soares_parathyroid_tumor_NHPPA Homo sapiens cDNA clone IMAGE:1668634 3' similar to TR:P97535 P97535 PS-PLA1 PRECURSOR ;
11754	18032		8.98	2.0E-03	AJ245187.1	NT	Camelus dromedarius cvhp19 gene for immunoglobulin heavy chain variable region
11967	25050		2.34	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCGXD05 5'
12062	24345	30964	1.49	2.0E-03	Y00508.1	NT	H. sapiens M1 gene for muscarinic acetylcholine receptor
12372	24542		2.06	2.0E-03	AF129756.1	NT	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
12551	24849		5.07	2.0E-03	AV697968.1	EST_HUMAN	AV697968 GKC Homo sapiens cDNA clone GKCGXD05 5'
464	13088	25589	1.33	1.0E-03	H98471.1	EST_HUMAN	Y68c08.r1 Soares_pitneal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232334 5'
862	13477	25992	1.47	1.0E-03	A1720263.1	EST_HUMAN	as70p08.x1 Barstead cdon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
862	13477	25993	1.47	1.0E-03	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE ;
1134	13737	26246	2.21	1.0E-03	A1865788.1	EST_HUMAN	Q13825 AU-BINDING PROTEINENYOYL-COA HYDRATASE ;
1154	13757	26267	1.31	1.0E-03	A1854572.1	EST_HUMAN	wk96a06.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2422258 3'
1208	13808	26321	1.87	1.0E-03	A1692616.1	EST_HUMAN	wk96a01.x1 NCI_CGAP_Maf15 Homo sapiens cDNA clone IMAGE:2651242 3'
2074	14654	27227	4.05	1.0E-03	P47808	SWISSPROT	wk96a01.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2338440 3' similar to contains Alu repetitive element;
2199	14775	27348	9.99	1.0E-03	AJ131018.1	NT	HIGH MOLECULAR WEIGHT FORM OF MYOSIN I (HMYWI)
3008	15624	28102	1.45	1.0E-03	AB033117.1	NT	Homo sapiens SCL gene locus Homo sapiens mRNA for KIAA1291 protein, partial cds
3225	15837	28315	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3225	15837	28316	1.81	1.0E-03	P18915	SWISSPROT	CARBONIC ANHYDRASE VI PRECURSOR (CARBONATE DEHYDRATASE VI) (CA-VI) (SECRETED CARBONIC ANHYDRASE) (SALIVARY CARBONIC ANHYDRASE)
3341	15951	28427	0.79	1.0E-03	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
3596	16200	28683	0.65	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3596	16200	28684	0.65	1.0E-03	U68061.1	NT	Human MUC2 gene, promoter region
3727	16328		1.31	1.0E-03	AB044400.1	NT	Homo sapiens SVMT gene for synaptic vesicle monoamine transporter, exons 14, 15
3997	16595	29067	0.75	1.0E-03	AW170552.1	EST_HUMAN	nt63d07.x1 Soares_NHCeC_cervical_tumor Homo sapiens cDNA clone IMAGE:2698381 3' similar to contains TAR1.11 TART repetitive element;
4008	16606	29080	0.81	1.0E-03	Z49649.1	NT	S cerevisiae chromosome X reading frame ORF YJR149w
4528	17112	29558	4.29	1.0E-03	BE939162.1	EST_HUMAN	RC1-TN0128-160800-021-g01 TN0128 Homo sapiens cDNA
4574	17157	29601	5.77	1.0E-03	BE246536.1	EST_HUMAN	TCBAP1D4909 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4909
4770	17351	29803	0.83	1.0E-03	U29449.1	NT	Caenorhabditis elegans spliced leader RNA (SL3 alpha), (SL4), and (SL5) genes
4950	17525	29968	2.83	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4950	17525	29967	2.83	1.0E-03	A1073485.1	EST_HUMAN	ov45c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640262 3'
4951	17528		5.92	1.0E-03	BE154067.1	EST_HUMAN	PMO-HT0339-200400-010-D02 HT0339 Homo sapiens cDNA
5236	17800	30219	11.45	1.0E-03	O48409	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
5511	18144	30556	2.02	1.0E-03	AA290951.1	EST_HUMAN	Zs44f01.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:700345 5'
5598	18228	30876	2.74	1.0E-03	AJ006345.1	NT	Homo sapiens KVLQ11 gene
5647	18275	30749	1.7	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5647	18275	30750	1.7	1.0E-03	K03332.1	NT	Epstein-Barr virus (AG876 isolate) U2-IR2 domain encoding nuclear protein EBNA2, complete cds
5761	18387	31101	0.92	1.0E-03	BE796491.1	EST_HUMAN	601589841F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943954 5'
5768	18392	31105	1.72	1.0E-03	Q02388	SWISSPROT	COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN)
6171	18783		2.62	1.0E-03	X07699.1	NT	Mouse nucleolin gene
6209	18819	31590	1.1	1.0E-03	BE963339.2	EST_HUMAN	601657519R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875693 3'
6339	18945		8.29	1.0E-03	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6478	19077	31860	1.21	1.0E-03	T87761.1	EST_HUMAN	yd83a11.1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:115772 5'
6541	19140		1.4	1.0E-03	AW902595.1	EST_HUMAN	QV3-NN1024-260400-171-g05 NN1024 Homo sapiens cDNA
6852	19441	32256	1.31	1.0E-03	L77570.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
7208	19737	32590	2.48	1.0E-03	D18626.1	NT	Human gene for fourth somatostatin receptor subtype
7498	20021		1.72	1.0E-03	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
							Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase 1 (CAMK1), creatine transporter (CRT), CDM protein (CDM), adrenoleukodystrophy protein >
7635	20147	33030	1.7	1.0E-03	U52111.2	NT	

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7694	20203	33080	3.21	1.0E-03	M63376.1	NT	Human TRPM-2 protein gene, exons 1,2 and 3
7734	20242	33133	1.13	1.0E-03	BE880044.1	EST_HUMAN	601491081F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893278 5'
7830	20372	33279	0.57	1.0E-03	AF274581.1	NT	Homo sapiens prolactin-releasing peptide receptor gene, 5' flanking region
7881	20433	33342	6.78	1.0E-03	AJ251973.1	NT	Homo sapiens partial steerin-1 gene
8086	20627	33541	1.29	1.0E-03	AA122270.1	EST_HUMAN	z897c09.s1 Soares_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:480768 3' similar to contains L1.t1 L1 repetitive element
8186	20727	33639	2.03	1.0E-03	AF153980.1	NT	Homo sapiens exostose-like protein 1 (EXTL1) gene, exons 2 through 11, and complete cds
8389	20909	33828	0.81	1.0E-03	U28397.1	NT	Rattus norvegicus plasma membrane Ca ²⁺ ATPase isoform 3 (PMCA3) gene, 5' flanking region
8530	21069	33988	0.52	1.0E-03	AA001613.1	EST_HUMAN	zh82e08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8530	21069	33989	0.52	1.0E-03	AA001613.1	EST_HUMAN	zh82e08.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:427810 3'
8873	21412		1.29	1.0E-03	Y11204.1	NT	V.carteri gene encoding volvoxapain
8900	21438	34361	0.59	1.0E-03	AW840353.1	EST_HUMAN	GM3-L1T0079-170200-092-507 L1T0079 Homo sapiens cDNA
9009	21546						Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca ²⁺ /Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
9047	21584	34514	0.68	1.0E-03	U52111.2	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9047	21584	34515	3.37	1.0E-03	M30471.1	NT	Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds
9525	22025	34982	1.96	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (ega1A) gene, complete cds
9525	22025	34983	1.96	1.0E-03	AF011400.1	NT	Thermotoga neapolitana alpha-1,6-galactosidase (ega1A) gene, complete cds
9734	22232	35210	0.94	1.0E-03	Q01129	SWISSPROT	BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG)
10088	22563	35558	0.57	1.0E-03	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
10073	22568		0.75	1.0E-03	AF097485.1	NT	Homo sapiens transducin beta-like 2 (TBL2) gene, complete cds
10218	22713	35705	1.25	1.0E-03	A024350.1	EST_HUMAN	ov75709.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643175 3' similar to contains MER39 b1
10545	23082	36095	1.71	1.0E-03	AW362393.1	EST_HUMAN	MER39 MER39 repetitive element
10545	23082	36096	1.71	1.0E-03	AW362393.1	EST_HUMAN	RC1-CT0279-181098-011-409 CT0279 Homo sapiens cDNA
10629	23161	36173	3.2	1.0E-03	BE170859.1	EST_HUMAN	RC1-CT0279-181098-011-409 CT0279 Homo sapiens cDNA
10703	23232		3.19	1.0E-03	A1583847.1	EST_HUMAN	QV3-HT0543-220300-130-503 HT0543 Homo sapiens cDNA
11036	23550		3.78	1.0E-03	AV759949.1	EST_HUMAN	tt73e12.x1 NCI_OGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246446 3' similar to TR:Q26195 Q26195 PVA1 GENE
11082	24099	37149	4.46	1.0E-03	BE894488.1	EST_HUMAN	AV759949 MDS Homo sapiens cDNA clone MDSDDF11 5'
12149	24392	30974	1.27	1.0E-03	9507203	NT	AV759949 MDS Homo sapiens cDNA clone IMAGE:3918524 5'
							Rattus norvegicus transformation related protein 63 (Trp63), mRNA

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12175	25030		5.89	1.0E-03	A1347355.1	EST_HUMAN	tc05h11.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2063013 3' similar to contains Alu repetitive element
12292	25052	30510	5.72	1.0E-03	BE780572.1	EST_HUMAN	601468878F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872035 5'
5862	18484		1.63	9.0E-04	P06727	SWISSPROT	APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV)
6612	19209	32017	1.08	9.0E-04	P02381	SWISSPROT	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1
9561	22061		1.56	9.0E-04	A8037203.1	NT	Glucyrrhiza glabra GgbA1 mRNA for beta-amylin synthase, complete cds
1636	14127		1.05	8.0E-04	X98469.1	NT	Xlaevis mRNA for C4SR protein
4259	16845		5.17	8.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4880	17455	28908	2.55	8.0E-04	U28185.1	NT	Homo sapiens p10n protein (P1P) gene, complete cds
11024	23538		2.15	8.0E-04	AA777084.1	EST_HUMAN	z24c10.s1 Scores. fetal heart_NbH19W Homo sapiens cDNA clone IMAGE:377874 3'
11175	23682		2.5	8.0E-04	A1571089.1	EST_HUMAN	tr55e08.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:2176310 3'
12500	24626	30892	1.65	8.0E-04	AW578954.1	EST_HUMAN	PM2-HT0353-130100-002-f10 HT0353 Homo sapiens cDNA
1867	14453	27012	0.99	7.0E-04	L1825.1	NT	Homo sapiens CYP17 gene, 5' end
2442	15009	27581	0.92	7.0E-04	U28185.1	NT	Homo sapiens p10n protein (P1P) gene, complete cds
2739	15284	27881	1.75	7.0E-04	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3319	15929	28406	1.23	7.0E-04	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
6246	18555	31626	0.75	7.0E-04	AA516212.1	EST_HUMAN	ng65g12.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:939718 similar to contains L1.B3 L1 L1 repetitive element
6636	19232		2.63	7.0E-04	A1769331.1	EST_HUMAN	hg36f09.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
7279	19807		0.79	7.0E-04	AK024445.1	NT	Homo sapiens mRNA for FLJ00035 protein, partial cds
9719	22217	35191	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
9719	22217	35192	0.57	7.0E-04	P13497	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
11440	23690		3.42	7.0E-04	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
11463	23913	36980	2.68	7.0E-04	Z40561.1	EST_HUMAN	HSC28A072 normalized infant brain cDNA Homo sapiens cDNA clone c-28a07 3'
12222	24443		11.57	7.0E-04	BE077941.1	EST_HUMAN	CM1-BT0814-110300-142-BT2 BT0814 Homo sapiens cDNA
12472	24597		4.94	7.0E-04	R17336.1	EST_HUMAN	yg13c06.r1 Scores infant brain 1N1B Homo sapiens cDNA clone IMAGE:32298 5'
12505	24628		7.97	7.0E-04	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
2720	15276		0.93	6.0E-04	BF341380.1	EST_HUMAN	602013339F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4149297 5'
4033	16631	29100	1.61	6.0E-04	A1862525.1	EST_HUMAN	Wt15a11.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402876 3'
4163	16754	29205	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4163	16754	29208	0.6	6.0E-04	K01315.1	NT	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, 5' flanking region
4264	16850	29298	3.2	6.0E-04	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
4538	17122	29567	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-109 HT0560 Homo sapiens cDNA

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4538	17122	29568	0.93	6.0E-04	BE173435.1	EST_HUMAN	RC2-HT0560-190200-011-109 HT0560 Homo sapiens cDNA
5413	17970	30379	0.9	6.0E-04	A1906667.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
5413	17970	30380	0.9	6.0E-04	A1906667.1	EST_HUMAN	RC-BT122-180399-057 BT122 Homo sapiens cDNA
7807	20350		3.04	6.0E-04	P46408	SWISSPROT	GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE (FRUCTOSE TRANSPORTER)
7958	20500		0.67	6.0E-04	H92947.1	EST_HUMAN	y94c11.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:231956 3' similar to contains LOR1 repetitive element;
9890	22387		3.74	6.0E-04	AL048507.2	EST_HUMAN	DKFZ586M2024_r1 586 (synonym: huter1) Homo sapiens cDNA clone DKFZ586M2024
9924	22420		0.77	6.0E-04	A1858286.1	EST_HUMAN	w35g02.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2426930 3'
9992	22487	35475	2.18	6.0E-04	BE005850.1	EST_HUMAN	RC2-BN0120-250400-012-h11 BN0120 Homo sapiens cDNA
10242	22737		0.64	6.0E-04	AF287478.1	NT	Lytechinus variegatus embryonic blastocoele extracellular matrix protein precursor (ECM3) mRNA, complete cds
11358	23812	36872	2.9	6.0E-04	AJ228042.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 2/3
11441	23891	36956	5.11	6.0E-04	AW013847.1	EST_HUMAN	U1-H-B10-aab-e-09-0-U1.s1 NCL CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
11495	23944		2.28	6.0E-04	Q01768	SWISSPROT	NUCLEOSIDE DIPHOSPHATE KINASE B (NDK B) (NDP KINASE B) (NM23-M2) (P18)
11869	24928		3.55	6.0E-04	AW380519.1	EST_HUMAN	RC1-HT0289-281199-012-408 HT0289 Homo sapiens cDNA
12671	24739		1.61	6.0E-04	A1817088.1	EST_HUMAN	w176g11.x1 NCL CGAP_Lu18 Homo sapiens cDNA clone IMAGE:2408804 3' similar to contains element L1 repetitive element;
679	13303	25785	8.64	5.0E-04	O10341	SWISSPROT	HYPOTHETICAL 28.3 KD PROTEIN (ORF92)
1549	14141		1.68	5.0E-04	AW851844.1	EST_HUMAN	QV0-CT0225-021099-030-a07 CT0225 Homo sapiens cDNA
3460	16067	28540	1.53	5.0E-04	AA548631.1	EST_HUMAN	nk27e11.s1 NCL CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014764 3' similar to contains Alu repetitive element;
3778	16378	28843	1.02	5.0E-04	Q9UKP4	SWISSPROT	ADAM-TS 7 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 7) (ADAMTS-7) (ADAM-TS7)
5664	18291	30770	1.98	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6740	19334	32141	6.37	5.0E-04	AA156080.1	EST_HUMAN	z033b08.r1 Streptagene cdon (#937204) Homo sapiens cDNA clone IMAGE:588663 5'
7411	19336	32801	16.91	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
7898	20440	33346	4.97	5.0E-04	A1188382.1	EST_HUMAN	qd13f06.x1 Soares_placenta_8to6weeks_2NbHP8c9W Homo sapiens cDNA clone IMAGE:1723619 3' similar to gb:X51602_cds1 VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 1 (HUMAN); contains Alu repetitive element;
8245	20786	33705	0.91	5.0E-04	AA814519.1	EST_HUMAN	ab96e02.s1 NCL CGAP_GCBT1 Homo sapiens cDNA clone IMAGE:1339226 3' similar to contains element MER22 repetitive element;
9201	21718	34662	1.37	5.0E-04	AA846545.1	EST_HUMAN	dj56h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1394357 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9293	21893	34840	0.6	5.0E-04	N83765.1	EST_HUMAN	KK2745F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone KK2745 5' similar to REPETITIVE ELEMENT
9437	21963	34912	0.65	5.0E-04	P29126	SWISSPROT	BIFUNCTIONAL ENDO-1,4-BETA-XYLANASE XYLA PRECOURSOR
9527	22027	34968	4.43	5.0E-04	AW270938.1	EST_HUMAN	xs06602.x1 NCI_CGAP_KR11 Homo sapiens cDNA clone IMAGE:2769858 3'
10855	23376		4.52	5.0E-04	AL048507.2	EST_HUMAN	DKFZp566M2024_r1 586 (synonym: hute1) Homo sapiens cDNA clone DKFZp566M2024
11559	18281	30770	11.05	5.0E-04	AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
11631	19936	32801	1.84	5.0E-04	M23604.1	NT	Gorilla gorilla involucrin gene medium allele, complete cds
11809	24657		3.21	5.0E-04	AA568513.1	EST_HUMAN	nf15h02.s1 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:913875
12353	24883		1.77	5.0E-04	U63834.1	NT	Human KIT protein and alternatively spliced KIT protein (KIT) gene, complete cds
415	13050		0.84	4.0E-04	BF241482.1	EST_HUMAN	601676534F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4104897 5'
701	13323	25810	1.12	4.0E-04	U32748.1	NT	Haemophilus influenzae Rd section 63 of 163 of the complete genome
880	13494	26012	1.46	4.0E-04	A1720263.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
880	13494	26013	1.46	4.0E-04	A1720263.1	EST_HUMAN	Q13825 AU-BINDING PROTEIN/ENOYL-COA HYDRATASE. ;
1514	14108	26642	9.82	4.0E-04	AW763356.1	EST_HUMAN	as70b08.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2334039 3' similar to TR:Q13825
2130	14708	27280	1.59	4.0E-04	AL163278.2	NT	RC3-CT0254-130100-023-01 CT0254 Homo sapiens cDNA
2179	14756		1.34	4.0E-04	AL046704.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
2656	15215	27787	1.83	4.0E-04	O66815	SWISSPROT	DKFZp434D059_r1 434 (synonym: hites3) Homo sapiens cDNA clone DKFZp434D059 5'
3200	15812	28286	2.59	4.0E-04	AF281074.1	NT	SERPIN-2 (SILK GUM PROTEIN 2)
3405	16014	28493	0.58	4.0E-04	AV696824.1	EST_HUMAN	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3935	16533		0.94	4.0E-04	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4415	17000	29442	3.2	4.0E-04	AA576331.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
4415	17000	29443	3.2	4.0E-04	AA576331.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
4635	17218	29871	1.94	4.0E-04	AA086324.1	EST_HUMAN	nh10a10.s1 NCI_CGAP_Cot1 Homo sapiens cDNA clone IMAGE:951930 3' similar to gb:M21121 T-CELL
5249	17812	30235	6.04	4.0E-04	BE560680.1	EST_HUMAN	SPECIFIC RANTES PROTEIN PRECURSOR (HUMAN);
							zn61c08.s1 Stragene muscle 837209 Homo sapiens cDNA clone IMAGE:562870 3'
							601345895F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3678910 5'
							EXTRACELLULAR CALCIUM-SENSING RECEPTOR PRECURSOR (CASR) (PARATHYROID CELL
7312	19840	32669	1.25	4.0E-04	P48442	SWISSPROT	CALCIUM-SENSING RECEPTOR
7541	20061		2.42	4.0E-04	AL161566.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 66
8473	21013	33929	1.42	4.0E-04	BF240712.1	EST_HUMAN	601875985F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099700 5'
8481	21020	33935	1.85	4.0E-04	N25507.1	EST_HUMAN	yx39e12.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:264142 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9608	22108	35070	2.79	4.0E-04	AI025699.1	EST_HUMAN	ov87h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644341 3'
9754	22252		1.22	4.0E-04	AF022855.1	NT	Mus musculus neuropilin-2(a17) mRNA, alternatively spliced, complete cds
12186	24833		2.4	4.0E-04	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
187	12830	25316	2.71	3.0E-04	AL119426.1	EST_HUMAN	DKFZp761J221_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J221 5'
209	12870	25356	3.63	3.0E-04	P49259	SWISSPROT	180 KD SECRETORY PHOSPHOLIPASE A2 RECEPTOR PRECURSOR (PLA2-R)
913	13526	26045	1.72	3.0E-04	U83991.1	NT	Human short chain acyl CoA dehydrogenase gene, exons 1 and 2
1879	14465	27022	5.5	3.0E-04	AI262100.1	EST_HUMAN	qz28d03.y1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028197 5'
1894	14478		1.08	3.0E-04	AI399874.1	EST_HUMAN	th23a02.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2119082 3'
3349	15958	26434	4.95	3.0E-04	P25147	SWISSPROT	INTERVALIN B PRECURSOR
4036	16634	29103	3.07	3.0E-04	P49448	SWISSPROT	GLUTAMATE DEHYDROGENASE 2 PRECURSOR (GDH)
4131	16723		1.37	3.0E-04	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
4167	16758		1.14	3.0E-04	BE140609.1	EST_HUMAN	RCO-HT0014-310599-028 HT0014 Homo sapiens cDNA
4941	17516		5.05	3.0E-04	BE153778.1	EST_HUMAN	PMO-HT0339-190200-007-g12 HT0339 Homo sapiens cDNA
5192	17731	30156	0.57	3.0E-04	Q09472	SWISSPROT	ETA-ASSOCIATED PROTEIN P300
6292	18900		5.93	3.0E-04	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
6909	19568	32395	1.67	3.0E-04	AL163276.2	NT	Homo sapiens chromosome 21 segment HS21C078
7590	20105	32981	1.04	3.0E-04	P23468	SWISSPROT	PROTEIN-TYROSINE PHOSPHATASE DELTA PRECURSOR (R-PTP-DELTA)
8202	20743	33656	6.76	3.0E-04	P22607	SWISSPROT	FIBROBLAST GROWTH FACTOR RECEPTOR 3 PRECURSOR (FGFR-3)
9834	22332	35313	1.46	3.0E-04	AA454055.1	EST_HUMAN	z48d08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795471 5' similar to gb:M62762
10080	22575	35570	0.5	3.0E-04	AI992139.1	EST_HUMAN	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (HUMAN);
10356	22850	35844	8.78	3.0E-04	AA781201.1	EST_HUMAN	w75e11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
11758	25072	30514	3.55	3.0E-04	AA228301.1	EST_HUMAN	aj24g05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:2513276 3'
12140	24909	30713	4.29	3.0E-04	AB018292.1	NT	nc38a04.r1 NCL_CGAP_P12 Homo sapiens cDNA clone IMAGE:1010430 similar to contains L1.12 L1
12574	24671		3.54	3.0E-04	AL134483.1	EST_HUMAN	repetitive element ;
187	12848	25333	1.23	2.0E-04	AF217796.1	NT	Homo sapiens mRNA for KIAA0749 protein, partial cds
504	13136	25624	2.86	2.0E-04	AU146707.1	EST_HUMAN	DKFZp547L185_r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547L185 5'
940	13553	26069	5.4	2.0E-04	M86524.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NHL, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
940	13553	26070	5.4	2.0E-04	M86524.1	NT	AU146707 HEMBBT Homo sapiens cDNA clone HEMBB1001253 3'
1221	13821		3.94	2.0E-04	AI286021.1	EST_HUMAN	Human dystrophin gene
						NT	Human dystrophin gene
						EST_HUMAN	qh98a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3.b2 MER3 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1228	13827		1.95	2.0E-04	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1872	14458		1.12	2.0E-04	AF224288.1	NT	Mus musculus 5' flanking region of Pip3 gene
2227	14802		0.9	2.0E-04	AA478980.1	EST_HUMAN	zu39505.s1 Soares ovary tumor NBH0T Homo sapiens cDNA clone IMAGE:740337 3' similar to contains Alu repetitive element
2810	15172						Human germline T-cell receptor beta chain TCRBV17S1A1T, TCRBV2S1, TCRBV10S1P, TCRBV28S1P, TCRBV16S1P, TCRBV15S1, TCRBV11S1A1T, HVB relic, TCRBV28S1P, TCRBV34S1, TCRBV14S1, TCRBV3S1, TCRBV4S1A1T, TRY4, TRY5, TRY6, TRY7, TRY8, TCRBD1, TCRBL1S1, TCRBL1S2, >
3016	15632	27740	0.83	2.0E-04	U66061.1	NT	am58c09.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539760 3'
3377	15986	28109	1.13	2.0E-04	AI124529.1	EST_HUMAN	Homo sapiens tubulin, beta, 4 (TUBB4) mRNA
3483	16089	28581	2.53	2.0E-04	BE082317.1	EST_HUMAN	QV2-BT0636-070500-194-b07 BT0636 Homo sapiens cDNA
3983	16591	29052	0.85	2.0E-04	AW978441.1	EST_HUMAN	EST390550 IMAGE resequences, MAGP Homo sapiens cDNA
4224	16812		6.34	2.0E-04	U01029.1	NT	Phascolus vulgaris nitrate reductase (PVRN2) gene, complete cds
4776	17357	29809	1.34	2.0E-04	H66265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232558 5'
4776	17357	29810	1.34	2.0E-04	H66265.1	EST_HUMAN	yu01e11.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:232558 5'
4913	17488		1.79	2.0E-04	U09226.1	NT	Gallus gallus proteasome 28 kDa subunit homolog mRNA, complete cds
5215	17780	30199	1.44	2.0E-04	AB037897.1	NT	Danio rerio hagerorn gene, exons 1 to 6, partial cds
5733	18359	31095	1.92	2.0E-04	AV654352.1	EST_HUMAN	AV654352 GLC Homo sapiens cDNA clone GLODUH10 3'
5745	18371	31079	1.87	2.0E-04	AI680862.1	EST_HUMAN	tp03b11.x1 NCI_CGAP_U18 Homo sapiens cDNA clone IMAGE:2207709 3'
5924	18546	31272	0.87	2.0E-04	AA296652.1	EST_HUMAN	EST11191 Uterus Homo sapiens cDNA 5' end similar to EST containing O family repeat
6102	18718	31470	1.06	2.0E-04	4758179	NT	Homo sapiens cell cycle progression 3 protein (DNJ3) mRNA
6385	18989	31769	0.81	2.0E-04	AF140708.1	NT	Mus musculus G protein coupled receptor gene, complete cds; and unknown gene
7281	19809		2.44	2.0E-04	AU121712.1	EST_HUMAN	AU121712 MAMMA1 Homo sapiens cDNA clone MAMMA1000798 5'
7916	20129		13.08	2.0E-04	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7826	20138	33017	1.26	2.0E-04	P64286	SWISSPROT	MYOMESIN 2 (M-PROTEIN) (165 KD TITIN-ASSOCIATED PROTEIN) (165 KD CONNECTIN-ASSOCIATED PROTEIN)
7897	20439	33344	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
7897	20439	33345	2.74	2.0E-04	U32444.2	NT	Solanum lycopersicum phytochrome F (PHYF) gene, partial cds
8226	20767	33685	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8226	20767	33686	0.97	2.0E-04	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8500	21039	33980	1.77	2.0E-04	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8678	21217	34137	0.56	2.0E-04	X57931.1	NT	Human immunoglobulin C(mu) and C(delta) heavy chain genes (constant regions)
9257	21783	34736	0.47	2.0E-04	AA725700.1	EST_HUMAN	ai22a12.s1 Soares testis_NHT Homo sapiens cDNA clone 1343518 3'
9340	21854	34803	0.5	2.0E-04	P18715	SWISSPROT	GASTRULA ZINC FINGER PROTEIN XLGPF26.1
9885	22382	35357	1.4	2.0E-04	BE149303.1	EST_HUMAN	RC3-HT0254-151099-011-b05 HT0254 Homo sapiens cDNA
9930	22426	35400	2.39	2.0E-04	AA405777.1	EST_HUMAN	zu66c11.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742984 5'
10731	23257	36273	6.22	2.0E-04	AV730373.1	EST_HUMAN	AV730373 HTF Homo sapiens cDNA clone HITFAA01 5'
11185	23690	36737	5.43	2.0E-04	AI440282.1	EST_HUMAN	g01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
11303	23786	36854	2.72	2.0E-04	AW136740.1	EST_HUMAN	UIH-B11-adm-c-04-0-UJ.s1 NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717190 3'
799	13416	25920	1.41	1.0E-04	H98646.1	EST_HUMAN	yz26c09.s1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262864 3' similar to contains L1.1 L1 repetitive element ;
1113	13717	26227	2.57	1.0E-04	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1153	13756	26265	4.04	1.0E-04	AW013847.1	EST_HUMAN	ENDONUCLEASE]
1153	13756	26266	4.04	1.0E-04	AW013847.1	EST_HUMAN	UIH-B10-aab-e-09-0-UJ.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
1377	13970		3.95	1.0E-04	U62918.1	NT	UIH-B10-aab-e-09-0-UJ.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2708825 3'
							Anguilla anguilla dopamine D1A1 receptor (d1A1) gene, complete cds
1669	14262	26795	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 69 gene, partial cds, and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1669	14262	26796	2.57	1.0E-04	AF148805.1	NT	Kaposi's sarcoma-associated herpesvirus ORF 69 gene, partial cds; and ORF 69, kaposin, v-FLIP, v-cyclin, latent nuclear antigen, ORF K14, v-GPCR, putative phosphoribosylglycinamide synthase, and LAMP (LAMP) genes, complete cds
1901	14486	27047	2.44	1.0E-04	AB048342.1	NT	Equus caballus DNA, chromosome 24q14, microsatellite TKY38
2711	15266	27835	1.09	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
2711	15268	27836	1.09	1.0E-04	BE218833.1	EST_HUMAN	h45c08.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176366 3'
3323	15933	28410	1.1	1.0E-04	Q62203	SWISSPROT	SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SPLICING FACTOR 3A SUBUNIT 2) (SF3A66)
3789	16369	28864	2.7	1.0E-04	AI440282.1	EST_HUMAN	g01f11.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140269 3' similar to contains Alu repetitive element;
4134	16726	29180	1.72	1.0E-04	M14042.1	NT	Mouse alpha 1 type-IV collagen mRNA
4156	16748	29201	1.27	1.0E-04	AV647727.1	EST_HUMAN	AV647727 GLC Homo sapiens cDNA clone GLCBB04 3'
5263	17825	30250	0.95	1.0E-04	A1357156.1	EST_HUMAN	q02h04.x1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:2005975 3'
6021	18640	31380	1.5	1.0E-04	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6568	19168	31862	0.97	1.0E-04	AA177111.1	EST_HUMAN	nc02e12.s1 NCL_CGAP_Pf3 Homo sapiens cDNA clone IMAGE:252

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
6925	19884	32414	0.78	1.0E-04	AA584561.1	nt25a04.s1 NCI_CGAP_AA1 Homo sapiens cDNA clone IMAGE:993486 3' similar to gb:M97252
7237	19767	32823	14.08	1.0E-04	A1251980.1	KALLMANN SYNDROME PROTEIN PRECURSOR (HUMAN); contains Alu repetitive element;
7572	19787	32823	14.23	1.0E-04	A1251980.1	q147d10.x1 NCI_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
7937	20479	33389	1.02	1.0E-04	AA630453.1	q147d10.x1 NCI_CGAP_Ox32 Homo sapiens cDNA clone IMAGE:1985683 3'
9260	21786	34738	2.34	1.0E-04	A1808220.1	eb94g08.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:854654 3'
9270	21786	34745	1.71	1.0E-04	O88969	wf26e08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358742 3'
9346	21860		0.78	1.0E-04	T77153.1	CYSTATIN-RELATED EPIDIDYMAL SPERMATOGENIC PROTEIN PRECURSOR (CYSTATIN 8)
8564	22064	35023	2.2	1.0E-04	10863876	yf72c08.r1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:113774 5'
10081	22576		2.87	1.0E-04	P08547	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
10116	22611	35601	0.83	1.0E-04	P08548	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11218	23721		2.08	1.0E-04	M28587.1	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11503	23952	37020	1.98	1.0E-04	AB032968.1	Mouse alpha leukocyte interferon gene, complete cds
11540	23988	37059	2.1	1.0E-04	AW269081.1	Homo sapiens mRNA for KIAA1142 protein, partial cds
11570	24017	37086	1.87	1.0E-04	O03696	xy49g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2816518 3'
11570	24017	37087	1.87	1.0E-04	O03696	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11670	24082		1.57	1.0E-04	BE686769.1	NEURONAL-GLIAL CELL ADHESION MOLECULE PRECURSOR (NG-CAM)
11919	24876		1.99	1.0E-04	BE676399.1	GM0-CT0404-130700-476-103 CT0404 Homo sapiens cDNA
727	13347	25839	1.98	9.0E-05	AA718933.1	7728a10.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286058 3' similar to contains L1.13 L1
2047	14629	27198	0.92	9.0E-05	AW866218.1	repetitive element;
8117	18733	31486	1.45	9.0E-05	Q60716	ah45c11.s1 Soares testis_NHT Homo sapiens cDNA clone 1292468 3'
8397	21820		2.71	9.0E-05	D85606.1	QV4-SN0023-070400-166-504 SN0023 Homo sapiens cDNA
9399	21822	34771	2.79	9.0E-05	AF120982.1	PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11017	23531	36567	2.86	9.0E-05	AW073078.1	Homo sapiens gene for cholesterylkinin type-A receptor, complete cds
11121	23629	36671	1.99	9.0E-05	A1287878.1	Homo sapiens methyl-CpG binding protein 1 (MBD1) gene, exon 15b
11483	18733	31486	3.89	9.0E-05	Q60716	q147d10.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568728 3' similar to contains L1.12 L1
						repetitive element;
						q147d10.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
						MIR repetitive element;
						PROLYL 4-HYDROXYLASE ALPHA-2 SUBUNIT PRECURSOR
11974	24939		4.26	9.0E-05	AF129756.1	Homo sapiens MSH55 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G5b, G6d, G6e, G6f, BAT5, G5b,
854	13470	25981	1.21	8.0E-05	AJ251648.1	CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LTA genes, complete cds
897	13511		9.89	8.0E-05	AJ251646.1	Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)
						Pisum sativum mRNA for beta-1,3 glucanase (gns2 gene)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2877	15593		0.71	8.0E-05	M83575.1	NT	Human platelet-derived growth factor A chain (PDGFA) gene, exons only
4579	17182	29604	1.87	8.0E-05	AW044605.1	EST_HUMAN	wy78a04.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2554638 3'
8683	21222	34142	0.49	8.0E-05	Y11688.1	NT	Mus musculus gene for hexokinase II, exon 1 (and joined CDS)
11030	23544	36581	2.32	8.0E-05	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
12613	24921		2.72	8.0E-05	AA276333.1	EST_HUMAN	zs88h01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704593 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element
369	13018	25501	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
369	13018	25502	8.81	7.0E-05	AW847445.1	EST_HUMAN	RC3-CT0208-220999-011-E04 CT0208 Homo sapiens cDNA
593	13223	25697	3.82	7.0E-05	L48075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
593	13223	25698	3.82	7.0E-05	L49075.1	EST_HUMAN	HUM072014F Human fovea cDNA Homo sapiens cDNA clone EST HFD072014
1093	13698	26208	1.41	7.0E-05	Q22949	SWISSPROT	PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (GPAT)
2744	15299	27665	3.67	7.0E-05	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
3194	15806	28279	4.69	7.0E-05	AB009080.1	NT	Dicystellum discoideum gene for TRFA, complete cds
4462	17048	28492	1.73	7.0E-05	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4543	17127	29570	0.58	7.0E-05	U60680.1	NT	Caenorhabditis elegans Stp1p homolog mRNA, complete cds
8167	20708	33624	1.11	7.0E-05	AA905882.1	EST_HUMAN	in93g01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:966098 3'
9472	21871	34820	3.74	7.0E-05	T07095.1	EST_HUMAN	EST04984 Fetal brain, Stragene (cat#36206) Homo sapiens cDNA clone HFBED60
11040	23554		7.95	7.0E-05	10835046	NT	Homo sapiens sercoglycan, epsilon (SGCE), mRNA
2073	14653	27225	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2073	14653	27226	2.03	6.0E-05	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2824	15186	27753	1.34	6.0E-05	AI85241.1	EST_HUMAN	TOPOISOMERASE I (HUMAN);
2709	15266	27833	0.9	6.0E-05	Z84506.1	NT	w654h06.x1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:2309531 3' similar to gb:J03250 DNA
2709	15266	27834	0.9	6.0E-05	Z84506.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
2840	13329	25815	2.88	6.0E-05	AF053630.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28B10
5352	17912	30327	1.3	6.0E-05	AW962309.1	EST_HUMAN	Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds
6071	18688	31432	3.12	6.0E-05	Q12860	SWISSPROT	EST1374382 MAGG resequences, MAGG Homo sapiens cDNA
6071	18688	31433	3.12	6.0E-05	Q12860	SWISSPROT	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
6535	19135	31928	1.45	6.0E-05	N72829.1	EST_HUMAN	CONTACTIN PRECURSOR (GLYCOPROTEIN GP135)
7013	19511	32332	0.79	6.0E-05	AA897880.1	EST_HUMAN	w50g11.1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:246212 5'
8029	20571	33475	0.97	6.0E-05	BE064410.1	EST_HUMAN	q80a03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1504588 3'
8029	20571	33476	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-h06 BT0311 Homo sapiens cDNA
8029	20571	33476	0.97	6.0E-05	BE064410.1	EST_HUMAN	RC4-BT0311-141198-011-h06 BT0311 Homo sapiens cDNA

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8381	20921	33841	0.65	6.0E-05	AA150482.1	EST_HUMAN	z08c08.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491726 3' similar to contains element MER28 repetitive element ;
8385	20925	33845	2.3	6.0E-05	AW866329.1	EST_HUMAN	PM4-NN0050-310300-001-110 NN0050 Homo sapiens cDNA
8516	21055	33978	0.62	6.0E-05	Q60401	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR
9176	21753	34699	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9178	21753	34700	1.09	6.0E-05	P08607	SWISSPROT	C4B-BINDING PROTEIN PRECURSOR (C4BP)
9440	21968	34915	1.13	6.0E-05	T04148.1	EST_HUMAN	y028c12.r1 Strategene lung (#937210) Homo sapiens cDNA clone IMAGE:119062 5'
9637	22137	35103	0.57	6.0E-05	AW627985.1	EST_HUMAN	h137a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974444 3'
10627	23159	36172	3.96	6.0E-05	R75639.1	EST_HUMAN	y09d08.s1 Soares placentia Nb2HP Homo sapiens cDNA clone IMAGE:143535 3' similar to contains Alu repetitive element; contains L TR7 repetitive element ;
11394	23846	36911	4.18	6.0E-05	AA044015.1	EST_HUMAN	z68f02.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487035 5'
12193	24919	30716	10.26	6.0E-05	AW890110.1	EST_HUMAN	MRO-NT0038-250400-001-109 NT0038 Homo sapiens cDNA
1449	14041	26569	18.37	5.0E-05	AW392086.1	EST_HUMAN	QV4-ST0234-241199-040-h11 ST0234 Homo sapiens cDNA
1903	14489		1.75	5.0E-05	8923891	NT	Homo sapiens 22kDa peroxisomal membrane protein-like (LOC55695), mRNA
4051	16648	29116	3.88	5.0E-05	AJ251884.1	NT	Homo sapiens partial SLC22A3 gene for extraneuronal monoamine transporter (EMT), exon 1
5716	18342	30848	11.26	5.0E-05	X58855.1	NT	Human ML C1emb gene for embryonic myosin alkaline light chain, 3'UTR
6144	18768	31516	2.97	5.0E-05	AV653544.1	EST_HUMAN	AV653544 GLC Homo sapiens cDNA clone GLCMA06 3'
6316	18923	31700	0.97	5.0E-05	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
7370	19896		1.22	5.0E-05	AB037964.1	NT	Mus musculus gene for calretinin, exon 1
11971	24460		5.73	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
12249	24460		9.18	5.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
2833	12906		3.49	4.0E-05	U12821.1	NT	Human renin (REN) gene, 5' flanking region
4580	17163	29605	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
4580	17163	29605	1.37	4.0E-05	P49193	SWISSPROT	RETINAL-BINDING PROTEIN (RALBP)
5166	17735	30182	0.58	4.0E-05	AF212313.1	NT	Drosophila melanogaster senseless protein (sens) gene, complete cds
7020	19518	32340	0.75	4.0E-05	U01947.1	NT	Macaca mulatta haptoglobin (HP) gene, 5' region
9442	21968		7.26	4.0E-05	AF202635.1	NT	Homo sapiens PP1200 mRNA, complete cds
9912	22408	35384	0.55	4.0E-05	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE; ENDONUCLEASE]
10305	22799	35780	0.73	4.0E-05	P23780	SWISSPROT	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (ACID BETA-GALACTOSIDASE)
10848	23180	36193	5.05	4.0E-05	AW627948.1	EST_HUMAN	h136c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2974380 3' similar to contains element MIR repetitive element ;
11850	24210	31041	3.27	4.0E-05	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
11929	24264		1.38	4.0E-05	AW117560.1	EST_HUMAN	xd93e09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605192 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
709	13330	25817	0.64	3.0E-05	AI248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
1067	13702	26212	1.46	3.0E-05	AW273851.1	EST_HUMAN	xv24g03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2814100 3'
1170	13772	26280	1.51	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3865142 5'
1170	13772	26281	1.51	3.0E-05	BF037898.1	EST_HUMAN	601461463F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3865142 5'
2746	15301	27867	1.17	3.0E-05	Q62234	SWISSPROT	SKELEMIN
3331	15941		0.69	3.0E-05	AI288919.1	EST_HUMAN	q191g11.x1 Soares_NihHMPu_S1 Homo sapiens cDNA clone IMAGE:1879748 3' similar to TR:O08632
4471	17057	29503	7.22	3.0E-05	BE169211.1	EST_HUMAN	O08632 GLYCINE TYROSINE-RICH HAIR PROTEIN ;
4471	17057	29504	7.22	3.0E-05	BE169211.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4565	17148	29594	1.06	3.0E-05	AA368679.1	EST_HUMAN	PM1-HT0521-120200-001-e10 HT0521 Homo sapiens cDNA
4565	17148	29595	1.06	3.0E-05	AA368679.1	EST_HUMAN	EST179996 Placenta1 Homo sapiens cDNA similar to similar to p53-associated protein
4692	17274		0.71	3.0E-05	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4728	17307	29751	0.75	3.0E-05	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4963	13330	25817	0.65	3.0E-05	AI248061.1	EST_HUMAN	qh64c10.x1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:1849458 3' similar to contains Alu repetitive element; contains element KER repetitive element ;
5746	18372	31080	1.73	3.0E-05	11072102	NT	Mus musculus myosin light chain 2, precursor lymphocyte-specific (Myc2pl), mRNA
5854	19442	32257	1.28	3.0E-05	AJ225762.1	NT	Homo sapiens SYBL1 gene, exons 6-8
5854	19442	32258	1.28	3.0E-05	AJ225762.1	NT	Homo sapiens SYBL1 gene, exons 6-8
7839	20381	33286	1.9	3.0E-05	BE733157.1	EST_HUMAN	601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842282 5'
8233	20834	33756	1.29	3.0E-05	AA284049.1	EST_HUMAN	zs60b05.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701841 3'
8824	21363	34288	1.78	3.0E-05	AW770982.1	EST_HUMAN	h194608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009638 3'
8828	21367	34291	1.22	3.0E-05	6912431	NT	Homo sapiens Interleukin-1 receptor antagonist homolog 1 (IL1HY1), mRNA
8832	21371	34296	0.47	3.0E-05	P43361	SWISSPROT	MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN)
9058	21595		0.88	3.0E-05	X03273.1	NT	Human Alu-family cluster 5' of alpha(1)-acid glycoprotein gene
9244	21770	34718	1.3	3.0E-05	AA372562.1	EST_HUMAN	EST84475 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
9581	22081		2.97	3.0E-05	A1769331.1	EST_HUMAN	wg36f09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2367209 3'
10428	22922	35925	0.85	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
10428	22922	35926	0.85	3.0E-05	Q62918	SWISSPROT	PROTEIN KINASE C-BINDING PROTEIN NELL2 PRECURSOR (NELL-LIKE PROTEIN 2)
12055	24338		1.48	3.0E-05	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12387	25101		1.52	3.0E-05	AW518689.1	EST_HUMAN	xs89d06.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2776811 3'
2362	14933	27506	1.55	2.0E-05	AI266021.1	EST_HUMAN	qh98e11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1855052 3' similar to contains MER3 b2 MER3 repetitive element ;
2619	15181	27747	10.26	2.0E-05	M13792.1	NT	Human adenosine deaminase (ADA) gene, complete cds

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2738	15293		6.76	2.0E-05	AA160562.1	EST_HUMAN	zq46a12.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:632734 5' similar to contains Alu repetitive element; contains element L1 repetitive element ;
3171	15785	28257	1.59	2.0E-05	BE066036.1	EST_HUMAN	RC3-BT0319-120200-014-H08 BT0319 Homo sapiens cDNA
3391	15999	28477	0.63	2.0E-05	AF184814.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
3416	16024	28508	1.04	2.0E-05	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
3541	16146		0.72	2.0E-05	X95465.1	NT	S.cerevisiae 12.8 Kbp fragment of the left arm of chromosome XV
3680	16478		0.67	2.0E-05	AL039107.1	EST_HUMAN	DKFZp5681064_r1 568 (synonym: hfkd2) Homo sapiens cDNA clone DKFZp5681064 5'
5010	17583	30028	0.83	2.0E-05	AJ131018.1	NT	Homo sapiens SCL gene locus
5176	17743		2.42	2.0E-05	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
5933	18555	31282	1.84	2.0E-05	AJ011712.1	NT	Homo sapiens TNNT1 gene, exons 1-11 (and joined CDS)
6125	18740	31492	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6125	18740	31493	1.4	2.0E-05	Q13183	SWISSPROT	RENAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA(+)/DICARBOXYLATE COTRANSPORTER)
6305	18912	31686	0.73	2.0E-05	A1149272.1	EST_HUMAN	qc72a02.x1 Soares_placenta_8to9weeks_2NBHP8to9W Homo sapiens cDNA clone IMAGE:1715114 3'
6736	19330	32136	2.12	2.0E-05	AA714330.1	EST_HUMAN	similar to contains L1.13 L1 repetitive element ;
6982	19480	32301	2.2	2.0E-05	Y08926.1	NT	nm006d12.s1 NCI CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238519 3'
6994	19492	32313	1.34	2.0E-05	A1492960.1	EST_HUMAN	P. falciparum mRNA for AARP1 protein, partial
7002	19500		8.08	2.0E-05	A1891025.1	EST_HUMAN	qz47b06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2030003 3' similar to TR:O02711
							O02711 PRO-POL-DUTPASE POLYPROTEIN ;
							wu35h07.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
7207	19738	32591	2.2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7207	19738	32592	2.2	2.0E-05	AF224262.1	NT	Heterodontus francisci HoxA10 (HoxA10), HoxA9 (HoxA9), HoxA7 (HoxA7), HoxA6 (HoxA6), HoxA5 (HoxA5), HoxA4 (HoxA4), HoxA3 (HoxA3), HoxA2 (HoxA2), and HoxA1 (HoxA1) genes, complete cds
7403	19928		0.91	2.0E-05	AF128847.1	NT	Homo sapiens indolethylamine N-methyltransferase (INMT) mRNA, INMT-2 allele, complete cds
7626	20368	33276	1.41	2.0E-05	A1381040.1	EST_HUMAN	tg20h05.x1 NCI CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2109369 3'
9191	21708	34651	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9191	21708	34652	0.49	2.0E-05	P49457	SWISSPROT	COMPLEMENT DECAY-ACCELERATING FACTOR (CD55)
9837	22335	35317	0.48	2.0E-05	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
10041	22536	35532	0.74	2.0E-05	BF055939.1	EST_HUMAN	7175g09.y1 NCI CGAP_Bm20 Homo sapiens cDNA clone IMAGE:3340576 5'

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10482	22976	35984	2.62	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10482	22976	35985	2.62	2.0E-05	N41751.1	EST_HUMAN	yw91a06.r1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:259570 5'
10524	19500		2.44	2.0E-05	A1991025.1	EST_HUMAN	wu35h07.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2522077 3'
11327	23025	36034	2.74	2.0E-05	BE175801.1	EST_HUMAN	RC5-HT0582:280300-012-E12 HT0582 Homo sapiens cDNA
11983	24844		4.91	2.0E-05	BE348229.1	EST_HUMAN	hw21a03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3183532 3' similar to TR:Q12832
							Q12832 GLYCOPHORIN HEP2;
							xa89a03.x1 NCI CGAP_Co17 Homo sapiens cDNA clone IMAGE:2573932 3' similar to contains L1.b3 L1
12090	25018		13.02	2.0E-05	AW074604.1	EST_HUMAN	repetitive element;
12144	24831		2.54	2.0E-05	AF275948.1	NT	Homo sapiens ABCA1 (ABCA1) gene, complete cds
12855	24727		2.35	2.0E-05	A1200970.1	EST_HUMAN	qf68g11.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755236 3'
2719	15475	27841	1.45	1.0E-05	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
3711	16312	28780	1.91	1.0E-05	AF088273.1	NT	Drosophila melanogaster strain Lemito 120 Suppressor of Hairless (Su(H)) gene, partial cds
4039	16637	29105	11.9	1.0E-05	P81274	SWISSPROT	MOSAIC PROTEIN LGN
4252	16840	29289	0.98	1.0E-05	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4364	16951	29391	1.89	1.0E-05	AA431119.1	EST_HUMAN	zw69g04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781494 5'
4976	17550	29992	2.24	1.0E-05	AW419134.1	EST_HUMAN	xy49g11.x1 NCI CGAP_Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
							os64d07.x6 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1610125 3' similar to contains Alu repetitive element;
5395	17963		0.94	1.0E-05	A1733566.1	EST_HUMAN	
5426	17983	30388	0.91	1.0E-05	L27595.1	NT	Mus musculus bradykinin B2 receptor (B2R) gene, complete cds
6848	19438	32252	1.32	1.0E-05	AJ246003.1	NT	Homo sapiens Spast gene for spastin protein
							ns19g02.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1184114 3' similar to contains L1.1 L1
7140	19520	32342	3.88	1.0E-05	AA641846.1	EST_HUMAN	L1 repetitive element;
7142	19675	32515	14.32	1.0E-05	4505844	NT	Homo sapiens phospholipase A2, group X (PLA2G10) mRNA, and translated products
7655	20167	33054	0.76	1.0E-05	BF222848.1	EST_HUMAN	7p57d01.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:3649845 3' similar to contains MER10.b3
7754	20262		2.22	1.0E-05	P19474	SWISSPROT	MER10 repetitive element;
8846	21385		2.56	1.0E-05	AL163227.2	NT	52 KD RO PROTEIN (SJOJGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
							Homo sapiens chromosome 21 segment HS21C027
8990	21528	34457	2.18	1.0E-05	AA452578.1	EST_HUMAN	zc35h12.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788519 3' similar to
							gbL02932 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
9211	21728	34671	13.74	1.0E-05	AA236110.1	EST_HUMAN	zs05e11.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684332 5' similar to contains Alu
9288	21898	34834	0.6	1.0E-05	AV732190.1	EST_HUMAN	repetitive element; contains element TAR1 repetitive element;
							AV732190 HTF Homo sapiens cDNA clone HTFBIH01 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9752	22250	35232	0.76	1.0E-05	AW510902.1	EST_HUMAN	h441b02.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFR.11 OFR repetitive element.
9752	22250	35233	0.76	1.0E-05	AW510902.1	EST_HUMAN	h441b02.x1 Soares_NFL_T_OBC_S1 Homo sapiens cDNA clone IMAGE:2812043 3' similar to contains OFR.11 OFR repetitive element.
9830	22326	35309	1.58	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-aggk-a-08-Q-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
9830	22326	35310	1.58	1.0E-05	AW291521.1	EST_HUMAN	UI-H-B12-aggk-a-08-Q-UI.s1 NCI CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724398 3'
10087	22592		1.73	1.0E-05	AW468985.1	EST_HUMAN	h407c10.x1 NCI CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2873010 3' similar to contains L1.L2 L1 repetitive element.
10799	23322	36332	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
10799	23322	36333	2.32	1.0E-05	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
12493	25011	30616	1.67	1.0E-05	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2696	15253	27824	4.74	9.0E-06	AI583811.1	EST_HUMAN	tt73a06.x1 NCI CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246386 3'
3130	15744	28213	5.23	9.0E-06	AI218983.1	EST_HUMAN	qg11b08.x1 Soares_placenta_8to9weeks_2Nb1-IP8to9W Homo sapiens cDNA clone IMAGE:1759191 3'
3670	16271		3.37	9.0E-06	M61755.1	NT	Human alanine:glyoxylate aminotransferase (AGXT) gene, exons 1 and 2
6084	18681	31423	2.25	9.0E-06	L23416.1	NT	Homo sapiens differentiation antigen CD20 gene, exons 5, 6
6947	19524	32346	0.84	9.0E-06	BE065042.1	EST_HUMAN	RC1-BT0313-110500-017-a07 BT0313 Homo sapiens cDNA
7466	19986	32853	0.85	9.0E-06	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
7751	20259	33156	12.47	9.0E-06	AI034370.1	EST_HUMAN	ox20g01.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1656912 3' similar to contains Alu repetitive element.
8400	20940	33863	1.18	9.0E-06	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8913	21451	34372	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
8913	21451	34373	2.48	9.0E-06	Q63769	SWISSPROT	SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR (DRS PROTEIN) (DOWN-REGULATED BY V-SRC)
9149	21684	34628	4.6	9.0E-06	U35114.1	NT	Human apolipoprotein E (APOE) gene, hepatic control region HCR-2
10818	23339	36353	3.76	9.0E-06	Q10384	SWISSPROT	PUTATIVE SERINE/THREONINE-PROTEIN KINASE C22E12.14C
2569	15469	27701	1.48	8.0E-06	AW362539.1	EST_HUMAN	RC3-CT0283-201199-011-p11 CT0283 Homo sapiens cDNA
10424	22818	35619	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)
10424	22818	35620	0.64	8.0E-06	P34083	SWISSPROT	FASCICLIN II, PHOSPHATIDYLINOSITOL-LINKED ISOFORM PRECURSOR (FAS II)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1015	13625		1.71	7.0E-06	AA689729.1	EST_HUMAN	ab90f10.s1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:854251 3' similar to contains MER20.t1 MER20 repetitive element ;
1487	14080	26619	3.36	7.0E-06	7652177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
2177	14754	27324	1.55	7.0E-06	AW593215.1	EST_HUMAN	hg11b12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2945279 3' similar to gb:XB2048.cds1 WEE1-LIKE PROTEIN KINASE (HUMAN);
2897	15514		7.94	7.0E-06	AI368252.1	EST_HUMAN	qw16g09.x1 NCI_CGAP_U13 Homo sapiens cDNA clone IMAGE:1991296 3' similar to contains Alu repetitive element;
3620	19223		1	7.0E-06	AA385542.1	EST_HUMAN	EST199205 Thyroid Homo sapiens cDNA 5' end similar to EST containing L1 repeat
5874	18498		5.81	7.0E-06	AW883141.1	EST_HUMAN	QV2-OT0062-250400-173-h01 OT0062 Homo sapiens cDNA
5972	18593	31327	0.94	7.0E-06	N98645.1	EST_HUMAN	yy65c07.r1 Soares_multiple_sclerosis_2NBHMS Homo sapiens cDNA clone IMAGE:278412 5'
8724	21263	34183	0.72	7.0E-06	11420709	NT	Homo sapiens DNA segment, numerous copies, expressed probes (GS1 gene) (DXF68S1E), mRNA
9814	22312		2.32	7.0E-06	Q61147	SWISSPROT	GERULOPLASMIN PRECURSOR (FERROXIDASE)
11710	25043	30508	1.62	7.0E-06	BF215972.1	EST_HUMAN	601881522F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083972 5'
2842	15558	28032	1.29	6.0E-06	BE069189.1	EST_HUMAN	QV3-BT0379-010300-105-d11 BT0379 Homo sapiens cDNA
4865	15584	28085	2.03	6.0E-06	Q01456	SWISSPROT	OVARIAN ABUNDANT MESSAGE PROTEIN (OAM PROTEIN)
4875	17450	29901	1.47	6.0E-06	AI040099.1	EST_HUMAN	ox08a02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1655738 3' similar to contains MER12 MER8 repetitive element ;
5552	18184	30599	1.3	6.0E-06	AF167441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
5605	18234	30685	1.15	6.0E-06	Q02040	SWISSPROT	PROTEIN XE7
9770	22288		1.67	6.0E-06	AW801912.1	EST_HUMAN	IL6-UJ0070-110400-063-g02 UJ0070 Homo sapiens cDNA
12602	24688	30881	1.47	6.0E-06	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 11 subunit (CACNA11), mRNA
5361	17921	30335	1.02	5.0E-06	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
6211	18821	31592	3.73	5.0E-06	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
6479	19080	31863	2.04	5.0E-06	U07591.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
7284	19812	32668	1.11	5.0E-06	AB007548.1	NT	Homo sapiens gene for LECT2, complete cds
10013	22508	35499	6.57	5.0E-06	AA313620.1	EST_HUMAN	EST185498 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
10406	22800	35895	0.54	5.0E-06	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
12482	24615	30890	13.8	5.0E-06	AI05045.1	EST_HUMAN	HA0877 Human fetal liver cDNA library Homo sapiens cDNA
675	13289	25780	6.05	4.0E-06	R16287.1	EST_HUMAN	ya48c03.r1 Soares_infant_brain_1NIB Homo sapiens cDNA clone IMAGE:53254 5' similar to contains Alu repetitive element; contains L1 repetitive element ;
879	13493	26011	6.94	4.0E-06	AW103354.1	EST_HUMAN	xc69g12.x1 NCI_CGAP_Esc2 Homo sapiens cDNA clone IMAGE:2589574 3' similar to contains Alu repetitive element; contains element MER21 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1379	13972	26469	3.92	4.0E-06	AB34928.1	EST_HUMAN	IB33a09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1379	13972	26500	3.92	4.0E-06	AB34928.1	EST_HUMAN	IB33a09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2056168 3'
1522	14114	26651	3.17	4.0E-06	BF365612.1	EST_HUMAN	QV2-NT0048-200600-250-h07 NT0048 Homo sapiens cDNA
2305	14878	27454	1.68	4.0E-06	AW016401.1	EST_HUMAN	UI-H-B10-aat-f05-Q-UI.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2710425 3'
3099	15714	28186	1.26	4.0E-06	AF198349.1	NT	Gallus gallus Daoh2 protein (Daoh2) mRNA, complete cds
3963	16561	29030	1.35	4.0E-06	AW948285.1	EST_HUMAN	IL3-CT0214-150200-074-B03 CT0214 Homo sapiens cDNA
4930	17505	29851	1.86	4.0E-06	AB86939.1	EST_HUMAN	wl94c10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2432562 3' similar to contains element
5053	17628	30070	2.12	4.0E-06	AL163279.2	NT	MER22 repetitive element;
8436	20976	33890	0.53	4.0E-06	O15393	SWISSPROT	Homo sapiens chromosome 21 segment HS21C079
8735	21274	34195	2.66	4.0E-06	AF009660.1	NT	TRANSMEMBRANE PROTEASE, SERINE 2
9624	22124	35089	1.11	4.0E-06	AJ272285.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
11324	23022	36031	3.84	4.0E-06	AB007955.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
2208	14784	27357	1.31	3.0E-06	AA700562.1	EST_HUMAN	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0486
2208	14784	27358	1.31	3.0E-06	AA700562.1	EST_HUMAN	234b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2307	14879		1.54	3.0E-06	AF202635.1	NT	234b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
2648	15584	28038	1.02	3.0E-06	AA868218.1	EST_HUMAN	234b08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:432663 3' similar to contains L1.11 L1 repetitive element;
3304	15915		2.41	3.0E-06	AB87779.1	EST_HUMAN	Homo sapiens PPI200 mRNA, complete cds
3851	16449	28911	1.06	3.0E-06	BE047094.1	EST_HUMAN	LTR1 repetitive element;
3851	16449	28912	1.06	3.0E-06	BE047094.1	EST_HUMAN	wl22a05.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2425616 3' similar to TR:O60734 O60734
4573	17156	28600	0.68	3.0E-06	T50266.1	EST_HUMAN	LINE-1 LIKE PROTEIN, contains L1.12 L1 repetitive element;
4681	17243	28697	4.82	3.0E-06	X54816.1	NT	Hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
5045	17618	30063	0.94	3.0E-06	JO4038.1	NT	Hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
5045	17618	30064	0.94	3.0E-06	JO4038.1	NT	Hq64d12.x1 NCI_CGAP_HN13 Homo sapiens cDNA clone IMAGE:3124151 3'
6308	18915	31689	0.78	3.0E-06	AJ159412.1	EST_HUMAN	yb78b10.r1 Stratiogene ovary (#837217) Homo sapiens cDNA clone IMAGE:77275 5' similar to contains L1 repetitive element
7280	19808		2.79	3.0E-06	P08548	SWISSPROT	Homo sapiens gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)
8027	20569	33473	0.72	3.0E-06	BE562864.1	EST_HUMAN	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8818	21157	34070	0.69	3.0E-06	P07743	SWISSPROT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds

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12152	24394		13.37	3.0E-06	AW385262.1	EST_HUMAN	RCOL-T0001-281189-011-A03 LT0001 Homo sapiens cDNA
216	12877		2.91	2.0E-06	P54398	SWISSPROT	HOMEOBOX PROTEIN GOOSECOID
1614	14207		4.46	2.0E-06	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
2418	14986	27560	2.2	2.0E-06	A1872138.1	EST_HUMAN	w604a03.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2297068 3' similar to contains MER30.b1
2506	15070	27643	1.79	2.0E-06	P04929	SWISSPROT	MER30 repetitive element;
2601	15163	27731	1.34	2.0E-06	P06719	SWISSPROT	HISTIDINE-RICH GLYCOPROTEIN PRECURSOR
3570	16174	28656	1.04	2.0E-06	AV657555.1	EST_HUMAN	KNOB-ASSOCIATED HISTIDINE-RICH PROTEIN PRECURSOR (KAHRP)
3825	16426	28887	1.85	2.0E-06	AA173518.1	EST_HUMAN	AV657555 GLC Homo sapiens cDNA clone GLCFDB05 3'
3836	16435	28897	0.63	2.0E-06	AW450215.1	EST_HUMAN	zp02603.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone IMAGE:595232 5'
3844	16443	28904	1.74	2.0E-06	AB030896.1	NT	UI-H-B13-aky-g-05-Q-UJ.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736176 3'
6239	18848		0.79	2.0E-06	AA974932.1	EST_HUMAN	Mus musculus gene for odorant receptor A18, complete cds
6287	18875	31643	0.87	2.0E-06	AI539448.1	EST_HUMAN	on34f01.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1558609 3' similar to contains Alu repetitive element;
6570	19168	31965	4.94	2.0E-06	A1819424.1	EST_HUMAN	tes1f05.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2090241 3' similar to TR:Q13537
7858	20400		0.89	2.0E-06	AW869223.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
8033	20575	33480	0.75	2.0E-06	T12238.1	EST_HUMAN	wj90b04.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410063 3'
8770	21309		0.59	2.0E-06	AA772497.1	EST_HUMAN	MR3-SN0087-120400-002-R02 SN0087 Homo sapiens cDNA
8782	21321	34245	1.54	2.0E-06	H62051.1	EST_HUMAN	A447R Heart Homo sapiens cDNA clone A447
9143	21878	34621	0.91	2.0E-06	AF003529.1	NT	zh27c11.s1 Soares_pineal_gland_NHHPG Homo sapiens cDNA clone IMAGE:413300 3' similar to
9143	21878	34622	0.91	2.0E-06	AF003529.1	NT	TR:P70487 P70487 REVERSE TRANSCRIPTASE;
9617	22117	35080	0.72	2.0E-06	N30576.1	EST_HUMAN	yu37c04.r1 Soares ovary tumor NHOT Homo sapiens cDNA clone IMAGE:235974 5' similar to gb:X74929
9833	22331		0.63	2.0E-06	AV748969.1	EST_HUMAN	KERATIN, TYPE II CYTOSKELETAL 8 (HUMAN);
12052	25046	30508	1.61	2.0E-06	P23249	SWISSPROT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
12210	24434		6.63	2.0E-06	BE328232.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
36	12715	25174	1.77	1.0E-06	O76082	SWISSPROT	hw66a03.s1 Soares_placenta_8tc9weeks_2NbHP8tc9W Homo sapiens cDNA clone IMAGE:257212 3'
685	13309	25794	1.45	1.0E-06	AF084364.1	NT	AV748969 NPC Homo sapiens cDNA clone NPCAXD05 5'
1500	14092	26631	2.08	1.0E-06	P09125	SWISSPROT	PROTEIN MOV-10
							hs9202.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3144699 3' similar to contains L1.12 L1 repetitive element;
							ORGANIC CATION/CARNITINE TRANSPORTER 2 (SOLUTE CARRIER FAMILY 22, MEMBER 5) (HIGH-AFFINITY SODIUM-DEPENDENT CARNITINE COTRANSPORTER)
							Mus musculus D6Mm5E protein (D6Mm5e) mRNA, complete cds
							MEROZOITE SURFACE PROTEIN CMZ-8

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1571	14164	26695	1.12	1.0E-06	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
1827	14220		1.54	1.0E-06	P27625	SWISSPROT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
2037	14619	27186	8.38	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
2037	14619	27187	8.38	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
4459	17045	29488	14.7	1.0E-06	U07561.1	NT	Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds
5269	17831	30258	0.99	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5269	17831	30257	0.99	1.0E-06	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5494	18128	30538	4.84	1.0E-06	BF333015.1	EST_HUMAN	MR1-BT0800-030700-002-c06 BT0800 Homo sapiens cDNA
5518	18150	30563	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-c04 FN0004 Homo sapiens cDNA
5518	18150	30564	1.08	1.0E-06	BE834518.1	EST_HUMAN	MR3-FN0004-090600-001-c04 FN0004 Homo sapiens cDNA
5667	18294	30774	1.13	1.0E-06	O60813	SWISSPROT	15 KDA SELENOPROTEIN PRECURSOR
6954	19531	32358	5.96	1.0E-06	P02671	SWISSPROT	FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR
7943	20485		0.86	1.0E-06	AA912623.1	EST_HUMAN	d29c08.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:1524878 3'
8218	20757	33671	1.21	1.0E-06	AI347010.1	EST_HUMAN	qp54602.x1 NCI_CGAP_C08 Homo sapiens cDNA clone IMAGE:1928842 3'
8425	20885	33879	1.23	1.0E-06	AI287878.1	EST_HUMAN	q23106.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1982435 3' similar to contains element
9228	21950	34859	0.98	1.0E-06	N74635.1	EST_HUMAN	z65501.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:296472 3'
9301	21901	34950	0.5	1.0E-06	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
8600	22100	35062	3.34	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
8600	22100	35063	3.34	1.0E-06	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
8643	22143	35111	4.36	1.0E-06	AA132811.1	EST_HUMAN	z017608.r1 Stratagene colon (#837204) Homo sapiens cDNA clone IMAGE:587174 5'
9703	22202		3.84	1.0E-06	AA449257.1	EST_HUMAN	z04411.s1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:785493 3' similar to
10382	22876		1.81	1.0E-06	AL163203.2	NT	gb:D26129 RIBONUCLEASE PANCREATIC PRECURSOR (HUMAN);
11502	23951		6.24	1.0E-06	AW890641.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
12087	24356	30868	7.83	1.0E-06	L78810.1	NT	RC4-NT0054-120500-012-b03 NT0054 Homo sapiens cDNA
12185	14619	27186	1.87	1.0E-06	AF184614.1	NT	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
12185	14619	27187	1.87	1.0E-06	AF184614.1	NT	Homo sapiens p47-phox (NCF1) gene, complete cds
12603	14220		1.38	1.0E-06	P27625	SWISSPROT	Homo sapiens p47-phox (NCF1) gene, complete cds
383	13030	25518	2.01	9.0E-07	AF003529.1	NT	DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT
383	13030	25519	2.01	9.0E-07	AF003529.1	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
8346	20887		0.57	9.0E-07	AL163280.2	NT	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
11126	23634	36875	2.95	9.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C080
							Homo sapiens chromosome 21 segment HS21C081

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4885	17460	28912	5.02	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
4885	17460	28913	5.02	8.0E-07	AI288596.1	EST_HUMAN	q182g07.x1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:1878876 3'
6047	18666		7.49	8.0E-07	P21414	SWISSPROT	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE: ENDONUCLEASE]
7944	20486		9.51	8.0E-07	AF135416.1	NT	Homo sapiens UDP-glucuronosyltransferase gene, complete cds
11486	23935		8.73	8.0E-07	T07770.1	EST_HUMAN	EST05860 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBEN89
11660	24106		7.98	8.0E-07	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
1908	14491	27052	1.14	7.0E-07	AF167341.1	NT	Homo sapiens membrane interleukin 1 receptor accessory protein (IL1RAP) gene, exons 10 and 11
5710	18336	30841	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
5710	18336	30842	0.69	7.0E-07	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCA8), mRNA
10842	23174	36186	1.59	7.0E-07	BE676648.1	EST_HUMAN	7133g01.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3286496 3' similar to TR:Q98897 Q98897
1956	14540	27096	2.56	6.0E-07	AW855558.1	EST_HUMAN	ENDOGENOUS RETROVIRUS-K, LTR US AND GAG GENE. ;
							CM3-CT0277-221089-024-e11 CT0277 Homo sapiens cDNA
2534	15098	27671	2.3	6.0E-07	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-
4044	16842		1.76	6.0E-07	P41479	SWISSPROT	hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes. >
							HYPOPHYSICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION
							7d94f07.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314149 3' similar to TR:O75920 O75920
9068	21605	34536	1.94	6.0E-07	BF001867.1	EST_HUMAN	4F5L. ;
11625	24067	37131	1.83	6.0E-07	AF792950.1	EST_HUMAN	cm87d05.y6 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1554177 5'
11949	24989		2.85	6.0E-07	AW803222.1	EST_HUMAN	CM4-NN1029-250300-121-h12 NN1029 Homo sapiens cDNA
348	12999		1.19	5.0E-07	AB31893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
1095	13700		2.21	5.0E-07	AA380630.1	EST_HUMAN	EST03615 Supt cells Homo sapiens cDNA 5' end
3066	15681		0.64	5.0E-07	AB31893.1	EST_HUMAN	wh84f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2385547 3'
4751	17332	29775	1.32	5.0E-07	AF149774.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 4 through 14 and complete cds
6268	18876	31644	1.13	5.0E-07	U85067.1	NT	Mus musculus OG-2 homeodomain protein (OG-2) gene, partial cds
7124	19484	32281	1.56	5.0E-07	AB93981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu
							repetitive element; contains element A3R repetitive element ;
7124	19484	32282	1.56	5.0E-07	AB93981.1	EST_HUMAN	tg06b05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2107953 3' similar to contains Alu
							repetitive element; contains element A3R repetitive element ;
7386	19912	32776	16.07	5.0E-07	AW070885.1	EST_HUMAN	ya31a02.x1 NCI_CGAP_Br18 Homo sapiens cDNA clone IMAGE:2568362 3' similar to gb:X15341
							CYTCHROME C OXIDASE POLYPEPTIDE VIA-LIVER (HUMAN);
8217	20758	33672	0.82	5.0E-07	Q9WUQ1	SWISSPROT	ADAM-TS 1 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8427	20967		1.08	5.0E-07	P09593	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
10270	22765	35752	4.46	5.0E-07	A1805587.1	EST_HUMAN	CM-BT178-220499-014 BT178 Homo sapiens cDNA
10542	23079	36093	1.58	5.0E-07	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11391	23843	36907	4.94	5.0E-07	P11087	SWISSPROT	COLLAGEN ALPHA 1(I) CHAIN PRECURSOR
11492	23902		2.43	5.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
12391	24899		2.85	5.0E-07	AW662537.1	EST_HUMAN	QV0-CT0383-210400-204-b12 CT0383 Homo sapiens cDNA
4071	16867	28128	1.94	4.0E-07	AV009602.1	EST_HUMAN	we84h05.x1 NCI CGAP C63 Homo sapiens cDNA clone IMAGE:2504697 3'
7230	19761		0.88	4.0E-07	AJ272265.1	NT	Homo sapiens SPP2 gene for secreted phosphoprotein 24 precursor, exons 1-8
7311	19839	32697	1.35	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7311	19839	32698	1.35	4.0E-07	Q9Z2V6	SWISSPROT	HISTONE DEACETYLASE 5 (HD5) (HISTONE DEACETYLASE MHDA1)
7863	20405	33312	0.65	4.0E-07	AL183207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8981	21519	34445	5.37	4.0E-07	AW419134.1	EST_HUMAN	xy49g11.x1 NCI CGAP Lu34.1 Homo sapiens cDNA clone IMAGE:2856548 3'
10228	22723	36715	0.5	4.0E-07	AL183218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10817	23338	36351	4.05	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCI CGAP Kd12 Homo sapiens cDNA clone IMAGE:2399703 3'
10817	23338	36352	4.05	4.0E-07	A1765528.1	EST_HUMAN	w81b08.x1 NCI CGAP Kd12 Homo sapiens cDNA clone IMAGE:2399703 3'
11100	23610		2.06	4.0E-07	BE001828.1	EST_HUMAN	PM1-BN0083-030300-003-e12 BN0083 Homo sapiens cDNA
469	13100	25591	4.51	3.0E-07	U19719.1	NT	Human microfilament-associated glycoprotein (MFAP2) gene, putative promoter region and alternatively spliced untranslated exons
609	13237	25711	2.64	3.0E-07	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1417	14010	26539	1.65	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
1687	14280		1.95	3.0E-07	M84857.1	NT	Human Igk subgroup I germline gene, exons 1 and 2, V-region 018 allele
2090	14670		3.87	3.0E-07	AA526763.1	EST_HUMAN	n156b09.s1 NCI CGAP Ov2 Homo sapiens cDNA clone IMAGE:980825 similar to contains Alu repetitive element; contains L1.3 L1 repetitive element;
2327	14898	27471	1.72	3.0E-07	M99149.1	NT	Human polymorphic microsatellite DNA
2508	15072	27645	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
2508	15072	27646	6.56	3.0E-07	BE005077.1	EST_HUMAN	MRO-BN0115-020300-001-f11 BN0115 Homo sapiens cDNA
3069	15684	28156	0.79	3.0E-07	T84704.1	EST_HUMAN	yc50f12.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:111695 5'
3195	15907	28280	2.03	3.0E-07	P38739	SWISSPROT	HYPOPHYSICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR
4788	17368		0.58	3.0E-07	P20740	SWISSPROT	OVOSTATIN PRECURSOR (OVOMACROGLOBULIN)
4834	17412	28865	7.74	3.0E-07	AV650201.1	EST_HUMAN	AV650201 GLC Homo sapiens cDNA clone GLCCD01 3'
4878	17453	29905	0.71	3.0E-07	A1797236.1	EST_HUMAN	we88b12.x1 Scores_NFL_T_CBC_S1 Homo sapiens cDNA clone IMAGE:2347967 3'
5222	17787	30205	1.81	3.0E-07	T57850.1	EST_HUMAN	yc14h06.s1 Stragene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb-M62982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5222	17787	30206	1.81	3.0E-07	T57850.1	EST_HUMAN	yc14h09.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80705 3' similar to similar to gb:162982 ARACHIDONATE 12-LIPOXYGENASE (HUMAN)
5847	18471	31197	12.79	3.0E-07	O89807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
6128	18743	31498	0.71	3.0E-07	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
6804	19395		5.41	3.0E-07	AA815175.1	EST_HUMAN	oc04c10.s1 NCI CGAP GC81 Homo sapiens cDNA clone IMAGE:1339890 3'
7519	20039	32608	3.22	3.0E-07	AW797168.1	EST_HUMAN	QV1-UM0036-200300-115-g02 UM0036 Homo sapiens cDNA
7659	20171		1.8	3.0E-07	A1591085.1	EST_HUMAN	tw28f11.x1 NCI CGAP CV635 Homo sapiens cDNA clone IMAGE:2261037 3' similar to contains Alu repetitive element/contains element MSR1 MSR1 repetitive element;
11373	23825		1.68	3.0E-07	BE439409.1	EST_HUMAN	HTM1-025F1 HTM1 Homo sapiens cDNA
12841	24716		6.74	3.0E-07	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
31	12710	25168	3.36	2.0E-07	AF262988.1	NT	Homo sapiens TRF2-interacting telomeric RAP1 protein (RAP1) mRNA, complete cds
185	12828	25314	7.91	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
165	12828	25315	7.91	2.0E-07	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
194	12854	25338	45.53	2.0E-07	U38849.1	NT	Fugu rubripes beta-cytoplasmic(vascular) actin gene, complete cds
778	13397	25898	2.58	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
778	13397	25899	2.58	2.0E-07	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
791	13409		0.91	2.0E-07	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE];
979	13591	26106	2.56	2.0E-07	AA223260.1	EST_HUMAN	z08b07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:650869 3' similar to gb:131860 GLYCOPHORIN A PRECURSOR (HUMAN); contains Alu repetitive element;
980	13592	26107	6.66	2.0E-07	T63042.1	EST_HUMAN	yc15g04.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:80790 3' similar to contains L1 repetitive element;
1205	13805	26318	0.78	2.0E-07	Q28768	SWISSPROT	I/6 AUTOANTIGEN
1644	14236	26771	1.88	2.0E-07	Q09701	SWISSPROT	HYPOTHETICAL 72.6 KD PROTEIN C2F7.10 IN CHROMOSOME 1
3679	16280		0.65	2.0E-07	BF131397.1	EST_HUMAN	601818916F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4044891 5'
3751	16352	28820	22.38	2.0E-07	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
5547	18179	30593	1.81	2.0E-07	AW898086.1	EST_HUMAN	RC3-NN0066-280400-021-g11 NN0066 Homo sapiens cDNA
6769	19362	32171	1.59	2.0E-07	AI208715.1	EST_HUMAN	gg56405.x1 Soares testis NIH-Homo sapiens cDNA clone IMAGE:1839177 3'
8405	20945		3.57	2.0E-07	AV729390.1	EST_HUMAN	AV729390 HTC Homo sapiens cDNA clone HTCAEG02 5'
8628	21167	34082	1.1	2.0E-07	AA035198.1	EST_HUMAN	zk27g09.s1 Soares_pregnant_uterus_NbH-IPU Homo sapiens cDNA clone IMAGE:471808 3'
9676	22175		2.27	2.0E-07	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10168	22663	35658	5.85	2.0E-07	AW892507.1	EST_HUMAN	GM4-NN0003-280300-124-e08 NN0003 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10383	22877	35868	0.76	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
10383	22877	35869	0.75	2.0E-07	P00751	SWISSPROT	COMPLEMENT FACTOR B PRECURSOR (C3/C5 CONVERTASE) (PROPERDIN FACTOR B) (GLYCINE-RICH BETA GLYCOPROTEIN) (GBG) (PBF2)
11842	24603		2.57	2.0E-07	BE163717.1	EST_HUMAN	PM0-HT0339-260100-006-H07 HT0339 Homo sapiens cDNA
11734	24890		3.56	2.0E-07	A1732462.1	EST_HUMAN	zn85h11.x5 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565029 3' similar to contains THR.b2 THR repetitive element.
1141	13744		1.17	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
2013	14595	27157	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2013	14595	27158	0.97	1.0E-07	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
2424	14982	27565	0.93	1.0E-07	P10263	SWISSPROT	RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
2854	14162	26693	2.94	1.0E-07	P09256	SWISSPROT	GLYCOPROTEIN GPV
3807	13744		1.22	1.0E-07	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
4380	16967	29413	2.75	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
4380	16967	29414	2.75	1.0E-07	AV718662.1	EST_HUMAN	AV718662 GLC Homo sapiens cDNA clone GLCFNF04 5'
6627	19223	32028	1.57	1.0E-07	U92871.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltractin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>
6850	19527	32349	4.57	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
6950	19527	32350	4.57	1.0E-07	BE047871.1	EST_HUMAN	tz43d06.y1 NCI CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291339 5'
7504	20026	32860	8.62	1.0E-07	N55081.1	EST_HUMAN	y43c07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:245484 3'
7644	20156	33042	0.82	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7644	20156	33043	0.82	1.0E-07	BF375909.1	EST_HUMAN	PM4-TN0024-030800-002-b05 TN0024 Homo sapiens cDNA
7669	20181	33068	1.35	1.0E-07	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
8157	20698	33611	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8157	20698	33612	2.52	1.0E-07	P97435	SWISSPROT	ENTEROPEPTIDASE (ENTEROKINASE)
8884	21422	34347	2.7	1.0E-07	AA693576.1	EST_HUMAN	z151e10.s1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone IMAGE:434348 3'
9194	21711	34654	1.05	1.0E-07	P57110	SWISSPROT	ADAM-TS 8 PRECURSOR (A DISINTEGRIN AND METALLOPROTEINASE WITH THROMBOSPONDIN MOTIFS 8) (ADAMTS-8) (ADAM-TS8) (METH-2)
9535	22035	34995	0.49	1.0E-07	BE327843.1	EST_HUMAN	hu28h08.x1 NCI CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171419 3' similar to contains MER18.13
9849	22347	35329	2.51	1.0E-07	BF674524.1	EST_HUMAN	MER18 repetitive element.
9855	22353	35334	1.19	1.0E-07	AA386311.1	EST_HUMAN	602137714F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4274426 5'
10362	22856		3.53	1.0E-07	AL163282.2	NT	EST185054 Brain IV Homo sapiens cDNA
							Homo sapiens chromosome 21 segment HS21C082

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12013	24860	30704	2.42	1.0E-07	BE048770.1	EST_HUMAN	h53c11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132212 3' similar to TR:095722 O95722
7325	19852	32714	0.87	9.0E-08	AI539362.1	EST_HUMAN	DJ1163J1.1;
9802	22300	35285	2.1	9.0E-08	AV734819.1	EST_HUMAN	te51b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2090195 3'
11061	23573	36610	3.41	9.0E-08	AI891052.1	EST_HUMAN	AV734819 cdA Homo sapiens cDNA clone cdABFB06 5'
11519	23987	37039	4.51	9.0E-08	AL163301.2	NT	wn30a07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2446932 3' similar to contains OFR.12
11981	24283		2.98	9.0E-08	AJ251973.1	NT	OFR repetitive element;
635	15420		2.27	8.0E-08	AI811352.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
1088	13693		0.79	8.0E-08	BE795469.1	EST_HUMAN	Homo sapiens partial steirin-1 gene
3598	16202		1.05	8.0E-08	BE795469.1	EST_HUMAN	wd16b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328273 3'
8674	21213	34133	3.54	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8674	21213	34133	3.54	8.0E-08	AI752367.1	EST_HUMAN	601590133F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943976 5'
8674	21213	34133	3.54	8.0E-08	AI752367.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
9545	22045	35006	3.32	8.0E-08	AW970693.1	EST_HUMAN	cn15c02.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
11124	23632		2.81	8.0E-08	AF253417.1	NT	EST382776 IMAGE resequences, MAGK Homo sapiens cDNA
84	12760	25243	2.82	7.0E-08	Q02357	SWISSPROT	Homo sapiens microsomal epoxide hydrolase (EPHX1) gene, complete cds
1405	13998	26527	11.08	7.0E-08	X04809.1	NT	ANKYRIN 1 (ERYTHROCYTE ANKYRIN)
3635	16238	28714	0.7	7.0E-08	P15305	SWISSPROT	Rat mRNA for ribosomal protein L31
3635	16238	28714	0.7	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
4002	16900	29073	0.89	7.0E-08	P01606	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
4002	16900	29074	0.89	7.0E-08	P01606	SWISSPROT	IG KAPPA CHAIN V-J REGION OU
10683	23223		6.5	7.0E-08	AI535743.1	EST_HUMAN	IG KAPPA CHAIN V-J REGION OU
11523	23971	37041	6.1	7.0E-08	U24070.1	NT	cong3.P11.A5 conorm Homo sapiens cDNA 3'
12450	16238	28713	3.59	7.0E-08	P15305	SWISSPROT	Rattus norvegicus Munc13-1 mRNA, complete cds
12450	16238	28714	3.59	7.0E-08	P15305	SWISSPROT	DYNEIN HEAVY CHAIN (DYHC)
850	13468	25974	3.81	6.0E-08	AL163248.2	NT	DYNEIN HEAVY CHAIN (DYHC)
850	13468	25974	3.81	6.0E-08	AL163248.2	NT	DYNEIN HEAVY CHAIN (DYHC)
2401	14989	27543	2.01	6.0E-08	BE144398.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
4334	16921	28363	1.14	6.0E-08	AL163248.2	NT	MR0-HT0166-191196-004-g09 HTO166 Homo sapiens cDNA
7892	20434		0.68	6.0E-08	P08547	SWISSPROT	Homo sapiens chromosome 21 segment HS21C048
9251	21777		0.6	6.0E-08	AA827075.1	EST_HUMAN	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							obs56c05.s1 NCI_CGAP_GC81 Homo sapiens cDNA clone IMAGE:1335368 3' similar to contains
							MER12.b3 MER12 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11293	23745	36802	2.61	6.0E-08	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
11407	23858		1.77	6.0E-08	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
88	12764	25247	2.33	5.0E-08	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2277	14851	27429	1.23	5.0E-08	AA493851.1	EST_HUMAN	rh03b09.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943193 similar to contains Alu repetitive element;
11692	24107		7.32	5.0E-08	P06681	SWISSPROT	COMPLEMENT C2 PRECURSOR (C3/C5 CONVERTASE)
11898	24233	31004	1.48	5.0E-08	AW851878.1	EST_HUMAN	QVO-CT0225-131099-034-a12 CT0225 Homo sapiens cDNA
1797	14387	26931	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
1797	14387	26932	1.53	4.0E-08	P25723	SWISSPROT	DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR
2910	15527		1.49	4.0E-08	AL079581.1	EST_HUMAN	DKFZp434J0426_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434J0426 5'
3100	15715		1.01	4.0E-08	AI078417.1	EST_HUMAN	oxd5e02.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674458 3' similar to contains Alu repetitive element;
3986	16584	29055	0.67	4.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
6537	19136	31929	1.14	4.0E-08	P52624	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8733	21272	34192	0.97	4.0E-08	O15393	SWISSPROT	TRANSMEMBRANE PROTEASE, SERINE 2
9066	21603	34533	0.92	4.0E-08	L42671.1	NT	Cricetulus griseus ribosomal transcription factor (UBF2) mRNA, complete cds
9563	22063		0.97	4.0E-08	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
10233	22728		0.71	4.0E-08	AI016342.1	EST_HUMAN	α78d12.s1 Soares_fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1622903 3'
10287	22782	35774	3.59	4.0E-08	AI050027.1	EST_HUMAN	an22d10.x1 Gessler_Wilms_tumor_Homo sapiens cDNA clone IMAGE:1699411 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
10782	23306		1.7	4.0E-08	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (tRNA48 gene)
10968	23483	36510	3.7	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
10968	23483	36511	3.7	4.0E-08	BF692493.1	EST_HUMAN	602248024F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4333300 5'
11697	25022		1.4	4.0E-08	W78159.1	EST_HUMAN	zd65g03.r1 Soares_fetal_heart_Nb1HH19W Homo sapiens cDNA clone IMAGE:345556 5' similar to contains L1.1 L1 repetitive element ;
12378	24546		3.48	4.0E-08	AI343353.1	EST_HUMAN	tb95a11.x1 NCI_CGAP_Cot18 Homo sapiens cDNA clone IMAGE:2062076 3' similar to contains MER18.b3 MER18.MER18 repetitive element ;
5795	18420	31136	3.12	3.0E-08	BE018348.1	EST_HUMAN	bb79a10.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048570 5' similar to TR:Q9Z158 Q9Z158 SYNTAXIN 17. ;
7052	18071	30462	3.77	3.0E-08	AI792737.1	EST_HUMAN	qs76f11.y5 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:1944045 5'
7845	20065	32939	1.41	3.0E-08	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7730	20238		4.17	3.0E-08	AI436352.1	EST_HUMAN	th93h09.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2128273 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
9812	22310		0.51	3.0E-08	AF055086.1	NT	Homo sapiens MHC class 1 region
11662	24087		38.65	3.0E-08	R18420.1	EST_HUMAN	YG02R04.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:30948 5' similar to contains Alu repetitive element;
220	12881		6.74	2.0E-08	AW302998.1	EST_HUMAN	x7f706.x1 NCL CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2767139 3'
247	12907		6.48	2.0E-08	AA425598.1	EST_HUMAN	zw48f07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773317 5' similar to contains Alu repetitive element; contains element MER15 repetitive element;
522	13154	25637	2.59	2.0E-08	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
688	13312	25798	10.99	2.0E-08	AW886438.1	EST_HUMAN	NR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
688	13312	25797	10.99	2.0E-08	AW886438.1	EST_HUMAN	NR0-OT0080-240200-001-g08 OT0080 Homo sapiens cDNA
1027	13638		22.86	2.0E-08	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
1387	13981	26508	2.09	2.0E-08	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21G047
1777	14367		1.3	2.0E-08	BE734871.1	EST_HUMAN	601570463F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845199 5'
1895	14480		4.65	2.0E-08	AW270271.1	EST_HUMAN	xp43f11.x1 NCL CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743149 3'
2482	15029	27587	0.97	2.0E-08	AA731948.1	EST_HUMAN	hw64h01.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1251409 3' similar to contains L1.13 L1 repetitive element;
2580	15143		2.21	2.0E-08	K00218.1	NT	Sheep 'His-RNA-GUG
3243	15855	28337	6.85	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3243	15855	28338	6.85	2.0E-08	O42280	SWISSPROT	WNT-14 PROTEIN PRECURSOR
3928	16524		1.93	2.0E-08	AW813620.1	EST_HUMAN	RC3-ST0197-161099-012-b03 ST0197 Homo sapiens cDNA
4152	18744	29198	0.57	2.0E-08	U82668.1	NT	Homo sapiens shox gene, alternatively spliced products, complete cds
4494	17079		1.74	2.0E-08	AA459040.1	EST_HUMAN	aa28c07.r1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814380 5' similar to contains L1.12 L1 repetitive element;
5092	17665		3.83	2.0E-08	AW572881.1	EST_HUMAN	het17h08.x2 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918327 3' similar to contains Alu repetitive element;
5817	18441	31163	0.87	2.0E-08	AA813204.1	EST_HUMAN	aa80h11.s1 Soares testis NHT Homo sapiens cDNA clone 1377189 3'
5998	18618	31354	0.87	2.0E-08	AW088924.1	EST_HUMAN	xd32c04.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595462 3' similar to contains MER18 b3
7946	20488	33398	1.07	2.0E-08	P10272	SWISSPROT	MER18 MER18 repetitive element;
8054	20596	33503	1.2	2.0E-08	AA490121.1	EST_HUMAN	POL POLYPYRROLINE [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; ENDONUCLEASE]
9014	21551		1.41	2.0E-08	AU139878.1	EST_HUMAN	ab02g06.s1 Strabagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:839674 3'
							AU139878 PLACE1 Homo sapiens cDNA clone PLACE1011719 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10413	22807	35804	0.78	2.0E-08	N78097.1	EST_HUMAN	W7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1 b3 LTR1 repetitive element:
10413	22807	35905	0.78	2.0E-08	N78097.1	EST_HUMAN	W7202.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:248283 5' similar to contains LTR1 b3 LTR1 repetitive element:
11982	24293		1.74	2.0E-08	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
12559	25073		1.44	2.0E-08	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
1812	14402	26947	0.99	1.0E-08	AF125348.1	NT	Homo sapiens caveolin 1 (CAV1) gene, exon 3 and partial cds
2095	14874		2.74	1.0E-08	BE141959.1	EST_HUMAN	PM2-HT0130-150989-001-r12 HT0130 Homo sapiens cDNA
5785	18410	31128	4.23	1.0E-08	AJ010770.1	NT	Homo sapiens hyperin gene, exons 1-50
7746	20254	33148	1.14	1.0E-08	P19474	SWISSPROT	52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A))
7978	20520	33428	0.55	1.0E-08	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
8070	20612	33525	0.85	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8070	20612	33528	0.85	1.0E-08	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8484	21023	33940	1.84	1.0E-08	AJ015304.1	EST_HUMAN	o35a05.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1818736 3'
8132	21667	34608	0.75	1.0E-08	BE072572.1	EST_HUMAN	PM2-BT0546-210100-004-002 BT0546 Homo sapiens cDNA
9878	22373	35350	1.16	1.0E-08	P79110	SWISSPROT	TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (GTP)
10449	22943	35953	0.84	1.0E-08	P89063	SWISSPROT	(TRICARBOXYLATE CARRIER PROTEIN)
11195	23700	36751	3.79	1.0E-08	AF044083.1	NT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
12081	24353		2.27	1.0E-08	X51755.1	NT	Homo sapiens major histocompatibility locus class III region
4327	16913	28356	3.93	9.0E-08	AL163279.2	NT	Human lambda-immunoglobulin constant region complex (germline)
4327	16913	28357	3.93	9.0E-08	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079
9874	22469		0.49	9.0E-08	T07950.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
7308	19836	32684	8.63	8.0E-08	AJ183500.1	EST_HUMAN	qq42607.x1 Soares fetal heart NBH19W Homo sapiens cDNA clone IMAGE:121918 3'
7942	20484	33398	2.86	8.0E-08	AW600159.1	EST_HUMAN	yes8a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:1732184 3' similar to contains MSR1.11 MSR1 repetitive element:
8919	21457		2.77	8.0E-08	AA838992.1	EST_HUMAN	OMG-NN1004-100300-273-008 NN1004 Homo sapiens cDNA
3667	16268		1.87	7.0E-08	D86842.1	NT	op74d08.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1582575 3'
4080	16878		1	7.0E-08	U50871.1	NT	Homo sapiens DNA for 3-ketacyl-CoA thiolase beta-subunit of mitochondrial trfunctional protein, exon 2, 3 Human familial Alzheimer's disease (STM2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7843	20385		0.5	7.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
7991	20533		0.78	7.0E-09	AA356200.1	EST_HUMAN	zr80c05.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:681992 5' similar to contains L1.12 L1 repetitive element;
9184	21701	34944	2.99	7.0E-09	L09709.1	NT	Human lysosomal membrane glycoprotein-2 (LAMP2) gene, 5' end and flanking region
10086	22581	35574	1.3	7.0E-09	BE254850.1	EST_HUMAN	601111173F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351834 5'
10248	22743		0.63	7.0E-09	AA058628.1	EST_HUMAN	zfs9e07.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381156 3' similar to contains L1.12 L1 repetitive element;
10552	23088		2.78	7.0E-09	T97950.1	EST_HUMAN	ye58a12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121918 3'
2198	14774		1.16	6.0E-09	AL040439.1	EST_HUMAN	DKFZp434C0514_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C0514 5'
5116	17688	30126	5.44	6.0E-09	BE169421.1	EST_HUMAN	PM1-HT0527-160200-001-h05 HT0527 Homo sapiens cDNA
5246	17810	30232	1	6.0E-09	AW593471.1	EST_HUMAN	hg1612.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:X63743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5246	17810	30233	1	6.0E-09	AW593471.1	EST_HUMAN	hg1612.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2945807 3' similar to gb:X63743 FIBULIN-1, ISOFORM C PRECURSOR (HUMAN);
5582	18213	30662	12.11	6.0E-09	AW195784.1	EST_HUMAN	xn85h08.x1 Soares_NFL_T_QBC_S1 Homo sapiens cDNA clone IMAGE:2701311 3'
8512	21051	33973	0.81	6.0E-09	BE161653.1	EST_HUMAN	MR3-HT0448-260300-201-h12 HT0448 Homo sapiens cDNA
9103	21839	34578	2.37	6.0E-09	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
10177	22672		3.89	6.0E-09	AF200923.2	NT	Homo sapiens testis-specific kinase substrate (TSKS) gene, complete cds
10610	23143	36154	1.68	6.0E-09	BF108755.1	EST_HUMAN	7145e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to contains MER29.b2 MER29 repetitive element;
1460	14052	26584	3.95	5.0E-09	BE149284.1	EST_HUMAN	RC2-HT0252-120200-014-h10 HT0252 Homo sapiens cDNA
1893	14478	27038	0.93	5.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
6542	19141	31933	2.29	5.0E-09	AA359454.1	EST_HUMAN	EST08746 Fetal lung II Homo sapiens cDNA 5' end
8521	21060	33983	0.59	5.0E-09	P37071	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN COR5
10007	22502	35493	2.27	5.0E-09	AW799897.1	EST_HUMAN	PM2-UM0053-240300-005-c09 UM0053 Homo sapiens cDNA
547	13178		1.69	4.0E-09	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1000	13611		1.99	4.0E-09	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1518	14110	26846	1.81	4.0E-09	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
2473	15040	27608	4.54	4.0E-09	AA308078.1	EST_HUMAN	EST58365 Infant brain Homo sapiens cDNA 5' end similar to heat shock protein, 90 kDa
7788	20331	33237	0.72	4.0E-09	AA495747.1	EST_HUMAN	zw04c08.r1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:768298 5'
8459	20999	33915	0.62	4.0E-09	T84942.1	EST_HUMAN	jd11a07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:66804 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10996	23510		1.73	4.0E-09	AA195142.1	EST_HUMAN	z34a12.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:665278 5' similar to gb:L07807 DYNAMIN-1 (HUMAN);
2390	14958	27530	6.63	3.0E-09	BE222239.1	EST_HUMAN	hu09609.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
2589	15151	27717	0.95	3.0E-09	BE222239.1	EST_HUMAN	hu09609.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
2677	15235	27802	1.22	3.0E-09	P23249	SWISSPROT	PROTEIN MOV-10
3372	15980	28457	1.05	3.0E-09	BE222239.1	EST_HUMAN	hu09609.x1 NCJ_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166120 3' similar to contains MER18.13 MER18 repetitive element ;
3423	16031		3.13	3.0E-09	AA442272.1	EST_HUMAN	z54a04.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757422 5'
4172	16763		3.54	3.0E-09	X16874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
4517	17101	29548	5.18	3.0E-09	AF175325.1	NT	Homo sapiens eukaryotic initiation factor 4A1 (EIF4A1) gene, partial cds
4610	17193	29639	1.52	3.0E-09	O8Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)
7841	20383	33287	1.29	3.0E-09	BE465780.1	EST_HUMAN	hx8a02.x1 NCJ_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3194090 3' similar to TR:O55081 O55091 IMPACT PROTEIN ;
10146	22641	35631	1.98	3.0E-09	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10900	23420	36437	3.87	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
10900	23420	36438	3.97	3.0E-09	BF109943.1	EST_HUMAN	7172c08.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3527030 3'
845	13461		1.01	2.0E-09	X16874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
1301	13895	28417	6.02	2.0E-09	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1698	14291		10.31	2.0E-09	AL116573.1	EST_HUMAN	DKFZp761B1710.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761B1710 5'
2364	14935	27507	2.79	2.0E-09	O8Y3R5	SWISSPROT	258.1 KDA PROTEIN C21ORF5 (KIAA0833)
4011	16809	26082	4.13	2.0E-09	O60241	SWISSPROT	BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 2 PRECURSOR
4083	16679	28139	0.94	2.0E-09	AI283479.1	EST_HUMAN	q107d09.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1855793 3'
6876	19610		0.74	2.0E-09	AA357407.1	EST_HUMAN	EST66142 Kidney IX Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7474	19996	32861	8.48	2.0E-09	AA461430.1	EST_HUMAN	z63h06.r1 Soares_total_fetus_Nb2-HF8_9w Homo sapiens cDNA clone IMAGE:796187 5' similar to contains Alu repetitive element;
7532	20052	32925	0.88	2.0E-09	W28834.1	EST_HUMAN	52d11 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8646	21185	34104	1.72	2.0E-09	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11634	24074		1.72	2.0E-09	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
12338	13461		27.08	2.0E-09	X16874.1	NT	H.sapiens PADPRP-1 gene for NAD(+) ADP-ribosyltransferase
12310	25094		2.25	2.0E-09	AA226070.1	EST_HUMAN	nc11c02.r1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:1007810 similar to contains Alu repetitive element;

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1032	13642		1.14	1.0E-09	W78152.1	EST_HUMAN	zsf78d03.s1 Soares_fetal_hear NbHH19W Homo sapiens cDNA clone IMAGE:346853 3' similar to
1148	13751	26260	2.3	1.0E-09	5031624	NT	gb:L02892 PEROMYSOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN);
1148	13751	26261	2.3	1.0E-09	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2914	15531	28003	1.74	1.0E-09	U80017.1	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
2952	15568	28042	3.98	1.0E-09	M28699.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (hapi) and survival motor neuron protein (smn) genes, complete cds
2852	15568	28043	3.98	1.0E-09	M28699.1	NT	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
3073	15688	28160	0.77	1.0E-09	BE535440.1	EST_HUMAN	Homo sapiens nuclear phosphoprotein B23 (NPM1) mRNA, complete cds
4916	17491		5.48	1.0E-09	AA719297.1	EST_HUMAN	601058602F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3445177 5'
5694	18320	30819	0.87	1.0E-09	AL163283.2	NT	zsf35603.s1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:414029 3' similar to contains
5696	18616	31352	1.46	1.0E-09	U07000.1	NT	Alu repetitive element; contains element MER22 repetitive element ;
6293	18901	31671	3.17	1.0E-09	P26694	SWISSPROT	Homo sapiens chromosome 21 segment HS21C083
8329	20870	33794	0.87	1.0E-09	A1888474.1	EST_HUMAN	Human breakpoint cluster region (BCR) gene, complete cds
10216	22711		2.57	1.0E-09	AL163283.2	NT	CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS)
12136	25032	30820	3.3	1.0E-09	11418127	NT	w439p05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330481 3' similar to contains
12593	24944		1.82	1.0E-09	AF260225.1	NT	MER25.11 MER25 repetitive element ;
1352	13947	28471	1.48	9.0E-10	AW867740.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
							Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2880	15479	27955	6.87	9.0E-10	A1870071.1	EST_HUMAN	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
6922	19581	32410	4.35	9.0E-10	A1452982.1	EST_HUMAN	MRO-SN0040-050500-002-c07 SN0040 Homo sapiens cDNA
158	12821	25309	10.47	8.0E-10	U63630.2	NT	w478d03.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2347253 3' similar to
3368	15995	28472	0.59	8.0E-10	BE080748.1	EST_HUMAN	SW:RL28_HUMAN P47914 60S RIBOSOMAL PROTEIN L29 ; contains element PTR5 repetitive element ;
4279	18665	28311	4.11	8.0E-10	AA376832.1	EST_HUMAN	q46809.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2144537 3' similar to
9875	22372		2.34	8.0E-10	U36308.2	NT	TR:O00372 O00372 PUTATIVE P150 ;
730	13350	25844	24.84	7.0E-10	7706225	NT	Homo sapiens MCM4 (MCM4) and DNA-PKcs (PRKDC) genes, partial cds
730	13350	25845	24.84	7.0E-10	7706225	NT	QV1-BT0631-150200-071-01 BT0631 Homo sapiens cDNA
1663	14256	26791	2.13	7.0E-10	Q13342	SWISSPROT	EST789584 Small intestine I Homo sapiens cDNA 5' end
2087	14647		1.31	7.0E-10	P08548	SWISSPROT	Homo sapiens lens major intrinsic protein (MIP) gene, complete cds
2594	15158		13	7.0E-10	P08547	SWISSPROT	Homo sapiens TPA inducible protein (LOC51586), mRNA
							Homo sapiens TPA inducible protein (LOC51586), mRNA
							LYSP100 PROTEIN (LYMPHOID-RESTRICTED HOMOLOG OF SP100)
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
							LINE-1 REVERSE TRANSCRIPTASE HOMOLOG

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3124	15738	28206	2.84	7.0E-10	X00856.1	NT	H.sapiens DHFR gene, exon 3
6332	18938	31714	5.28	7.0E-10	AA345220.1	EST_HUMAN	EST151247 Gall bladder II Homo sapiens cDNA 5' end
7446	19970	32838	1.2	7.0E-10	BF352883.1	EST_HUMAN	IL3-HT0619-110700-209-D12 HT0619 Homo sapiens cDNA
7852	20184		1.43	7.0E-10	P35084	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT
7916	20458	33364	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
7916	20458	33365	1.68	7.0E-10	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2
10212	22707	35701	0.57	7.0E-10	L08895.1	NT	Homo sapiens MADS/MEF2-family transcription factor (MEF2C) mRNA, complete cds
11511	23959	37030	1.54	7.0E-10	AW778769.1	EST_HUMAN	ho12g02.x1 NCI_CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3037202 3' similar to contains Alu repetitive element; contains MER7.b1 MER7 repetitive element;
946	13559	28072	3.68	6.0E-10	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
2702	15259	27827	1.89	6.0E-10	AI424405.1	EST_HUMAN	RC3-CT0254-031089-012-g12 CT0254 Homo sapiens cDNA
4847	17425		2.15	6.0E-10	AW853719.1	EST_HUMAN	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1)
8718	21257	34177	0.94	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (ELAM-1)
8718	21257	34178	0.94	6.0E-10	P33730	SWISSPROT	(LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E)
9552	22052	35015	0.52	6.0E-10	P88073	SWISSPROT	E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 2) (LECAM2) (CD62E)
11731	24136		1.47	6.0E-10	AW971923.1	EST_HUMAN	ENTEROPEPTIDASE PRECURSOR (ENTEROKINASE)
792	13410		5.2	5.0E-10	AL046804.1	EST_HUMAN	EST384012 MAGE sequences, MAGL Homo sapiens cDNA
3522	16127	28607	0.86	5.0E-10	Q01033	SWISSPROT	DKFZp434N219_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N219 5'
5002	17575	30018	1.05	5.0E-10	AW028877.1	EST_HUMAN	HYPOTHETICAL GENE 48 PROTEIN
5002	17575	30019	1.05	5.0E-10	AW028877.1	EST_HUMAN	ww97b03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542061 3' similar to contains MER10.11
5128	17700	30134	1.37	5.0E-10	AF181897.1	NT	ww97b03.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542061 3' similar to contains MER10.11
7363	18889		1.84	5.0E-10	BF105159.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
9455	21981	34932	1.65	5.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
9455	21981	34933	1.65	5.0E-10	P34678	SWISSPROT	601822184F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4042413 5'
116	12787		1.02	4.0E-10	AI221083.1	EST_HUMAN	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
607	13235	25709	0.73	4.0E-10	AA515280.1	EST_HUMAN	HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME III
2039	14621	27189	1.17	4.0E-10	AW594709.1	EST_HUMAN	hg09099.x1 Soares_placenta_8cd9weeks_2NNHP80c9W Homo sapiens cDNA clone IMAGE:1759049 3' similar to contains LTR8.b2 LTR8 repetitive element;
							hg58g03.x1 NCI_CGAP_Go3 Homo sapiens cDNA clone IMAGE:924948 3'
							hg58g03.x1 NCI_CGAP_Go3 Homo sapiens cDNA clone IMAGE:2949844 3' similar to contains Alu repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2609	15171	27739	4.19	4.0E-10	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7228	19759	32814	22.35	4.0E-10	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
10087	22592	35584	0.62	4.0E-10	AW293243.1	EST_HUMAN	(UBE2D3) genes, complete cds
10342	22838	35831	1.01	4.0E-10	AI287342.1	EST_HUMAN	U1-H-B12-ah1-e-07-0-J1.s1 NCL CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727061 3'
948	13560	26074	1.95	3.0E-10	N38113.1	EST_HUMAN	eq63h11.s1 Stanley Frontal SN pool 2 Homo sapiens cDNA clone IMAGE:2035653
1395	13989		4.43	3.0E-10	AY005150.1	NT	y63206.s1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:272963 3' similar to contains L1.1 L1 repetitive element;
4633	17218	28687	1.07	3.0E-10	AL163203.2	NT	Homo sapiens extracellular glycoprotein lactin precursor, gene, complete cds
4633	17216	28668	1.07	3.0E-10	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
5646	18274	30748	0.92	3.0E-10	N50109.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
6350	18955	31734	1.87	3.0E-10	P20350	SWISSPROT	y217g08.s1 Soares, multiple_sclerosis_2NblHMSP Homo sapiens cDNA clone IMAGE:282782 3'
6492	18093	31877	2.86	3.0E-10	BE302970.1	EST_HUMAN	RHOMBLOID PROTEIN (VEINLET PROTEIN)
7737	20245	33136	2.3	3.0E-10	AV743302.1	EST_HUMAN	ba76d08.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2806319 5'
7737	20245	33137	2.3	3.0E-10	AV743302.1	EST_HUMAN	AV743302 CB Homo sapiens cDNA clone CBFBGD08 5'
8665	21204	34122	1.08	3.0E-10	H87208.1	EST_HUMAN	y674b12.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:220511 3' similar to contains MER29 repetitive element;
8979	21517	34442	1.61	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
8979	21517	34443	1.61	3.0E-10	AW850731.1	EST_HUMAN	IL3-CT0219-160200-064-B08 CT0219 Homo sapiens cDNA
9284	21790		0.86	3.0E-10	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
10359	22853		2.13	3.0E-10	T65891.1	EST_HUMAN	y611e12.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:80398 5'
10485	22979		1.71	3.0E-10	AA769284.1	EST_HUMAN	n238g03.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1289908 3'
12415	24568	30911	3.44	3.0E-10	BE179517.1	EST_HUMAN	IL3-HT0618-110500-136-E07 HT0618 Homo sapiens cDNA
38	12717	25176	92.79	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
38	12717	25177	92.78	2.0E-10	P48988	SWISSPROT	MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B)
1942	14526		2.33	2.0E-10	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (napi) and survival motor neuron protein (smn) genes, complete cds
3015	15631		0.66	2.0E-10	BF675047.1	EST_HUMAN	602136640F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273377 5'
5971	18592		7.24	2.0E-10	Q28640	SWISSPROT	(HPRG)
8398	19001	31779	1.42	2.0E-10	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7414	18839	32803	7.79	2.0E-10	BE761082.1	EST_HUMAN	601588208F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940824 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7956	20498	33407	0.54	2.0E-10	P28809	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
7956	20498	33408	0.54	2.0E-10	P28809	SWISSPROT	POLYPROTEIN [CONTAINS: PROTEASE; REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
9226	21742		0.85	2.0E-10	BF434585.1	EST_HUMAN	7078d08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3642303 3' similar to contains L1.13 L1 repetitive element;
1556	14148		2.26	1.0E-10	AW667767.1	EST_HUMAN	MRO-SN0038-280300-001-f01 SN0038 Homo sapiens cDNA
1650	14242	26776	2.41	1.0E-10	AV652123.1	EST_HUMAN	AV652123 GLC Homo sapiens cDNA clone GLCXA11 3'
2618	15180		1.78	1.0E-10	AW852001.1	EST_HUMAN	QV0-CT0225-191189-058-e08 CT0225 Homo sapiens cDNA
3548	16152	28634	0.73	1.0E-10	AW832912.1	EST_HUMAN	QV2-TT0003-161189-013-g10 TT0003 Homo sapiens cDNA
3563	16197		0.62	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
3911	16197		0.89	1.0E-10	AL041685.1	EST_HUMAN	DKFZp434N1317.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N1317 5'
4087	16683		6.83	1.0E-10	AF213884.1	NT	Homo sapiens nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (NFKB1) gene, complete cds
4207	16786	29243	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4207	16786	29244	5.77	1.0E-10	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI1), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
4214	16803	29253	1.95	1.0E-10	AB031069.1	NT	Homo sapiens PCCX1 mRNA for protein containing CXC domain 1, complete cds
4249	16837		2.53	1.0E-10	M30629.1	NT	Human pregnancy-specific glycoprotein beta-1 (SP1) mRNA, test exon
5343	17904		1	1.0E-10	A1787745.1	EST_HUMAN	web2704.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2347615 3' similar to contains
8182	20723	33637	1.06	1.0E-10	AW406890.1	EST_HUMAN	MER31.11 MER31 repetitive element;
8589	21128		1.03	1.0E-10	A1268340.1	EST_HUMAN	FB_6A4 Fetal brain library Homo sapiens cDNA
10103	22598		4.16	1.0E-10	AA081888.1	EST_HUMAN	qm04e10.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1860874 3' similar to contains L1.11 L1 repetitive element;
10793	23516	36525	3.47	1.0E-10	A1038280.1	EST_HUMAN	zr23g08.11 Stralagene neuroepithelium NT2RAM1 937234 Homo sapiens cDNA clone IMAGE:548314 5'
11672	18038		1.58	1.0E-10	X87344.1	NT	ov65h03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1672681 3'
283	12939	25425	0.98	9.0E-11	BE145600.1	EST_HUMAN	H.sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
2152	14729	27302	6.73	9.0E-11	AL134395.1	EST_HUMAN	IL2-HT0203-291099-016-c08 HT0203 Homo sapiens cDNA
2152	14729	27303	6.73	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'
3430	16038	28520	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D225 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3430	18038	28521	2.33	9.0E-11	AL134395.1	EST_HUMAN	DKFZp547D225.11 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D225 5'
4598	17182	29829	0.69	9.0E-11	AA775985.1	EST_HUMAN	aa7801.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970287 3'
5763	18389		3.77	9.0E-11	BE079780.1	EST_HUMAN	RC6-BT0627-140200-011-E06 BT0627 Homo sapiens cDNA
10058	22553	35548	0.98	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
10058	22553	35549	0.98	9.0E-11	AA324960.1	EST_HUMAN	EST27872 Cerebellum II Homo sapiens cDNA 5' end
12059	24342	30989	3.52	9.0E-11	C16635.1	EST_HUMAN	C16635 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-506B08 5'
3150	15764		9.38	8.0E-11	H19971.1	EST_HUMAN	y5311.1 s1 Soares adult brain N255HB55Y Homo sapiens cDNA clone IMAGE:172173 3' similar to contains L1 repetitive element
4035	16633	29102	0.68	8.0E-11	A1478617.1	EST_HUMAN	hm54c09.s1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2181936 3'
4117	18711	29165	5.2	8.0E-11	N23712.1	EST_HUMAN	yw46e06.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255288 3'
1497	14089	26629	2.94	7.0E-11	AA330642.1	EST_HUMAN	EST34392 Embryo, 6 week I Homo sapiens cDNA 5' end
3939	16537	29004	0.94	7.0E-11	AJ277548.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
8435	20975	33889	2.61	7.0E-11	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
10129	22624		1.1	7.0E-11	P11369	SWISSPROT	RETROVIRUS-RELATED POL POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE)
12206	24430		1.52	7.0E-11	AV701656.1	EST_HUMAN	AV701656 ADB Homo sapiens cDNA clone ADBABC09 5'
437	13070	25566	5.57	6.0E-11	IM55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
437	13070	25567	5.57	6.0E-11	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
6822	19412	32229	1.03	6.0E-11	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's
7680	20191	33080	3.28	6.0E-11	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
8305	20846	33769	3.25	6.0E-11	AV727859.1	EST_HUMAN	AV727859 HTC Homo sapiens cDNA clone HTCASC06 5'
12	12891	25147	0.9	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3411	12691	25147	1.29	5.0E-11	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
4312	16898	29343	1.04	5.0E-11	P48034	SWISSPROT	ALDEHYDE OXIDASE
6639	19235	32037	3.02	5.0E-11	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
7537	20057	32831	12.3	5.0E-11	11416798	NT	Homo sapiens protocadherin beta 3 (PCDH83), mRNA
1446	14038		1.41	4.0E-11	AA336042.1	EST_HUMAN	zu01b12.11 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730559 5'
2816	15368	27837	8.36	4.0E-11	BE885900.1	EST_HUMAN	601507531F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906295 5'
2997	15613	28093	1.17	4.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4725	17306	28750	0.93	4.0E-11	D44686.1	EST_HUMAN	HUMSUPY069 Human brain cDNA Homo sapiens cDNA clone 069
6602	19198	32005	3.5	4.0E-11	P20095	SWISSPROT	PRE-MRNA SPLICING FACTOR RNA HELICASE PRP2

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7409	19934		4.06	4.0E-11	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
8316	21830		1.44	4.0E-11	BE149425.1	EST_HUMAN	RC1-HT0256-210100-013-08 HT0256 Homo sapiens cDNA
9580	22080	35045	0.91	4.0E-11	A1609763.1	EST_HUMAN	h82g12.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:2105830 3' similar to WP:ZK353.1
12275	24479	30837	1.36	4.0E-11	11545732	NT	CE00385
1538	14130	26868	3.79	3.0E-11	6878077	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
4363	16950		1.47	3.0E-11	AA309248.1	EST_HUMAN	Mus musculus expressed in non-metastatic cells 2, protein (NM23B) (Nme2), mRNA
995	13607	26121	1.64	2.0E-11	A1150502.1	EST_HUMAN	EST180120 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
1227	13626	26342	5.04	2.0E-11	R24807.1	EST_HUMAN	qf36c04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752102 3' similar to contains MER10.13
1227	13828	26343	5.04	2.0E-11	R24807.1	EST_HUMAN	MER10 repetitive element
1655	14247	26780	6.04	2.0E-11	L17432.1	NT	y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
1655	14247	26781	6.04	2.0E-11	L17432.1	NT	y943e12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:35144 5'
							Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
							COR3'beta (COR3'beta) genes, complete cds
							Gallus gallus rho-globin, beta-H globin, beta-A globin, epsilon-globin, and olfactory receptor-like protein
							COR3'beta (COR3'beta) genes, complete cds
1659	14252	26786	1.09	2.0E-11	A1126371.1	EST_HUMAN	qc51c10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1713138 3' similar to
3230	15842	26323	6.98	2.0E-11	P10263	SWISSPROT	gb.L02892 PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR ALPHA (HUMAN); contains L1.11
3368	15976	28453	0.76	2.0E-11	A1478617.1	EST_HUMAN	L1 repetitive element
							RETROVIRUS-RELATED GAG POLYPROTEIN (VERSION 1)
							tm64c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161936 3'
							POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP
							ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N-
							ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1)
3409	18018	28497	0.65	2.0E-11	Q10473	SWISSPROT	
3544	18148		1.01	2.0E-11	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
4539	17123		0.89	2.0E-11	BE065537.1	EST_HUMAN	RC3-BT0316-170200-014-s05 BT0316 Homo sapiens cDNA
4711	17293		0.65	2.0E-11	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
5070	17843		1.37	2.0E-11	BE062558.1	EST_HUMAN	QV2-BT0256-261089-014-s01 BT0258 Homo sapiens cDNA
6284	18892	31661	1.2	2.0E-11	AW877808.1	EST_HUMAN	QV2-PT0073-280300-109-008 PT0073 Homo sapiens cDNA
6452	19053	31838	2.02	2.0E-11	AA581028.1	EST_HUMAN	nc83h05.r1 NCI_CGAP_GC1 Homo sapiens cDNA clone IMAGE:797433 5' similar to SW.PR16_YEAST
7248	18775	32632	0.78	2.0E-11	BF592945.1	EST_HUMAN	P15938 PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16 ;
7823	20385		0.66	2.0E-11	P37072	SWISSPROT	797c03.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:342565 3'
							OLFACTORY RECEPTOR-LIKE PROTEIN COR6

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8150	21685		1.27	2.0E-11	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and tyrosinogen gene families
10184	22678	35871	4.6	2.0E-11	Q13608	SWISSPROT	OLFACTORY RECEPTOR 511 (OLFACTORY RECEPTOR-LIKE PROTEIN OLF1)
10409	22603	35899	0.79	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10409	22603	35900	0.79	2.0E-11	AW885874.1	EST_HUMAN	RC4-OT0072-170400-013-c11 OT0072 Homo sapiens cDNA
10992	23508	36538	2.41	2.0E-11	AA035369.1	EST_HUMAN	ZK27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794.3
10992	23508	36539	2.41	2.0E-11	AA035369.1	EST_HUMAN	ZK27g02.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:471794.3
11805	25020		2.8	2.0E-11	AA704195.1	EST_HUMAN	Z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460824.3
11836	24200		2.49	2.0E-11	AA704195.1	EST_HUMAN	Z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
11860	24218	31043	2.25	2.0E-11	BF377859.1	EST_HUMAN	RC00-CN0027-210100-011-c01 CN0027 Homo sapiens cDNA
12135	24388		2.03	2.0E-11	D25217.2	NT	GM2-TN0140-070900-372-g01 TN0140 Homo sapiens cDNA
12293	24492		5.24	2.0E-11	P08547	SWISSPROT	Homo sapiens mRNA for KIAA0027 protein, partial cds
12629	24707		3.57	2.0E-11	11417968	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
704	13325	25812	2.83	1.0E-11	AL131016.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
816	13434	25939	0.84	1.0E-11	AL163209.2	NT	Homo sapiens SCL gene locus
1259	13656	26372	2.96	1.0E-11	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C009
1546	14138		1.66	1.0E-11	AF118914.1	NT	Homo sapiens chromosome 21 segment HS21C079
2171	14748	27317	2.81	1.0E-11	AF000573.1	NT	Homo sapiens PRO3078 mRNA, complete cds
3546	16150	28630	0.83	1.0E-11	BE004315.1	EST_HUMAN	Homo sapiens homogenisate 1,2-dioxigenase gene, complete cds
4805	17480		0.97	1.0E-11	AL163285.2	NT	CM0-BN0105-170300-292-d12 BN0105 Homo sapiens cDNA
5535	18167	30581	15.03	1.0E-11	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C085
5997	18617	31353	0.8	1.0E-11	BF222646.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
8143	20684	33598	3.16	1.0E-11	4885546	NT	7p57d01.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3649945.3 similar to contains MER10.b3
8517	21058	33978	4.69	1.0E-11	R13174.1	EST_HUMAN	MER10 repetitive element
8978	21516	34440	1.38	1.0E-11	BF365119.1	EST_HUMAN	Homo sapiens PHD finger protein 2 (PHF2) mRNA
8978	21516	34441	1.38	1.0E-11	BF365119.1	EST_HUMAN	Y73408.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:28166.5
11167	23674	36721	2.46	1.0E-11	BF680078.1	EST_HUMAN	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
2979	15595	28075	0.67	9.0E-12	P20742	SWISSPROT	QV4-NN1149-250900-423-a03 NN1149 Homo sapiens cDNA
9713	22211	35184	5.63	9.0E-12	AL163300.2	NT	602154807F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285977.5
9713	22211	35185	5.63	9.0E-12	AL163300.2	NT	PREGNANCY ZONE PROTEIN PRECURSOR
9261	21787		1	8.0E-12	BE074720.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C100
11911	24249		4.51	8.0E-12	AJ271736.1	NT	Homo sapiens chromosome 21 segment HS21C100
4766	17347	28796	1.68	7.0E-12	Q05904	SWISSPROT	IL5-BT0578-130300-036-G12 BT0578 Homo sapiens cDNA
							Homo sapiens Xa pseudautosomal region, segment 2/2
							34 KO SPICULE MATRIX PROTEIN PRECURSOR (LSN34)

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11228	23759	38815	12.18	7.0E-12	AA704735.1	EST_HUMAN	2/23g01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451152 3'
3601	16205		0.72	6.0E-12	AV730554.1	EST_HUMAN	AV730554 HTF Homo sapiens cDNA clone HTFAWF06 5'
4440	17026	29466	10.25	6.0E-12	AA732516.1	EST_HUMAN	nz88f11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1302573 3' similar to contains Alu repetitive element;
8926	21464	34380	0.92	6.0E-12	AF003249.1	NT	Morone saxatilis myosin heavy chain FM3A (FM3A) mRNA, complete cds
9395	21818		1.8	6.0E-12	AA847898.1	EST_HUMAN	cd10g11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1367588 similar to contains MER29 12 MER29 repetitive element;
1081	13686	26108	2.85	5.0E-12	T06873.1	EST_HUMAN	EST04462 Fetal brain, Striatum (cat#836206) Homo sapiens cDNA clone HFBDV33
3437	16045	28526	1.19	5.0E-12	BE047779.1	EST_HUMAN	tz42b05.Y1 NCI_CGAP_Bim52 Homo sapiens cDNA clone IMAGE:2261217 5'
3780	16390	28855	6.69	5.0E-12	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
6172	18784	31550	5.59	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6617	19214	32019	5.59	5.0E-12	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
7096	19448	32264	1.12	5.0E-12	AL040739.1	EST_HUMAN	EST386850 MAGE resequences, MAGN Homo sapiens cDNA
7108	19448	32264	1.14	5.0E-12	AL040739.1	EST_HUMAN	DKFZ434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8171	20712	33629	1.43	5.0E-12	AA033745.1	EST_HUMAN	DKFZp434B1615.s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B1615 3'
8602	21141		0.7	5.0E-12	AV687037.1	EST_HUMAN	201g12.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:375718 3' similar to contains L1.13 L1 repetitive element;
8925	21463		0.98	5.0E-12	AL078561.1	EST_HUMAN	RC1-OT0086-220300-011-507 OT0086 Homo sapiens cDNA
9037	21574	34504	2.42	5.0E-12	AJ271735.1	NT	DKFZp434J0426.J1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434J0426 5'
9344	21858	34806	1.04	5.0E-12	P34982	SWISSPROT	Homo sapiens Xq pseudautosomal region; segment 1/2
10176	22671		4.17	5.0E-12	AL163303.2	NT	OLFACTORY RECEPTOR 1D2 (OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E) (OLFACTORY RECEPTOR 17-4) (OR17-4)
10266	22761	35748	0.67	5.0E-12	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C103
10461	22955	35968	2.12	5.0E-12	6978754	NT	Homo sapiens chromosome 21 segment HS21C102
265	12923	25409	3.53	4.0E-12	AA700326.1	EST_HUMAN	Rattus norvegicus Deleted in colorectal cancer (rat homolog) (Dcc), mRNA
268	12923	25409	4.43	4.0E-12	AA700326.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
4727	17308	29752	0.82	4.0E-12	AL086984.1	EST_HUMAN	z174g11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460676 3'
7615	20128		0.7	4.0E-12	BF445140.1	EST_HUMAN	b226h05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR-O13539 Q13539 MARINER TRANSPOSASE;
8185	20726		2.2	4.0E-12	AF109907.1	NT	nad21b03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3366077 3' similar to contains MER7.b2 MER7 repetitive element;
8621	21160	34075	1.2	4.0E-12	AB042816.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
							Bos taurus Mch2 mRNA for mitochondrial carrier homolog 2, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10961	23476	36501	4.25	4.0E-12	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
12180	24416		1.61	4.0E-12	U78027.1	NT	Homo sapiens Brubn's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
644	13267	25744	2.73	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
644	13267	25745	2.73	3.0E-12	AW341683.1	EST_HUMAN	hd13d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2909377 3' similar to TR:O14517
5643	18272	30746	1.18	3.0E-12	AF111108.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
8316	20857	33783	0.52	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
9035	21572	34501	0.56	3.0E-12	O35453	SWISSPROT	SERINE PROTEASE HEPSIN
10535	23072	36085	3.26	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
10535	23072	36086	3.26	3.0E-12	U37672.1	NT	Human prostate specific antigen gene, 5' flanking region
1893	14285	26820	1.05	2.0E-12	AW802131.1	EST_HUMAN	IL5-UM0071-120400-065-e05 UM0071 Homo sapiens cDNA
3513	16118	28598	0.87	2.0E-12	0754495	NT	Mus musculus keratin-associated protein 6.2 (Krtap6-2), mRNA
4192	16781	29229	0.8	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4192	16781	29230	0.9	2.0E-12	J01884.1	NT	Rat U3A small nuclear RNA
4512	17098		2.58	2.0E-12	BE063509.1	EST_HUMAN	CMO-BT0281-031188-087-a03 BT0281 Homo sapiens cDNA
6603	19200		1.54	2.0E-12	AW971857.1	EST_HUMAN	EST383948 IMAGE resequences, MAGL Homo sapiens cDNA
7227	19758	32613	2.97	2.0E-12	T08169.1	EST_HUMAN	EST06060 Infant Brain, Banto Soares Homo sapiens cDNA clone HIBBA13 5' and
7362	19808	32773	1.21	2.0E-12	BE173035.1	EST_HUMAN	MR0-HT0559-200400-016-e08 HT0559 Homo sapiens cDNA
7656	20168	33055	2.38	2.0E-12	11422228	NT	Homo sapiens Ac-like transposable element (ALTE), mRNA
7894	20436		0.8	2.0E-12	AV683827.1	EST_HUMAN	AV683827 GKC Homo sapiens cDNA clone GKC7B04 5'
9232	21954		2.18	2.0E-12	AF196894.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
9896	22393		11.42	2.0E-12	BE165880.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
10408	22802	35888	0.69	2.0E-12	AI334130.1	EST_HUMAN	qq0702.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1831835 3' similar to TR:Q13538
11820	24190		2.46	2.0E-12	AL163283.2	NT	Q13538 ORF2: FUNCTION UNKNOWN ;
128	12796	25282	2.79	1.0E-12	AW627874.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C083
2031	14613		1.53	1.0E-12	AI871726.1	EST_HUMAN	hh90a09.x1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2970040 3' similar to contains MER18.t1
3106	15721	28191	1.33	1.0E-12	AF000991.1	NT	hm51f07.x1 NCL_CGAP_U02 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1
3106	15721	28192	1.33	1.0E-12	AF000991.1	NT	MER18 repetitive element ;
3943	16541	28007	38.65	1.0E-12	AU132248.1	EST_HUMAN	wm51f07.x1 NCL_CGAP_U02 Homo sapiens cDNA clone IMAGE:2439493 3' similar to contains L1.b3 L1

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3943	16541	29008	38.65	1.0E-12	AU132248.1	EST_HUMAN	AU132248 NT2RP3 Homo sapiens cDNA clone NT2RP3004070 5'
6121	18736		1.85	1.0E-12	U92828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
6182	18802		1.95	1.0E-12	Q9Y2G7	SWISSPROT	HYPOTHETICAL ZINC FINGER PROTEIN KIAA0961
6653	19249	32051	0.7	1.0E-12	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
7170	19702	32549	1.74	1.0E-12	AF198864.1	NT	Homo sapiens putative BPES syndrome breakpoint region protein gene, complete cds
7204	19735	32587	9.7	1.0E-12	A1248533.1	EST_HUMAN	gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
7204	19735	32588	9.7	1.0E-12	A1248533.1	EST_HUMAN	gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN); contains MER10.t1 MER10 repetitive element;
8426	20986	33880	0.54	1.0E-12	U66059.1	NT	Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TORBV7S3A2T, TCRBV13S2A1T, TCRBV5S2A2P, TCRBV7S2A1N4T, TCRBV13S913S>
8639	21178	34098	1.18	1.0E-12	AA782323.1	EST_HUMAN	ac28d05.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857577 3'
11723	24130	37154	4.65	1.0E-12	AW962164.1	EST_HUMAN	EST374237 MAGG resequences, MAGG Homo sapiens cDNA
11941	24273		1.6	1.0E-12	A1798592.1	EST_HUMAN	w33808.x1 NCI_CGAP_C616 Homo sapiens cDNA clone IMAGE:2392095 3'
12097	24990		2.72	1.0E-12	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
12424	24609		2.02	1.0E-12	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4019	16817	29002	0.91	9.0E-13	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
9519	22019		3.1	9.0E-13	NG9953.1	EST_HUMAN	za26b06.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:293851 3'
746	13366	25860	4.58	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
746	13366	25981	4.58	8.0E-13	U29185.1	NT	Homo sapiens prion protein (PrP) gene, complete cds
1878	14464	27021	3.95	8.0E-13	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds; neuronal apoptosis inhibitory protein (naip) and survival motor neuron protein (smn) genes, complete cds
8056	20598	33505	0.68	8.0E-13	AI884398.1	EST_HUMAN	wm31109.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
8056	20598	33506	0.68	8.0E-13	AI884398.1	EST_HUMAN	wm31109.x1 NCI_CGAP_U4 Homo sapiens cDNA clone IMAGE:2437601 3'
10051	22546		2.58	8.0E-13	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11609	24052	37117	2.51	8.0E-13	U68090.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S9A2T, TCRBV5S6A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S6A2T, TCRBV5S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12
8178	20717		0.63	7.0E-13	Q85155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
12212	24435		37.61	7.0E-13	BE778223.1	EST_HUMAN	601463285F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3866813 5'
12448	24583		1.71	7.0E-13	Q10473	SWISSPROT	POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN UDP
2149	14726	27299	6.02	6.0E-13	AL163207.2	NT	ACETYL GALACTOSAMINYLTRANSFERASE (UDP-GALNAC:POLYPEPTIDE, N-
3364	15972		0.78	5.0E-13	R78338.1	EST_HUMAN	ACETYL GALACTOSAMINYLTRANSFERASE (GALNAC-T1)
3444	16052		1.64	5.0E-13	AA435773.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
6959	19535	32359	0.68	5.0E-13	P08983	SWISSPROT	yf2204.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145759 5'
10739	23284	38279	2.49	5.0E-13	P07313	SWISSPROT	z177a12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728350 3' similar to contains Alu
1908	14493		3.69	4.0E-13	AW378614.1	EST_HUMAN	repetitive element; contains element MER22 repetitive element ;
2500	15084		1.71	4.0E-13	AF003529.1	NT	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 30) (CX30)
4858	17436		1.03	4.0E-13	AA454054.1	EST_HUMAN	MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)
5774	18399	31113	5.09	4.0E-13	BE169131.1	EST_HUMAN	PM2-HT0224-221099-001-e11 HT0224 Homo sapiens cDNA
7257	19785	32641	1.07	4.0E-13	AB037750.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
7607	20120	32997	0.81	4.0E-13	AA431529.1	EST_HUMAN	PM3-HT0520-230200-002-e08 HT0520 Homo sapiens cDNA
7705	20214		1.84	4.0E-13	N44291.1	EST_HUMAN	Homo sapiens mRNA for KIAA1329 protein, partial cds
8775	21314	34236	0.94	4.0E-13	AL043810.1	EST_HUMAN	z177g12.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:782182 5' similar to TR:G452763
9933	22426	35403	4.28	4.0E-13	A1289831.1	EST_HUMAN	y33g05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273080 5' similar to PIR:A32995
11046	23559	36595	1.91	4.0E-13	AA435819.1	EST_HUMAN	A32995 t complex sterility protein - mouse ;
11046	23559	36596	1.91	4.0E-13	AA435819.1	EST_HUMAN	DKFZp434A0128_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434A0128 5'
192	12852		4.5	3.0E-13	AF003528.1	NT	q132405.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1899945 3' similar to contains Alu
898	13512		4.67	3.0E-13	AA430310.1	EST_HUMAN	repetitive element;
2408	14976	27550	1.06	3.0E-13	AJ271738.1	NT	z177g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
2519	15083		6.72	3.0E-13	AL163210.2	NT	z177g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:728514 3'
							Homo sapiens X-linked arylidic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							z177g10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781406 5'
							Homo sapiens Xq pseudautosomal region; segment 2/2
							Homo sapiens chromosome 21 segment HS21C010

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2687	15245	27812	2.75	3.0E-13	BF372862.1	EST_HUMAN	CM3-FT0100-140700-242-h08 FT0100 Homo sapiens cDNA
3221	15833		3.1	3.0E-13	AA745844.1	EST_HUMAN	ob18d02.st NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1324035 3'
3551	16155	28637	1.04	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
3551	16155	28638	1.04	3.0E-13	P18616	SWISSPROT	DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)
5730	18356	31060	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR 12 THR repetitive element;
5730	18356	31061	0.7	3.0E-13	AA134017.1	EST_HUMAN	zn88h10.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565315 5' similar to contains THR 12 THR repetitive element;
6143	18757	31515	0.66	3.0E-13	AW005639.1	EST_HUMAN	wz88c02.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2565890 3' similar to TR:O75139 O75139 KIAA0644 PROTEIN;
7824	20366	33274	9.59	3.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
8021	20563	33464	0.66	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re- reactive factor
8021	20563	33465	0.66	3.0E-13	AA352487.1	EST_HUMAN	EST60487 Activated T-cells XX Homo sapiens cDNA 5' and similar to similar to serine protease P100, Re- reactive factor
10556	23092		4.07	3.0E-13	A084768.1	EST_HUMAN	HA0536 Human fetal liver cDNA library Homo sapiens cDNA
10924	23443	36464	2.91	3.0E-13	BE083508.1	EST_HUMAN	GM0-BT0281-031199-087-e03 BT0281 Homo sapiens cDNA
11469	23919	36988	2.49	3.0E-13	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
161	12824	25312	2.59	2.0E-13	U52111.2	NT	Homo sapiens X28 region near ALD locus containing dual specificity phosphatase 9 (DUSP9), ribosomal protein L18a (RPL18a), Ca2+/Calmodulin-dependent protein kinase I (CAMKI), creatine transporter (CRTR), CDM protein (CDM), adrenoleukodystrophy protein >
260	12919	25406	2.22	2.0E-13	U23839.1	NT	Danio rerio fibroblast growth factor receptor 4 mRNA, complete cds
1313	13907	26427	8.84	2.0E-13	AF239710.1	NT	Homo sapiens DNA polymerase delta small subunit (POLD2) gene, exons 1 through 11 and complete cds
3038	15654	28133	0.59	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3038	15654	28134	0.58	2.0E-13	8924119	NT	Homo sapiens hypothetical protein PRO2130 (PRO2130), mRNA
3320	15930	28407	1.2	2.0E-13	BF431899.1	EST_HUMAN	ncb76f05.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
3555	16159	28642	1.14	2.0E-13	AF109907.1	NT	Homo sapiens S164 gene, partial cds; PST and hypothetical protein genes, complete cds; and S171 gene, partial cds
4166	16776		1.9	2.0E-13	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
6271	18879	31647	5.27	2.0E-13	Q08652	SWISSPROT	CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1)

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6905	19639	32475	7.42	2.0E-13	X16912.1	NT	Human PFKFB3 gene for liver-type 8-phosphofructokinase (EC 2.7.1.11) exon 2
10355	22849	35843	4.58	2.0E-13	5031896	NT	Homo sapiens mab-21 (C. elegans)-like 1 (MAB21L1) mRNA
11893	24236		20.31	2.0E-13	AW892155.1	EST_HUMAN	CMO-NN0001-100300-274-e11 NN0001 Homo sapiens cDNA
313	12967	25456	1.6	1.0E-13	S74128.1	NT	FGF-1=fibroblast growth factor 1 [human, kidney, Genomic, 342 nt, segment 2 of 2]
921	13534	26052	4.35	1.0E-13	AJ007973.1	NT	Homo sapiens LGMD2B gene
1381	13974	28502	1.01	1.0E-13	X87344.1	NT	H. sapiens DMA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, DQB2 and RING8, 9, 13 and 14 genes
2088	14648	27220	1.6	1.0E-13	AA720574.1	EST_HUMAN	nm21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13
4116	16710		2.21	1.0E-13	AA324394.1	EST_HUMAN	THR repetitive element;
4866	17278	28724	1.51	1.0E-13	BF340987.1	EST_HUMAN	EST27235 Cerebellum II Homo sapiens cDNA 5' end similar to EST containing L1 repeat
7851	20393	33286	0.77	1.0E-13	AA577812.1	EST_HUMAN	602038009F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4185866 5'
7851	20393	33297	0.77	1.0E-13	AA577812.1	EST_HUMAN	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
10002	22497		0.9	1.0E-13	O15481	EST_HUMAN	repetitive element; contains element MER24 repetitive element;
10202	22697	35691	0.52	1.0E-13	AF300701.1	SWISSPROT	nm24d01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1084801 3' similar to contains Alu
						NT	repetitive element; contains element MER24 repetitive element;
						EST_HUMAN	MELANOMA-ASSOCIATED ANTIGEN B4 (MAGE-B4 ANTIGEN)
						EST_HUMAN	Mus musculus osteoclastic protein tyrosine phosphatase mRNA, complete cds
11258	23786	36842	15.07	1.0E-13	BF108755.1	EST_HUMAN	745e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3524443 3' similar to
11714	24124		1.87	1.0E-13	AV715377.1	EST_HUMAN	contains MER28 b2 MER28 repetitive element;
12393	24563		4.28	1.0E-13	AJ271735.1	NT	AV715377 DGB Homo sapiens cDNA clone DCBAIE03 5'
						EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
355	13004	25488	4.61	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19
						EST_HUMAN	repetitive element;
358	13005	25489	2.07	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19
2545	15109		3.84	9.0E-14	AW861577.1	EST_HUMAN	repetitive element;
2627	15189	27757	1.41	9.0E-14	AJ133127.1	NT	RC4-CT0322-080100-013-009 CT0322 Homo sapiens cDNA
2627	15189	27758	1.41	9.0E-14	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
2782	15335	27903	3.29	9.0E-14	AB038162.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
3145	15759	28225	4.32	9.0E-14	AW513286.1	EST_HUMAN	Homo sapiens TFF gene cluster for trefoil factor, complete cds
						EST_HUMAN	xs54h05.x1 NCI_CGAP_UH1 Homo sapiens cDNA clone IMAGE:2707833 3'
3275	13004	25488	0.71	9.0E-14	AA781159.1	EST_HUMAN	aj24c01.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391232 3' similar to contains MER19.11 MER19
3866	16464	28928	7.24	9.0E-14	D14547.1	NT	repetitive element;
4870	17446	29897	1.77	9.0E-14	AJ002153.1	NT	Human DNA, SINE repetitive element
						NT	Seguinus oedipus gene for seminal vesicle secreted protein semenogelin I

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3545	16149		0.97	8.0E-14	BE489263.1	EST_HUMAN	h271c08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213424 3'
4029	16627		3.29	8.0E-14	R76209.1	EST_HUMAN	y72e03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:144796 3'
6369	20308	33211	36.57	8.0E-14	X99211.1	NT	H sapiens DNA for endogenous retroviral like element
9479	21878	34825	4.61	8.0E-14	AA219316.1	EST_HUMAN	zq17c10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629870 3'
11310	23603		4.45	8.0E-14	BE062558.1	EST_HUMAN	QV2-BT0258-281099-014-a01 BT0258 Homo sapiens cDNA
12106	24368	30972	2.07	8.0E-14	AI688118.1	EST_HUMAN	wc92h08.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2326143 3'
							x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2823146 3' similar to contains MER10.12
1671	15447		2.78	7.0E-14	AW151673.1	EST_HUMAN	MER10 repetitive element;
8851	21390		0.54	7.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
390	13036	25525	14.21	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
9736	22234	35212	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
9738	22234	35213	3.27	6.0E-14	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
646	13269	25747	5.26	5.0E-14	Q63120	SWISSPROT	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1 (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN)
5209	17774	30197	1.53	5.0E-14	AW073791.1	EST_HUMAN	x63b05.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2575185 3' similar to contains L1.12 L1
5724	18350	31053	4.81	5.0E-14	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
1162	15434		1.61	4.0E-14	P04928	SWISSPROT	S-ANTIGEN PROTEIN PRECURSOR
1920	14505	27082	3.86	4.0E-14	AJ007973.1	NT	Homo sapiens LGMD2B gene
3816	16416		0.84	4.0E-14	AA046502.1	EST_HUMAN	z67a06.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
4378	16966	28412	0.9	4.0E-14	N46328.1	EST_HUMAN	y773c12.s1 Soares_multiple_sclerosis_2NbHMS Homo sapiens cDNA clone IMAGE:279190 3' similar to contains L1.13 L1 repetitive element;
7898	20441		0.49	4.0E-14	X87344.1	NT	H sapiens DNA, DMB, HLA-Z1, IPP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
11633	24073	37135	1.91	4.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12457	25107		4.37	4.0E-14	AI886224.1	EST_HUMAN	wm08c03.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2435332 3' similar to contains Alu repetitive element;
985	13597	26110	1.26	3.0E-14	X85466.1	NT	R.norvegicus mRNA for OPG2 protein
5059	17632	30075	0.74	3.0E-14	AW265354.1	EST_HUMAN	xp45112.x1 NCI_CGAP_HN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER9 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6832	19422	32237	1.08	3.0E-14	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
6832	19422	32238	1.08	3.0E-14	AI420786.1	EST_HUMAN	te91c12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2094070 3' similar to TR:O00519 O00519 FATTY ACID AMIDE HYDROLASE. ;
8722	21261	34181	0.96	3.0E-14	N42185.1	EST_HUMAN	yo7b10.r1 Soares melanocyte 2NBM Homo sapiens cDNA clone IMAGE:270523 5'
10872	23393	36408	2.75	3.0E-14	BE888016.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
11116	17632	30075	9.84	3.0E-14	AW265354.1	EST_HUMAN	xp45f12.x1 NCI_CGAP_HIN11 Homo sapiens cDNA clone IMAGE:2743343 3' similar to contains Alu repetitive element; contains element MER0 repetitive element ;
12369	24964		1.84	3.0E-14	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
413	13048	25539	2.51	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
413	13048	25540	2.51	2.0E-14	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
719	15422	25828	9.8	2.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2431	14998		1.48	2.0E-14	AW372868.1	EST_HUMAN	RCS-BT037-091299-031-D12 BT0377 Homo sapiens cDNA
2504	15088		1.07	2.0E-14	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
2567	15131	27699	1.03	2.0E-14	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
2699	15256		0.88	2.0E-14	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
5715	18341	30847	0.95	2.0E-14	BF380661.1	EST_HUMAN	IL2-UT0072-240800-142-D07 UT0072 Homo sapiens cDNA
5804	18428	31148	0.8	2.0E-14	AI312351.1	EST_HUMAN	la78h01.x2 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2050225 3' similar to contains L1.13 L1 repetitive element ;
5895	18517	31242	2.86	2.0E-14	U01317.1	NT	Human beta globin region on chromosome 11
6963	19540		0.98	2.0E-14	BE000550.1	EST_HUMAN	RC3-BN0072-240200-011-a06 BN0072 Homo sapiens cDNA
7329	19856	32719	1.12	2.0E-14	P56163	SWISSPROT	ZINC-FINGER PROTEIN NEURO-D4
7518	20038	32806	20.34	2.0E-14	BE158781.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
7518	20038	32907	20.34	2.0E-14	BE158781.1	EST_HUMAN	IL2-HT0397-071299-024-D04 HT0397 Homo sapiens cDNA
9831	22329	35311	0.54	2.0E-14	AI978795.1	EST_HUMAN	wf59g10.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2492034 3' similar to contains Alu repetitive element ;
10659	23191	36206	4.65	2.0E-14	AW139800.1	EST_HUMAN	UI-H-B11-adv-a-10-0-UJ s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2718234 3'
12366	24988		3.3	2.0E-14	AF008191.1	NT	Homo sapiens putative G6 protein (GR6) gene, complete cds
12617	15088		1.99	2.0E-14	7657528	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1105	13708	28218	1.89	1.0E-14	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1452	14044	28572	6.89	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
1452	14044	28573	6.89	1.0E-14	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
2044	14626	27195	7.63	1.0E-14	L44140.1	NT	Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2228	14803	27374	5.33	1.0E-14	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2453	15020	27591	5.89	1.0E-14	AF001688.1	NT	Homo sapiens ribosomal protein L23A (RPL23A) gene, complete cds
2971	15587	28069	1.51	1.0E-14	P05227	SWISSPROT	HISTIDINE-RICH PROTEIN PRECURSOR (CLONE PFHRP-II)
3203	15815	28260	3.91	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3203	15815	28291	3.91	1.0E-14	BF335227.1	EST_HUMAN	RC2-CT0432-310700-013-a09_1 CT0432 Homo sapiens cDNA
3955	16553	29022	2.1	1.0E-14	AA682994.1	EST_HUMAN	ae89c12.s1 Stratiogene schizo brain S11 Homo sapiens cDNA clone IMAGE:2753059 3'
4572	17155	29599	1.71	1.0E-14	AW275852.1	EST_HUMAN	xq39h10.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2753059 3'
5977	18597	31332	2.03	1.0E-14	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
6778	24770	32183	12	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
6778	24770	32184	12	1.0E-14	11437150	NT	Homo sapiens promitin (mouse)-like 1 (PROML1), mRNA
1620	14213	26744	1.19	9.0E-15	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPR1), mRNA
							Homo sapiens transcription factor GIM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel $\alpha 2$
2217	14792		1.39	9.0E-15	AF198779.1	NT	GAG POLYPEPTIDE [CONTAINS: CORE PROTEINS P15, P12, P30, P10]
7507	20029	32892	3.77	9.0E-15	P21416	SWISSPROT	601677750F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960166 5'
7959	20501	33410	1.36	9.0E-15	BE603559.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
12560	24680		1.76	9.0E-15	AL163247.2	NT	601148632F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3164023 5'
2837	13138		1.17	8.0E-15	BE261482.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
7233	19763	32619	1.29	7.0E-15	BF036327.1	EST_HUMAN	xn77d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700483 3' similar to contains THR12 THR repetitive element 1
10331	22825		2.53	7.0E-15	AW241958.1	EST_HUMAN	zs57d08.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:701583 5' similar to gbL21834 STEROL O-ACYLTRANSFERASE (HUMAN); contains L111 L1 repetitive element 1
11776	24164		1.76	7.0E-15	AA284465.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 2/2
1031	13641	26156	6.29	6.0E-15	AJ271736.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6077	18694	31440	1.18	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
6077	18694	31441	1.18	6.0E-15	X73462.1	NT	O.aries mRNA for hair keratin cysteine-rich protein
11182	25128		1.86	6.0E-15	AW836843.1	EST_HUMAN	QV1-LT0036-150200-070-c10 LT0036 Homo sapiens cDNA
12648	24722		1.3	6.0E-15	BF432200.1	EST_HUMAN	na81c12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE: 3'
435	13068	25563	5.19	5.0E-15	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
							Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
2789	15342	27912	2.35	5.0E-15	U091328.1	NT	UI-H-BW0-ajb-g-10-0-UI.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2731219 3'
3515	16120		1.06	5.0E-15	AW296817.1	EST_HUMAN	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5289	17861		1.28	5.0E-15	P11369	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; ENDONUCLEASE]
10555	23091		2.72	5.0E-15	AV730036.1	EST_HUMAN	AV730036 HTF Homo sapiens cDNA clone HTFAVE08 5'
452	12681	25137	2.33	4.0E-15	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
6771	19384	32173	0.79	4.0E-15	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
10940	20287	33184	2.54	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
10940	20287	33185	2.54	4.0E-15	AJ130894.1	NT	Homo sapiens mRNA for transcription factor
4297	16883		7.28	3.0E-15	N89452.1	EST_HUMAN	LY1142F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone LY1142 5' similar to ANF(CARDIODILATIN)
5060	17633		0.57	3.0E-15	P92485	SWISSPROT	NADH-JIBUQUINONE OXIDOREDUCTASE CHAIN 5
5179	17746	30175	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
5179	17746	30176	0.72	3.0E-15	AA078097.1	EST_HUMAN	7P01F03 Chromosome 7 Placental cDNA Library Homo sapiens cDNA clone 7P01F03
6904	19638		1.41	3.0E-15	Q64625	SWISSPROT	GLUTATHIONE PEROXIDASE RY2D1 PRECURSOR (ODORANT-METABOLIZING PROTEIN RY2D1)
7323	19850	32711	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
7323	19850	32712	3.48	3.0E-15	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
9839	22337		2.32	3.0E-15	AA807128.1	EST_HUMAN	cc36a07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351764 3' similar to contains MER19.11 MER19 repetitive element;
10873	23205	36218	3.36	3.0E-15	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
12114	24997		1.36	3.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
271	12928	25415	4.1	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
391	13037	25526	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
391	13037	25527	3.78	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2410	14978	27552	1.44	2.0E-15	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER29 repetitive element;
2410	14978	27553	1.44	2.0E-15	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28.b3 MER29 repetitive element;
3559	16103	28845	0.73	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3559	16103	28846	0.73	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4142	16734	28188	0.95	2.0E-15	AW238499.1	EST_HUMAN	xp26h01.x1 NC1_CGAP_HIN10 Homo sapiens cDNA clone IMAGE:2741521 3' similar to contains L1 t3 L1 repetitive element ;
4728	17310		2.72	2.0E-15	AI806335.1	EST_HUMAN	wf07f08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2349923 3' similar to TR:Q61043
5332	17893	30306	0.93	2.0E-15	P13993	SWISSPROT	REPTITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
5332	17893	30307	0.93	2.0E-15	P13993	SWISSPROT	REPTITIVE PROLINE-RICH CELL WALL PROTEIN 2 PRECURSOR
6328	18935	31711	1.02	2.0E-15	BE582352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
6328	18935	31712	1.02	2.0E-15	BE582352.1	EST_HUMAN	601344253F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677268 5'
7168	19700		1.37	2.0E-15	AJ400877.1	NT	Homo sapiens ASCL3 gene, CEGP1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
7315	19842	32703	2.51	2.0E-15	AA704195.1	EST_HUMAN	z177e03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:460924 3'
7427	19951	32816	4.49	2.0E-15	W05084.1	EST_HUMAN	z178d10.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:288675 5' similar to WP:F44F4.8 CE02227 TRANSPOSASE ;
8837	21376	34300	2.62	2.0E-15	D14547.1	NT	Human DNA, SINE repetitive element
9002	21539	34468	0.87	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9002	21539	34468	0.87	2.0E-15	AA397758.1	EST_HUMAN	z177g08.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728414 5'
9325	21839	34780	1.13	2.0E-15	AW379465.1	EST_HUMAN	CMD-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
9325	21839	34781	1.13	2.0E-15	AW379465.1	EST_HUMAN	CMD-HT0244-201099-078-a12 HT0244 Homo sapiens cDNA
10718	23246		3.59	2.0E-15	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
12487	16163	28645	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
12487	16163	28646	2.97	2.0E-15	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
2803	15355		2.08	1.0E-15	AI869884.1	EST_HUMAN	b26h05.x1 NC1_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2270745 3' similar to TR:Q13539 Q13539 MARINER TRANSPOSASE ;
3046	15662	28143	1.24	1.0E-15	BE043584.1	EST_HUMAN	hk40e02.v1 NC1_CGAP_Ox34 Homo sapiens cDNA clone IMAGE:2899162 5'
3176	15789	28281	1.05	1.0E-15	P08547	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
6510	19110	31886	1.71	1.0E-15	T95763.1	EST_HUMAN	ye40e10.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:120234 3' similar to contains MER8 repetitive element ;
7080	19652		1.91	1.0E-15	BE074217.1	EST_HUMAN	QV3-BT0568-270100-074-g05 BT0568 Homo sapiens cDNA
7105	19445	32262	0.77	1.0E-15	P39057	SWISSPROT	DYNEIN BETA CHAIN, CILIARY
8174	20715	33631	0.89	1.0E-15	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8359	20899	33819	4.97	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'
8359	20899	33820	4.97	1.0E-15	AI200976.1	EST_HUMAN	qf68h06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755227 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8969	21507	34428	0.51	1.0E-15	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
8972	21510	34432	1.99	1.0E-15	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
9171	21748	34691	0.87	1.0E-15	Q39575	SWISSPROT	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
9550	22050	35012	1.18	1.0E-15	AA884853.1	EST_HUMAN	oh37c03.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1
10698	23228	36242	6.86	1.0E-15	AF044083.1	NT	repetitive element;
12564	24820	30792	9.35	1.0E-15	AI783944.1	EST_HUMAN	Homo sapiens major histocompatibility locus class III region
4417	17002		0.83	9.0E-16	BF689487.1	EST_HUMAN	602120102F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4277422 5'
4602	17185	29632	1.11	9.0E-16	4503168	NT	Homo sapiens cut (Drosophila)-like 1 (CCAT displacement protein) (CUTL1) mRNA
10873	23394	36409	2.68	9.0E-16	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
5880	18502	31228	0.73	7.0E-16	4885120	NT	Homo sapiens chemokine (C-C motif) receptor 8 (CCR8) mRNA
7379	19905	32769	1.36	7.0E-16	O88807	SWISSPROT	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
7379	19905	32770	1.36	7.0E-16	O88807	SWISSPROT	(PEPTIDYLARGININE DEIMINASE TYPE ALPHA)
12509	24916		33.75	7.0E-16	T94149.1	EST_HUMAN	PROTEIN-ARGININE DEIMINASE TYPE IV (PEPTIDYLARGININE DEIMINASE IV) (PAD-R4)
2186	14762		29.26	6.0E-16	AW972811.1	EST_HUMAN	ye28c12.11 Stratagene lung (H937210) Homo sapiens cDNA clone IMAGE:119062 5'
5436	17891	30397	0.94	6.0E-16	BF365702.1	EST_HUMAN	EST384702 MAGE resequences, MAGL Homo sapiens cDNA
1539	14131	28867	1.21	5.0E-16	AJ251154.1	NT	QV2-NT0048-160800-318-412 NT0048 Homo sapiens cDNA
2705	15282	27829	2.6	5.0E-16	AA692176.1	EST_HUMAN	Mus musculus olfactory receptor cluster, OR37A, OR37B, OR37C, OR37E genes and OR37D pseudogene
11386	23848	36914	3.76	5.0E-16	BF217368.1	EST_HUMAN	ot80c04.s1 Soares fetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1623078 3' similar to
12806	24890		4.98	5.0E-16	11418127	NT	contains element L1 repetitive element;
2281	14855		1.23	4.0E-16	AB001523.1	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
2419	14987	27561	1.88	4.0E-16	AW797168.1	EST_HUMAN	Homo sapiens gene for TMEM1 and PWP2, complete and partial cds
2419	14987	27562	1.98	4.0E-16	AW797168.1	EST_HUMAN	QV1-JM00038-200300-115-g02 UM0036 Homo sapiens cDNA
3503	16108	28584	6.73	4.0E-16	Q16853	SWISSPROT	QV1-JM00038-200300-115-g02 UM0036 Homo sapiens cDNA
4223	16811	29258	4.28	4.0E-16	BE083875.1	EST_HUMAN	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR
4223	16811	29259	4.28	4.0E-16	BE083875.1	EST_HUMAN	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
7698	20207	34878	1.44	4.0E-16	11423161	NT	PM4-BT0650-010400-002-g09 BT0650 Homo sapiens cDNA
9219	21736		1.44	4.0E-16	11423161	NT	Homo sapiens chromosome 21 segment HS21C084
11098	23608	36648	1.66	4.0E-16	AV730030.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ10024 (FLJ10024), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11800	24180		1.34	4.0E-16	P08548	SWISSPROT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
11837	24232		13.78	4.0E-16	C05947.1	EST_HUMAN	C05947 Human pancreatic islet Homo sapiens cDNA clone hbc5355
11897	24239	31006	2.91	4.0E-16	6912459	NT	Homo sapiens Grb2-associated binder 2 (GAB2), mRNA
12178	24414		1.8	4.0E-16	R18591.1	EST_HUMAN	yf96b11.11 Soares infant brain (NIB) Homo sapiens cDNA clone IMAGE:30489 5'
138	12803	25292	0.93	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
138	12803	25293	0.93	3.0E-16	AW022862.1	EST_HUMAN	df45c01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2486376 5'
491	13124		1.24	3.0E-16	AL046445.1	EST_HUMAN	DKFZp434P037.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434P037 5'
501	13133		2.35	3.0E-16	AF135446.1	NT	Homo sapiens TSX (TSX) pseudogene, exon 5
1501	14083	26632	1.81	3.0E-16	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
							ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220]
3004	15620	28097	4.2	3.0E-16	P03200	SWISSPROT	EST06060 Infant Brain, Bento Soares Homo sapiens cDNA clone HIBBA13 5' end
4007	16605	29079	0.61	3.0E-16	T08189.1	EST_HUMAN	Human BXP20 gene
4031	16629		1.07	3.0E-16	U03887.1	NT	SW:KID1_MOUSE Q61751 RENAL TRANSCRIPTION FACTOR KID-1;
4689	17271	29720	0.97	3.0E-16	AW160828.1	EST_HUMAN	AV661393 GLC Homo sapiens cDNA clone GLCGSA01 3'
5077	17650	30091	1.14	3.0E-16	AV661393.1	EST_HUMAN	7B10F02 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B10F02
5482	18116		0.9	3.0E-16	AA077225.1	EST_HUMAN	Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions
5901	18428	31144	1.57	3.0E-16	AF003529.1	NT	am98h05 s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR.b2 THR repetitive element;
8592	21131	34047	4.08	3.0E-16	A002836.1	EST_HUMAN	602246558F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332032 5'
8805	22303		0.94	3.0E-16	BF690817.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
10027	22522	35518	5.15	3.0E-16	L78810.1	NT	DKFZp434L1623.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L1623 5'
12637	25078	30516	9.33	3.0E-16	AL043268.2	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
1007	13818		1.38	2.0E-16	AL163279.2	NT	af08404.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1030855 3'
2429	14998		1.01	2.0E-16	AA621761.1	EST_HUMAN	Human SSAV-related endogenous retroviral LTR-like element
2713	15270		1.53	2.0E-16	J03061.1	NT	H. sapiens DNA for endogenous retroviral like element
4257	16843	29292	1.34	2.0E-16	X89211.1	NT	RC3-BT0046-131198-003-H12 BT0046 Homo sapiens cDNA
5370	17930	30344	0.57	2.0E-16	BE081178.1	EST_HUMAN	HISTIDINE-RICH PROTEIN KE4
6839	19429	32245	0.89	2.0E-16	Q31125	SWISSPROT	fi19e11.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141708 3' similar to contains element
							MER33 repetitive element;
7701	20210	33097	0.76	2.0E-16	A1470723.1	EST_HUMAN	nz47f06.x6 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1290947 similar to TR:O54849 O54849 HYPOTHETICAL 42.9 KD PROTEIN. [2] TR:O08905 :contains MER7.1 MER7 repetitive element;
7808	20450	33357	1.81	2.0E-16	A1732837.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8099	20840	33551	0.7	2.0E-16	BE58028.1	EST_HUMAN	782h09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3'
8099	20840	33552	0.7	2.0E-16	BE58028.1	EST_HUMAN	782h09.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:3303521 3'
8464	21004	33921	0.6	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
8464	21004	33922	0.6	2.0E-16	AW877214.1	EST_HUMAN	CM4-PT0034-180200-506-a01 PT0034 Homo sapiens cDNA
10808	23331	36343	2.71	2.0E-16	5902145	NT	Homo sapiens ubiquitin carrier protein E2-G (UBCH10), mRNA
197	12857	25339	2.66	1.0E-16	AF200719.1	NT	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
405	13080		29.83	1.0E-16	AA628592.1	EST_HUMAN	af39g11.s1 Soares_tet101_263-a10 BNO148 Homo sapiens cDNA
2014	14596	27159	1.78	1.0E-16	BF327942.1	EST_HUMAN	QV0-BNO148-070700-263-a10 BNO148 Homo sapiens cDNA
5386	18518	31243	0.85	1.0E-16	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
6565	19163		27.66	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
6688	19284	32087	2.77	1.0E-16	Q0279	SWISSPROT	MITOGEN-ACTIVATED PROTEIN KINASE KINASE 10 (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST)
7556	19163		6.08	1.0E-16	U45983.1	NT	Homo sapiens CCR8 chemokine receptor (CMKBR8) gene, complete cds
9207	21724	34667	1.15	1.0E-16	AW876651.1	EST_HUMAN	QV2-PT0012-040400-124-a05 PT0012 Homo sapiens cDNA
3802	18402	28866	2.48	9.0E-17	AW900048.1	EST_HUMAN	CM1-NN1003-200300-153-a01 NN1003 Homo sapiens cDNA
6824	19414		1.94	9.0E-17	AI392964.1	EST_HUMAN	tg22c11.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2109524 3' similar to contains MER28.12
8052	20594		4.65	9.0E-17	AW150257.1	EST_HUMAN	MER28 repetitive element;
10124	22618		2.1	9.0E-17	AF200719.1	NT	repetitive element;
1056	13681		1.59	8.0E-17	AW880701.1	EST_HUMAN	Homo sapiens pituitary tumor transforming gene protein (PTTG) gene, complete cds
3961	16559		0.7	8.0E-17	AL163280.2	NT	QV0-OT0032-080300-155-a01 OT0032 Homo sapiens cDNA
5771	24748	31111	3.55	8.0E-17	BE172081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
7319	19846		1.82	8.0E-17	AV730759.1	EST_HUMAN	MR0-HT0559-060300-003-a04 HT0559 Homo sapiens cDNA
1505	14097		3.4	7.0E-17	6753097	NT	AV730759 HTF Homo sapiens cDNA clone HTFAQB07 5'
5526	18158		2.87	7.0E-17	AF216850.1	NT	Mus musculus adiponectin B editing complex 2 (Apobec2), mRNA
						NT	Homo sapiens putative MTAP (MTAP) mRNA, partial cds, alternatively spliced
6789	19380	32106	7.15	7.0E-17	AF229843.1	NT	Mus musculus WNT-2 gene, partial cds; putative ankyrin-related protein and cystic fibrosis transmembrane
217	12878	25365	7.43	6.0E-17	AW883880.1	EST_HUMAN	conductance regulator (CFTR) genes, section 1 of 2 of the complete cds; and unknown gene
6455	19056	31841	1.88	8.0E-17	AW662772.1	EST_HUMAN	RC1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
10192	22687	35680	0.52	6.0E-17	P20138	SWISSPROT	hi81d04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878695 3' similar to contains L1 t2
						SWISSPROT	L1 repetitive element;
						SWISSPROT	MYELOID CELL SURFACE ANTIGEN CD33 PRECURSOR (GP67)

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal:	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
446	12675	25131	2.78	5.0E-17	T64110.1	EST_HUMAN	yc05h08.r1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:76839 5'
7586	20101	32976	1.82	5.0E-17	T81043.1	EST_HUMAN	yt26b04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109327 5'
9284	21884	34829	1.12	4.0E-17	AW129165.1	EST_HUMAN	xt20e04.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2618622 3' similar to contains Alu repetitive element; contains MER19.b1 MER19 repetitive element;
11365	23817	36878	2.17	4.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
11816	24188		2.36	4.0E-17	A1073546.1	EST_HUMAN	ov45e04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640266 3' similar to TR:Q16530
1540	14132		1.03	3.0E-17	D14547.1	NT	Q16530 PMS3 MRNA; contains MER10.12 MER10 repetitive element;
2146	14723	27285	1.28	3.0E-17	AW119123.1	EST_HUMAN	Human DNA, SINE repetitive element
3227	15839		1.41	3.0E-17	P35410	SWISSPROT	xd89c09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604784 3'
3704	16305	28773	1.24	3.0E-17	BE326522.1	EST_HUMAN	MAS-RELATED G PROTEIN-COUPLED RECEPTOR MRG
3704	16305	28774	1.24	3.0E-17	BE326522.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
5181	17747		1.02	3.0E-17	BF511266.1	EST_HUMAN	hw05b04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3181999 3'
8212	20753	33667	1.09	3.0E-17	N68451.1	EST_HUMAN	UI-H-B14-eq-c-06-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085043 3'
9618	22118	35081	4.54	3.0E-17	AB028898.1	NT	za14b02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292491 3' similar to contains PTR5.13 PTR5 repetitive element;
10282	22777	35767	0.65	3.0E-17	BF327012.1	EST_HUMAN	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
10282	22777	35768	0.65	3.0E-17	BF327012.1	EST_HUMAN	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
11775	24163		3.77	3.0E-17	11417866	NT	QV3-BN0047-270700-283-a12 BN0047 Homo sapiens cDNA
375	13024	25510	3.38	2.0E-17	A1270080.1	EST_HUMAN	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
378	13024	25510	2.68	2.0E-17	A1270080.1	EST_HUMAN	q63e06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1956922 3' similar to contains Alu repetitive element;
1025	13636		1.12	2.0E-17	AA72832.1	EST_HUMAN	q63e06.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:1956922 3' similar to contains Alu repetitive element;
2490	15055	27627	2.43	2.0E-17	Q28983	SWISSPROT	zg81d04.s1 Soares_fetal_heart_NBH18W Homo sapiens cDNA clone IMAGE:399751 3'
2490	15055	27628	2.43	2.0E-17	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2956	15572	28049	8.06	2.0E-17	P12036	SWISSPROT	ZONADHESIN PRECURSOR
5569	18200	30648	1.57	2.0E-17	M27685.1	NT	NEUROFILAMENT TRIPLET H PROTEIN (200 KDA NEUROFILAMENT PROTEIN) (NEUROFILAMENT HEAVY POLYPEPTIDE) (NF-H)
5569	18200	30649	1.57	2.0E-17	M27685.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6410	19013		1.8	2.0E-17	AF05066.1	NT	Mus musculus ultra high sulfur keratin gene, complete cds
6816	19213		1.58	2.0E-17	AL134881.1	EST_HUMAN	Homo sapiens MHC class 1 region
7773	20282	33179	0.85	2.0E-17	AB037839.1	NT	DKFZp762J0610_r1 762 (synonym: hma2) Homo sapiens cDNA clone DKFZp762J0610 5'
							Homo sapiens mRNA for KIAA1418 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8028	20570	33474	1.64	2.0E-17	Q95156	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF3
8394	20934	33856	1.15	2.0E-17	AA300640.1	EST_HUMAN	EST13504 Testis tumor Homo sapiens cDNA 5' end similar to glycogenin
9783	22281	35287	2.45	2.0E-17	BE298988.1	EST_HUMAN	600944890F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960615 5'
9818	22316	35297	3.36	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
9818	22316	35298	3.36	2.0E-17	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
10160	22655	35650	7.23	2.0E-17	D13391.1	NT	Human CYP19 gene for aromatase cytochrome P-450, promoter region (containing two cis-acting transcriptional regulatory elements)
10281	22776	35765	0.58	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10281	22776	35766	0.58	2.0E-17	P98063	SWISSPROT	BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BMP-1)
10306	22800	35791	0.63	2.0E-17	A798802.1	EST_HUMAN	wes4b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
10306	22800	35792	0.63	2.0E-17	A798802.1	EST_HUMAN	wes4b04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348719 3'
780	13399	25902	3.38	1.0E-17	P08183	SWISSPROT	MULTIDRUG RESISTANCE PROTEIN 1 (P-GLYCOPROTEIN 1)
1746	14396		1.2	1.0E-17	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
1804	14394	26939	2.89	1.0E-17	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2162	14736	27309	2.11	1.0E-17	P02461	SWISSPROT	COLLAGEN ALPHA 1(III) CHAIN PRECURSOR
2373	14943	27515	1.86	1.0E-17	U79410.1	NT	Homo sapiens thrombospondin 2 (THBS2) gene, promoter region and exons 1A and 1B
3625	16228		0.89	1.0E-17	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
4217	16805		8.46	1.0E-17	R09842.1	EST_HUMAN	y30e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128388 5'
6759	18352	32161	1.55	1.0E-17	A1185642.1	EST_HUMAN	q65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
6759	18352	32162	1.55	1.0E-17	A1185642.1	EST_HUMAN	q65b05.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743825 3'
7146	18678	32520	1.28	1.0E-17	Q16831	SWISSPROT	URIDINE PHOSPHORYLASE (UDRPASE)
8528	21067	33986	1.23	1.0E-17	BE062744.1	EST_HUMAN	QV0-BT0263-101299-072-d07 BT0263 Homo sapiens cDNA
9619	22415	35390	0.94	1.0E-17	AW996338.1	EST_HUMAN	QV3-BN0046-220300-129-c10 BN0046 Homo sapiens cDNA
11295	23747	36805	1.82	1.0E-17	Q28824	SWISSPROT	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE (MLCK) [CONTAINS: TELOKIN]
2510	15074	27647	1.13	9.0E-18	AA174078.1	EST_HUMAN	zp18g12.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609862 3'
9418	21927		3.03	9.0E-18	AI472167.1	EST_HUMAN	y66d03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2148389 3'
3654	16452	28615	1.56	8.0E-18	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
371	13020	25504	32.66	7.0E-18	AW316976.1	EST_HUMAN	xx10b04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S
371	13020	25505	32.66	7.0E-18	AW316976.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);
7469	19991	32854	0.96	7.0E-18	AW887542.1	EST_HUMAN	RIBOSOMAL PROTEIN L4 (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12306	13020	25504	5.28	7.0E-18	AW316978.1	EST_HUMAN	xx10b04.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
12306	13020	25505	5.28	7.0E-18	AW316978.1	EST_HUMAN	xx10b04.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2837071 3' similar to gb:L20868 60S RIBOSOMAL PROTEIN L4 (HUMAN);
3334	15944	28419	1.36	6.0E-18	X71791.2	NT	Rattus norvegicus partial GdnPn-1 gene for glia-derived nexin/protease nexin I, enhancer region
4857	17435		3.95	6.0E-18	P52181	SWISSPROT	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE (TISSUE TRANSGLUTAMINASE) (TGASE C) (TGC)
8192	20733		2.75	6.0E-18	11428155	NT	Homo sapiens similar to high-mobility group (nucleosome) protein 4 (H. sapiens) (LOC634448), mRNA
8289	20830	33751	0.6	6.0E-18	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11014	23528	36584	1.87	6.0E-18	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11209	23713	36767	1.9	6.0E-18	X87344.1	NT	H. sapiens DNA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, TAP2, DOB, DOB2 and RING8, 9, 13 and 14 genes
11501	24034		2.22	6.0E-18	11429885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
12041	24328	30995	2.24	6.0E-18	U67929.1	NT	Human acetylase hydratase (ACO2) gene, exon 4
1187	13788	26299	11.3	5.0E-18	AI280214.1	EST_HUMAN	qm65g11.x1 Soares_placenta_8to9weeks_2NdbIP8to9W Homo sapiens cDNA clone IMAGE:1893668 3' similar to contains Alu repetitive element
5284	17846	30273	0.94	5.0E-18	D61517.1	EST_HUMAN	HUM411F05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-411F05 5'
5477	18111	30520	1.03	5.0E-18	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8654	21193	34111	4.62	5.0E-18	BE143312.1	EST_HUMAN	MR0-HT0161-221068-002-c08 HT0161 Homo sapiens cDNA
10857	23378	36398	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
10857	23378	36397	3.68	5.0E-18	10242378	NT	Homo sapiens lymphocyte activation-associated protein (LOC51088), mRNA
12170	24409		6.5	5.0E-18	AW867182.1	EST_HUMAN	MR1-SN0035-060400-001-g11 SN0035 Homo sapiens cDNA
12531	24844		51.19	5.0E-18	AV650547.1	EST_HUMAN	AV650547 GLO Homo sapiens cDNA clone GLCCGA02 3'
130	12797	25283	1.96	4.0E-18	BE044076.1	EST_HUMAN	hc36h04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element
130	12797	25284	1.96	4.0E-18	BE044076.1	EST_HUMAN	hc36h04.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element
1754	14344	26890	8.14	4.0E-18	AA621814.1	EST_HUMAN	nc24f11.s1 NCL CGAP_Co10 Homo sapiens cDNA clone IMAGE:1144845 3' similar to gb:M26326 KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
1933	14517		0.92	4.0E-18	AI736592.1	EST_HUMAN	w133h08.x1 NCL CGAP_Co18 Homo sapiens cDNA clone IMAGE:2392095 3'
2242	14817	27390	1.23	4.0E-18	Q06430	SWISSPROT	N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (IGNT)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2242	14817	27391	1.23	4.0E-18	006430	SWISSPROT	N-ACETYL LACTOSAMINIDE BETA-1,6-N-ACETYL GLUCOSAMINYL TRANSFERASE (N-ACETYL GLUCOSAMINYL TRANSFERASE) (L-BRANCHING ENZYME) (IGNT)
5566	18197	30843	2.32	4.0E-18	A1017565.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
5566	18197	30644	2.32	4.0E-18	A1017565.1	EST_HUMAN	cu23e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1627138 3'
7787	20330		0.81	4.0E-18	AA746811.1	EST_HUMAN	mx4a08.s1 NCI_CGAP_A101 Homo sapiens cDNA clone IMAGE:1266998 similar to contains L1.12 L1 repetitive element;
10894	23405	36424	7.68	4.0E-18	AA371807.1	EST_HUMAN	EST83633 Pituitary gland, subtracted (prolactin/growth hormone) II Homo sapiens cDNA 5' end similar to EST containing O family repeat
882	13496	26015	18.02	3.0E-18	AA814196.1	EST_HUMAN	ob23h11.s1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1324581 3' similar to SW_RS5_HUMAN
985	13578	26091	2.25	3.0E-18	BE088634.1	EST_HUMAN	P46782 40S RIBOSOMAL PROTEIN S5;
4022	16820	29093	1.25	3.0E-18	AL163247.2	NT	CMO-BT0890-210300-288-g07 BT0890 Homo sapiens cDNA
6917	19578	32405	8.98	3.0E-18	BE001671.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C047
12312	24504		8.85	3.0E-18	AW022015.1	EST_HUMAN	PMO-BN0081-100300-001-b08 BN0081 Homo sapiens cDNA
272	12929	25416	2.57	2.0E-18	AW838620.1	EST_HUMAN	df31h12.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2485126 5'
1192	13793		197.1	2.0E-18	BE256097.1	EST_HUMAN	QV1-L T0036-150200-070-e07 LT0036 Homo sapiens cDNA
3157	15771	28238	1.15	2.0E-18	Q39575	SWISSPROT	601114352F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355044 5'
5608	18235		3.99	2.0E-18	AA868810.1	EST_HUMAN	DYNEIN GAMMA CHAIN, FLAGELLAR OUTER ARM
5697	18323	30823	3.16	2.0E-18	D14547.1	NT	ak53a07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409652 3' similar to TR:O14577
5697	18323	30824	3.16	2.0E-18	D14547.1	NT	O14577 BAC CLONE RG114A06 FROM 7Q31, COMPLETE SEQUENCE.;
6038	18657		1.98	2.0E-18	BF347229.1	EST_HUMAN	Human DNA, SINE repetitive element
6313	18920	31695	1	2.0E-18	X60459.1	NT	Human DNA, SINE repetitive element
6313	18920	31696	1	2.0E-18	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
6424	19027	31810	0.84	2.0E-18	BF352940.1	EST_HUMAN	Human IFNAR gene for interferon alpha/beta receptor
6460	19061	31847	7.53	2.0E-18	AW865853.1	EST_HUMAN	IL3-HT0819-220700-222-C12 HT0819 Homo sapiens cDNA
9980	22455	35437	1.39	2.0E-18	AW151673.1	EST_HUMAN	hi84g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979984 3' similar to contains MER10.12
9980	22455	35438	1.39	2.0E-18	AW151673.1	EST_HUMAN	MER10.12 MER19 repetitive element;
10854	23375	36394	4.96	2.0E-18	AW470791.1	EST_HUMAN	x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
							MER10 repetitive element;
							x67e10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2623146 3' similar to contains MER10.12
							MER10 repetitive element;
							ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3
							THR repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11579	24025	37093	5.24	2.0E-18	AW151299.1	EST_HUMAN	xg47a09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2630728 3' similar to contains MER8 b2
11970	13793		20.18	2.0E-18	BE258097.1	EST_HUMAN	MER8 repetitive element;
4507	17091		0.85	1.0E-18	T95408.1	EST_HUMAN	ye43g05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120538 5' similar to contains L1 repetitive element;
5558	18190	30606	1.91	1.0E-18	AV653405.1	EST_HUMAN	AV653405 GLC Homo sapiens cDNA clone GLDKE11 3'
5759	18385	31099	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
5759	18385	31100	2.18	1.0E-18	D00099.1	NT	Homo sapiens mRNA for Na,K-ATPase alpha-subunit, complete cds
6582	19180	31980	1.37	1.0E-18	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8380	20820	33840	1.22	1.0E-18	AI148288.1	EST_HUMAN	cc69d09.x1 Soares, senescent, fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:1680593 3' similar to contains L1.11 L1 repetitive element;
9813	22311	35293	4.45	1.0E-18	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RbRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
11918	24255	31011	4.39	1.0E-18	AF003529.1	NT	Homo sapiens glycican 3 (GPC3) gene, partial cds and flanking repeat regions
571	13202	25684	3.33	9.0E-19	AA281981.1	EST_HUMAN	z111d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
572	13202	25684	2.66	9.0E-19	AA281981.1	EST_HUMAN	MER19 repetitive element;
7790	20333		5.63	9.0E-19	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-2305
8622	21181	34078	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8622	21181	34077	2.46	9.0E-19	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
11007	23521	36558	3.92	9.0E-19	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11678	13202	25684	28.32	9.0E-19	AA281981.1	EST_HUMAN	z111d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
1086	13691		1.38	8.0E-19	AW974902.1	EST_HUMAN	MER19 repetitive element;
8080	20631	33544	1	8.0E-19	BE158836.1	EST_HUMAN	EST387007 IMAGE resequences, MAGN Homo sapiens cDNA
2287	14861	27438	1.72	7.0E-18	4758139	NT	MRO-H10404-210200-001-g08 HT0404 Homo sapiens cDNA
6584	19182	31982	1.91	7.0E-18	AF092090.1	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6 (RNA helicase, 54kD) (DDX6) mRNA
7341	19868	32732	0.95	7.0E-19	P28444	SWISSPROT	Rattus norvegicus cp151 mRNA, partial cds
9925	22421	35395	0.47	7.0E-19	A1344951.1	EST_HUMAN	BETA CRYSTALLIN A2
11823	25088		2.85	7.0E-19	AA705884.1	EST_HUMAN	tb01c08.x1 NCL_CGAP_Lu26 Homo sapiens cDNA clone IMAGE:2052302 3'
3847	18446		1.21	6.0E-19	AW852830.1	EST_HUMAN	z60b01.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:435145 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E- Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4562	17145	28592	1.39	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4562	17145	28593	1.39	6.0E-19	P34986	SWISSPROT	OLFACTORY RECEPTOR 6 (M50)
4919	17494		1.15	6.0E-19	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
6019	18638	31378	5.29	5.0E-19	Q00193	SWISSPROT	ZONA PELLUCIDA SPERM-BINDING PROTEIN B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP-X) (RC55)
6365	18989	31747	0.79	5.0E-19	AW563302.1	EST_HUMAN	hh77008.yt NCL CGAP_GUT Homo sapiens cDNA clone IMAGE:2868787.5'
10322	22816	35812	0.66	5.0E-19	AJ297699.1	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exon 14
11412	23863	36924	7.61	5.0E-19	AW183725.1	EST_HUMAN	xi87b02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2864171.3' similar to contains element MSR1 repetitive element
12544	24823		1.36	5.0E-19	U66060.1	NT	Human germline T-cell receptor beta chain TCRBV13S1, TCRBV6S8A2T, TCRBV6S8A3N2T, TCRBV13S6A2T, TCRBV6S9P, TCRBV5S3A2T, TCRBV13S8P, TCRBV6S3A1N1T, TCRBV5S2, TCRBV6S8A2T, TCRBV6S7P, TCRBV13S4, TCRBV6S2A1N1T, TCRBV5S4A2T, TCRBV6S4A1, TCRBV23S1A2T, TCRBV12>
580	13210	25688	0.95	4.0E-19	AB007970.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501
2707	15294	27831	1.25	4.0E-19	BF697362.1	EST_HUMAN	602130910F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4287674.5'
5593	18223	30872	1.1	4.0E-19	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3919	16517	28982	1.58	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
3919	16517	28983	1.58	3.0E-19	Q28997	SWISSPROT	BETA-2 ADRENERGIC RECEPTOR
4373	16960	29405	0.9	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4373	16960	29406	0.8	3.0E-19	O43900	SWISSPROT	LIM-ONLY PROTEIN 6 (TRIPLE LIM DOMAIN PROTEIN 6)
4544	17128	29571	1.33	3.0E-19	AV708138.1	EST_HUMAN	AV708136 ADC Homo sapiens cDNA clone ADCAMA11.5'
5484	18118		0.8	3.0E-19	AF223487.1	NT	Homo sapiens NPD008 protein (NPD008) mRNA, complete cds
7418	19942		1.83	3.0E-19	11432214	NT	Homo sapiens similar to aldo-keto reductase family 1, member B11 (aldose reductase-like) (H. sapiens) (LOC63222), mRNA
9380	20319	33220	1.2	3.0E-19	X89885.1	NT	M.musculus mRNA for TPCR33 protein
12084	24347		16.44	3.0E-19	AF165520.1	NT	Homo sapiens phorbol 1 protein (PBI) mRNA, complete cds
2595	15157	27725	7.09	2.0E-19	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4542	17128		1.28	2.0E-19	AI311783.1	EST_HUMAN	qq61e02.x1 NCL CGAP_Ki65 Homo sapiens cDNA clone IMAGE:1915898.3' similar to TR-Q69386 Q69386 POLYV GENE
8272	20813	33735	8.35	2.0E-19	AA012854.1	EST_HUMAN	ze34c09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360880.5'
9823	22321	35306	0.81	2.0E-19	Q95155	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN OLF2
507	13140		1.65	1.0E-19	BE408611.1	EST_HUMAN	601304126F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310.5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2209	14785	27359	1.46	1.0E-19	H30795.1	EST_HUMAN	y079g07.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:184188 5' similar to contains
2743	15298		2.16	1.0E-19	D38044.1	NT	MER10 repetitive element;
2873	15491		5.99	1.0E-19	4758977	NT	Human gene for Ah-receptor, exon 7-9
3448	16055	28531	1.37	1.0E-19	AA834967.1	EST_HUMAN	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
5322	17884		2.47	1.0E-19	AW117377.1	EST_HUMAN	aj49b12.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1393631 3' similar to contains MER37.12
6225	18834	31607	3.54	1.0E-19	U12186.1	NT	MER37 repetitive element;
6366	25116		0.74	1.0E-19	AA595527.1	EST_HUMAN	xd88h10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2604739 3' similar to contains
7624	20137	33015	0.86	1.0E-19	U08813.1	NT	L1.b2 L1 L1 repetitive element;
7624	20137	33016	0.86	1.0E-19	U08813.1	NT	Oryctolagus cuniculus sodium/dicarboxylate cotransporter mRNA, partial cds
8387	20827	33847	1.79	1.0E-19	M64657.1	NT	nh22d03.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:953063 similar to contains L1.t1 L1
8676	21215		2.48	1.0E-19	T99920.1	EST_HUMAN	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
10090	22585	35578	25.84	1.0E-19	AW812259.1	EST_HUMAN	Oryctolagus cuniculus Na+/glucose cotransporter-related protein mRNA, complete cds
10099	22594	35587	1.69	1.0E-19	N44631.1	EST_HUMAN	Rabbit phosphorylase kinase beta subunit mRNA, complete cds
11353	23807		2.24	1.0E-19	AW023137.1	EST_HUMAN	y072b02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123243 5' similar to contains
11594	24037	37108	1.64	1.0E-19	U93163.1	NT	OFR repetitive element;
6754	19347	32155	2.39	8.0E-20	7657286	NT	RCO-ST0174-191099-031-b05 ST0174 Homo sapiens cDNA
6754	19347	32156	2.39	8.0E-20	7657286	NT	y031a09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:272872 5'
7527	20047	32917	1.4	8.0E-20	A1221371.1	EST_HUMAN	di49h01.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487000 5'
7527	20047	32918	1.4	8.0E-20	A1221371.1	EST_HUMAN	Homo sapiens IMAGE-B2 (MAGE-B2), IMAGE-B3 (MAGE-B3), IMAGE-B4 (MAGE-B4), and IMAGE-B1
3314	15924	28402	0.78	7.0E-20	BF326455.1	EST_HUMAN	(IMAGE-B1) genes, complete cds
7088	18087	30443	5.61	7.0E-20	AL138120.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1) mRNA
8433	20973	33887	9.45	7.0E-20	AA557657.1	EST_HUMAN	Mus musculus keratin-associated protein 9-1 (Krtap9-1) mRNA
8433	20973	33888	9.45	7.0E-20	AA557657.1	EST_HUMAN	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
11561	24008		9.21	7.0E-20	6912633	NT	qg86f09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1842089 3'
3611	18214	28694	4.64	6.0E-20	P39188	SWISSPROT	PM4-AN0096-050900-003-404 AN0096 Homo sapiens cDNA
4359	16946	29388	4	6.0E-20	BE622434.1	EST_HUMAN	DKFZp547D092.r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp547D092 5'
							n146c04.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
							MER29 repetitive element;
							n146c04.s1 NCI_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29.b2
							MER29 repetitive element;
							Homo sapiens ribosomal protein L13a (RPL13A) mRNA
							ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY
							601441231F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916231 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4700	17282		1.11	5.0E-20	AV725123.1	EST_HUMAN	AV725123 HTC Homo sapiens cDNA clone HTC8TA01 5'
7169	19701	32548	1.33	5.0E-20	AF075301.1	EST_HUMAN	AF075301 Human fetal liver cDNA library Homo sapiens cDNA clone HA0250
7866	20428	33336	4.79	5.0E-20	W90525.1	EST_HUMAN	z178d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
7866	20428	33337	4.79	5.0E-20	W90525.1	EST_HUMAN	z178d08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418191 3' similar to contains MER30.t1 MER30 repetitive element ;
8047	20589	33498	0.79	5.0E-20	BE165980.1	EST_HUMAN	MR3-H10487-150200-113-g01 HT0487 Homo sapiens cDNA
8769	21308	34231	1.53	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
8769	21308	34232	1.53	5.0E-20	AB028174.1	NT	Mus musculus MMAN-g mRNA, complete cds
9366	20305		1.08	5.0E-20	O60809	SWISSPROT	HYPOTHETICAL PROTEIN DJ845024.1
5630	18454		0.92	4.0E-20	Q39880	SWISSPROT	HISTONE H2B C (H2B/C)
7866	20408		5.98	4.0E-20	AI874352.1	EST_HUMAN	zb4g03.x1 NCI_CGAP_OV435 Homo sapiens cDNA clone IMAGE:2293396 3'
10393	22887	35882	1.36	4.0E-20	AW937469.1	EST_HUMAN	QV3-DT0043-090200-080-c04 DT0043 Homo sapiens cDNA
2184	14760	27330	1.11	3.0E-20	U03888.1	NT	Human BXP21 gene
4288	16874	29323	1.49	3.0E-20	P23273	SWISSPROT	OLFATORY RECEPTOR-LIKE PROTEIN 114
4408	16893	29436	0.67	3.0E-20	AF230376.1	NT	Meriones unguiculatus prestin (Pres) mRNA, complete cds
4731	17312	29755	0.83	3.0E-20	AA037618.1	EST_HUMAN	z136b12.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:484895 3' similar to contains L1.13 L1 repetitive element ;
8865	21404		2.94	3.0E-20	D14547.1	NT	Human DNA, SINE repetitive element
10223	22718	35708	0.82	3.0E-20	BF185284.1	EST_HUMAN	601843561F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4084343 5'
							RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
10543	23080		1.84	3.0E-20	P11369	SWISSPROT	ENDONUCLEASE
11387	23839	36902	2.42	3.0E-20	A1284244.1	EST_HUMAN	q170d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11387	23839	36903	2.42	3.0E-20	A1284244.1	EST_HUMAN	q170d02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1864803 3' similar to contains Alu repetitive element;
11839	24202	31039	17.42	3.0E-20	BE988422.1	EST_HUMAN	601514180F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3915522 5'
863	13478		23.08	2.0E-20	AW303868.1	EST_HUMAN	x24e10.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS5_MOUSE
1150	13753	28262	2.92	2.0E-20	AA516335.1	EST_HUMAN	ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
1150	13753	28263	2.92	2.0E-20	AA516335.1	EST_HUMAN	G1224066 ORF2: FUNCTION UNKNOWN ;
							ng69h09.s1 NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:940097 similar to TR:G1224066
							G1224066 ORF2: FUNCTION UNKNOWN ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2843	13478		16.26	2.0E-20	AW303868.1	EST_HUMAN	xr24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW_RS5_MOUSE
5081	17654	30094	4.35	2.0E-20	Q28983	SWISSPROT	P97461 40S RIBOSOMAL PROTEIN S5 ;
5081	17654	30095	4.35	2.0E-20	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5328	17889		1.43	2.0E-20	5174538	NT	ZONADHESIN PRECURSOR
8081	20603	33514	0.97	2.0E-20	AA309457.1	EST_HUMAN	Homo sapiens malate dehydrogenase 1, NAD (soluble) (MDH1) mRNA
9118	21654	34596	5.33	2.0E-20	D10083.1	NT	EST180326 Liver III Homo sapiens cDNA 5' end
9118	21654	34596	5.33	2.0E-20	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
11622	24084	37128	1.76	2.0E-20	AA766755.1	EST_HUMAN	Homo sapiens RGH1 gene, retrovirus-like element
11622	24084	37129	1.76	2.0E-20	AA766755.1	EST_HUMAN	oe35b08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306835 3' similar to contains MER4.b2
12236	24809	30789	2.84	2.0E-20	H55371.1	EST_HUMAN	oe35b08.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1306835 3' similar to contains MER4.b2
2058	15396	27211	3.02	1.0E-20	AA281961.1	EST_HUMAN	CHR220310 Chromosome 22 exon Homo sapiens cDNA clone C22_391.5'
4533	17117	29563	1.18	1.0E-20	BF115158.1	EST_HUMAN	z111d06.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712811 5' similar to contains MER19.12
6975	19551	32376	0.72	1.0E-20	AF049587.1	EST_HUMAN	hr84b08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3135155 3' similar to contains L1.12 L1
9090	21626	34562	2.48	1.0E-20	11418491	NT	repetitive element ;
11427	23878	36943	3.02	1.0E-20	AF223391.1	NT	AF049587 Human activated dendritic cell mRNA Homo sapiens cDNA clone GA05
11966	24286		6.39	1.0E-20	AA420453.1	EST_HUMAN	Homo sapiens Autosomal Highly Conserved Protein (AHCP), mRNA
11681	24098		3.9	9.0E-21	AW898189.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8746	21285		1.77	8.0E-21	AW874891.1	EST_HUMAN	nc60g08.r1 NCL_CGAP_Prl Homo sapiens cDNA clone IMAGE:745694 similar to contains L1.13 L1
11413	23864	36925	4.8	8.0E-21	AA809411.1	EST_HUMAN	repetitive element ;
11852	24212	27258	5.02	8.0E-21	Q21330	SWISSPROT	RC3-NN0068-090500-021-503 NN0068 Homo sapiens cDNA
2113	14691	27259	1.61	7.0E-21	PT15900	SWISSPROT	bb30a02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2984714 5' similar to SW:NIAM_HUMAN
3764	16365	28832	0.59	7.0E-21	AL163300.2	NT	Q95169 NADH-UBIQUINONE OXIDOREDUCTASE ASH1 SUBUNIT PRECURSOR ;
4341	16928		4.31	7.0E-21	AA046502.1	EST_HUMAN	cb71f06.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336835 3'
6564	19192	31680	0.79	7.0E-21	AL163218.2	NT	ATP SYNTHASE A CHAIN (PROTEIN 6)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) (LAMININ CHAIN B3)
							Homo sapiens chromosome 21 segment HS21C100
							z67a08.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
							Homo sapiens chromosome 21 segment HS21C018

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8327	20888	33791	1.47	7.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
8610	21149	34064	10.47	7.0E-21	D14718.1	NT	Human chromosomal protein HMG1 related gene
10022	22517	35512	0.73	7.0E-21	AW858922.1	EST_HUMAN	RCO-CT0301-271198-031-F03 CT0301 Homo sapiens cDNA
10575	23110	38123					zq73403.s1 Soares_fetal_heart_NbHH18W Homo sapiens cDNA clone IMAGE:398981 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);contains THR.13 OFR repetitive element
11147	23655	36697	3.16	7.0E-21	AA723404.1	EST_HUMAN	Homo sapiens PTD013 protein (PTD013), mRNA
4179	16770	29219	1.94	7.0E-21	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9063	21600	29219	0.89	6.0E-21	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-H09 HT0454 Homo sapiens cDNA
860	13571	26087	0.58	6.0E-21	5902031	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
4453	17039	29482	0.82	5.0E-21	BE968839.1	EST_HUMAN	601849871F1 NIH_MGC_74 Homo sapiens cDNA clone IMAGE:3933880 5'
4922	17497	29948	3.12	5.0E-21	4885474	NT	Homo sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
6860	19594		5.67	5.0E-21	AW 440864.1	EST_HUMAN	he05e10.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2918154 3'
7086	19657	32496	0.83	5.0E-21	BE585805.1	EST_HUMAN	783d11.x1 NCL CGAP_P728 Homo sapiens cDNA clone IMAGE:3303573 3' similar to contains OFR.11 OFR repetitive element
10466	22860	35970	1	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
10468	22860	35971	0.79	5.0E-21	Q91690	SWISSPROT	ZINC FINGER PROTEIN GLI1 (GLI-1)
11766	24157		0.79	5.0E-21	AA393574.1	EST_HUMAN	z72c04.t1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727878 5'
1769	14359	26904	1.49	5.0E-21	AA970713.1	EST_HUMAN	cc86e08.e1 NCL CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1573094 3' similar to TR:Q16530 Q16530 PMS3 MRNA ;contains OFR.t1 OFR repetitive element ;
6953	19530	32355	1.24	4.0E-21	AB019576.1	NT	Rattus norvegicus mRNA for RTIM, complete cds
6953	19530	32355	3.04	4.0E-21	AB019576.1	NT	
9695	22194	35167					Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
1877	14483	27020	0.61	4.0E-21	U91328.1	NT	
2313	14895	27460	5.92	3.0E-21	AA218891.1	EST_HUMAN	z15d006.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:629771 3'
3110	15730	28200	1.2	3.0E-21	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
			3.35	3.0E-21	AJ007973.1	NT	Homo sapiens LGMD2B gene
5691	18317	30816					
5691	18317	30816	0.97	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
5691	18317	30817					
5913	18535		0.97	3.0E-21	AJ277557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
6326	18932		0.75	3.0E-21	AV661044.1	EST_HUMAN	AV661044 GLC Homo sapiens cDNA clone GLCGOA10 3'
			60.27	3.0E-21	BF184739.1	EST_HUMAN	601844465F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4064945 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7129	19469	32287	7.35	3.0E-21	BF361093.1	EST_HUMAN	RC1-OT0083-100800-019-g08 OT0083 Homo sapiens cDNA
9609	22109	36071	0.88	3.0E-21	AW997780.1	EST_HUMAN	CM1-NIN0063-280400-203-H08 NN0063 Homo sapiens cDNA
12359	25013	30617	2.75	3.0E-21	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
157	12820		19.17	2.0E-21	BE163247.1	EST_HUMAN	QV3-HT0458-170200-090-g12 HT0458 Homo sapiens cDNA
970	13581	26093	0.71	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
970	13581	26094	0.71	2.0E-21	AB007857.2	NT	Homo sapiens mRNA for KIAA0397 protein, partial cds
1256	13853		2	2.0E-21	BED64410.1	EST_HUMAN	RC4-BT0311-141199-011-H06 BT0311 Homo sapiens cDNA
2665	15223	27765	2.45	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
2665	15223	27766	2.45	2.0E-21	Q28983	SWISSPROT	ZONADHESIN PRECURSOR
5675	18302	30784	1.81	2.0E-21	AI624582.1	EST_HUMAN	ts30f03.x1 NCI CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2230109 3' similar to TR:Q99854 Q99854
5765	18391	31103	0.91	2.0E-21	AA027211.1	EST_HUMAN	HYPOPHYSICAL 51.1 KD PROTEIN;
5765	18391	31104	0.91	2.0E-21	AA027211.1	EST_HUMAN	z997a12.11 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8304	20845	33768	5.08	2.0E-21	BE141785.1	EST_HUMAN	z997a12.11 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366910 5'
8757	21296	34216	3.84	2.0E-21	AU136779.1	EST_HUMAN	QV0-HT0103-091199-050-g11 HT0103 Homo sapiens cDNA
10937	23454		2.2	2.0E-21	BE350127.1	EST_HUMAN	AU136779 PLACE1 Homo sapiens cDNA clone PLACE1005052 5'
11199	23704	36754	2.24	2.0E-21	BE973829.1	EST_HUMAN	h09g01.x1 NCI CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29 b3
11199	23704	36755	2.24	2.0E-21	BE973829.1	EST_HUMAN	MER29 repetitive element;
12072	24351		10.78	2.0E-21	AF176815.1	NT	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1298	13892	26415	1.54	1.0E-21	AA557657.1	EST_HUMAN	601680636F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3951008 5'
1448	14040		3.58	1.0E-21	AI601284.1	EST_HUMAN	Homo sapiens putative 8-hydroxyguanine DNA glycosylase gene, complete cds
5397	17955	30366	14.37	1.0E-21	P08548	SWISSPROT	h46c04.s1 NCI CGAP_P14 Homo sapiens cDNA clone IMAGE:1043718 similar to contains MER29 b2
6613	19210		2.59	1.0E-21	AL079752.1	EST_HUMAN	MER29 repetitive element;
7243	19772	32629	4.56	1.0E-21	AI223104.1	EST_HUMAN	ar88d12.x1 Barstead cdon_HPLRB7 Homo sapiens cDNA clone IMAGE:2152343 3'
10477	22971		1.45	1.0E-21	5730038	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
12485	24616		2.46	1.0E-21	AF046133.1	NT	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG
4500	17084	29534	2.78	9.0E-22	AI702438.1	EST_HUMAN	DKFZp4340830_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4340830 5'
8540	21079	33968	1.2	9.0E-22	AL163201.2	NT	DKFZp4340830_r1 434 (synonym: htes3) Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 OM
8540	21079	33969	1.2	9.0E-22	AL163201.2	NT	gg47e05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838336 3' similar to gb:M64241 OM
10870	23202	36215	5.06	9.0E-22	AV761874.1	EST_HUMAN	PROTEIN (HUMAN);
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
							Homo sapiens chromosome Xp22.410-8
							ts94e03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2296204 3' similar to TR:Q15408 Q15408
							NEUTRAL PROTEASE LARGE SUBUNIT
							Homo sapiens chromosome 21 segment HS21C001
							Homo sapiens chromosome 21 segment HS21C001
							AV761874 MDS Homo sapiens cDNA clone MDSOCCG05 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11553	24001	37073	3.44	9.0E-22	AU140358.1	EST_HUMAN	AU140358 PLACE2 Homo sapiens cDNA clone PLACE2000394 5'
984	13596		4.19	8.0E-22	BE144748.1	EST_HUMAN	CMD-HIT0179-281089-078-h05 HIT0179 Homo sapiens cDNA
7837	20379		3.26	8.0E-22	AA046502.1	EST_HUMAN	ZK87806 r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:487858 5'
693	13316	25801	5.27	7.0E-22	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
4370	18957	29389	2.55	7.0E-22	Q61838	SWISSPROT	ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA2M)
5190	17765	30184	1.12	7.0E-22	A808881.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
8624	21163		1.99	7.0E-22	AF151054.1	NT	Homo sapiens HSPC220 mRNA, complete cds
8766	21305	34227	3.39	7.0E-22	MF78590.1	EST_HUMAN	EST00738 Fetal brain, Stragene (cat#936206) Homo sapiens cDNA clone HFBCF07
9520	22020	34977	1.83	7.0E-22	AF008660.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
8184	20725		2.67	6.0E-22	AW028123.1	EST_HUMAN	wo05g07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2542812 3'
8640	19236	32038	2.82	5.0E-22	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10221	22716	35707	7.63	5.0E-22	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12314	24508		2.92	5.0E-22	BF476611.1	EST_HUMAN	naa27b06.x1 NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:3255898 3' similar to contains Alu repetitive element;
3688	16289		0.83	4.0E-22	AJ271735.1	NT	Homo sapiens Xq pseudocentromeric region; segment 1/2
8049	20591		0.53	4.0E-22	AV703223.1	EST_HUMAN	AV703223 ADB Homo sapiens cDNA clone ADBAUE12 5'
8352	25122	33498	3.36	4.0E-22	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10901	23135	36149	2.85	4.0E-22	BF218030.1	EST_HUMAN	601882813F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095434 5'
12492	24821		3.39	4.0E-22	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
994	13806		0.99	3.0E-22	AI469679.1	EST_HUMAN	tm14h10.x1 NCI_CGAP_Co14 Homo sapiens cDNA clone IMAGE:2156611 3' similar to gb:L19593 HIGH AFFINITY INTERLEUKIN-8 RECEPTOR B (HUMAN); contains L1 t1 L1 repetitive element ;
3735	16336		1.44	3.0E-22	D14718.1	NT	Human chromosomal protein HMGI related gene
4921	17496	28947	3.04	3.0E-22	AI090125.1	EST_HUMAN	qb28c07.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697580 3' similar to contains MER12.12 MER12 repetitive element ;
6172	20713		1.07	3.0E-22	BE156613.1	EST_HUMAN	QV0-HIT0368-090200-098-f12 HIT0368 Homo sapiens cDNA
8177	20718	33633	2.55	3.0E-22	BE089841.1	EST_HUMAN	RC5-BT0707-150300-021-H10 BT0707 Homo sapiens cDNA
8301	20842	33762	1	3.0E-22	X60860.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
8301	20842	33763	1	3.0E-22	X60860.1	NT	R.rattus RY2G5 mRNA for a potential ligand-binding protein
1896	14578		2.49	2.0E-22	N24942.1	EST_HUMAN	y73405.s1 Soares_melanocyte 2N5HM Homo sapiens cDNA clone IMAGE:267369 3'
2584	15128	27897	1.61	2.0E-22	P24916	SWISSPROT	IMMEDIATE EARLY GENE 13 PROTEIN PRECURSOR
3467	16074	28547	5.3	2.0E-22	8394043	NT	Homo sapiens protein kinase, AMP-activated, gamma 3 non-catalytic subunit (PRKAG3), mRNA
4310	16896	29340	1.35	2.0E-22	AW817784.1	EST_HUMAN	PM1-ST0262-261199-001-d12 ST0262 Homo sapiens cDNA
6015	24763	31372	1.95	2.0E-22	W39456.1	EST_HUMAN	zo20f01.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:322873 5' similar to gb:X72308 MONOCYTE CHEMOTACTIC PROTEIN 3 PRECURSOR (HUMAN);

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6324	18930	31706	3.3	2.0E-22	BF092116.1	EST_HUMAN	RC0-TN0079-150900-025-h12 TN0079 Homo sapiens cDNA
9619	22119	35082	1.59	2.0E-22	A1276522.1	EST_HUMAN	q176h06.x1 Soares_Nhlh1Pu_S1 Homo sapiens cDNA clone IMAGE:1878299 3' similar to contains
9712	22210	35182	0.69	2.0E-22	AA715315.1	EST_HUMAN	MER29.b3 MER29 repetitive element ;
9712	22210	35183	0.69	2.0E-22	AA715315.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
11595	24038	37107	2.33	2.0E-22	AW418960.1	EST_HUMAN	nv04h11.s1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:1219269 3'
11644	24605	30886	2.57	2.0E-22	AL163280.2	NT	ha24f04.x1 NCI_CGAP_K1d12 Homo sapiens cDNA clone IMAGE:2874655 3'
1921	14508	27063	1.59	1.0E-22	AW865517.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
2620	15182	27748	1.88	1.0E-22	U50871.1	NT	PM4-SN0020-010400-009-h02 SN0020 Homo sapiens cDNA
3457	16084	28539	1.45	1.0E-22	D14547.1	NT	Human familial Alzheimer's disease (STM2) gene, complete cds
7723	20231	33120	1.29	1.0E-22	BE084667.1	EST_HUMAN	Human DNA, SINE repetitive element
10446	22840	35950	0.84	1.0E-22	A1365435.1	EST_HUMAN	MRO-BT0659-220200-002-h07 BT0659 Homo sapiens cDNA
10446	22840	35951	0.84	1.0E-22	A1365435.1	EST_HUMAN	q209b07.x1 NCI_CGAP_GLL1 Homo sapiens cDNA clone IMAGE:2020981 3' similar to contains MER28.b2
12540	24650	36259	12.67	9.0E-23	AW802801.1	EST_HUMAN	MER29 repetitive element ;
3629	19232	28707	0.64	8.0E-23	AF198349.1	NT	IL2-UM0076-070400-061-F11 UM0076 Homo sapiens cDNA
3352	15960	36458	2.37	7.0E-23	AV647246.1	EST_HUMAN	Gallus gallus Dact2 protein (Dact2) mRNA, complete cds
10918	23437	36458	4.4	7.0E-23	5031952	NT	AV647246 GLC Homo sapiens cDNA clone GLCAW007 3'
3481	16087	28384	1.63	6.0E-23	AF198333.1	NT	Homo sapiens Nci56 (D. melanogaster)-like protein (NOT56L) mRNA
4355	16942	28384	1.1	6.0E-23	AL183249.2	NT	Rattus norvegicus RIM1B (Rim1B) mRNA, complete cds
11790	24173	31026	3.44	6.0E-23	AF224689.1	NT	Homo sapiens chromosome 21 segment HS21C049
11790	24173	31027	3.44	6.0E-23	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
11690	24300	30985	4.29	6.0E-23	A1209130.1	EST_HUMAN	(UBE2D3) genes, complete cds
5635	18284	30736	5.78	5.0E-23	U82671.2	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
6388	24763	31770	3.66	5.0E-23	AF179818.1	NT	qg59c03.x1 Soares_Teslis_NHT Homo sapiens cDNA clone IMAGE:1839460 3' similar to
7463	24763	31770	3.02	5.0E-23	AF179818.1	NT	SW.MV10 MOUSE P23249 PROTEIN MOV-10 ;
5375	17934	30348	0.92	3.0E-23	AW846839.1	EST_HUMAN	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12
6569	19167	31963	1.01	3.0E-23	AL163227.2	NT	(MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), caltactin (CALT), NAD(P)H dehydrogenase-like protein (NSDHL), and LI>

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6569	19167	31964	1.01	3.0E-23	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
7780	20323	33228	4.27	3.0E-23	AA130165.1	EST_HUMAN	z35g09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503968 5' similar to contains MER29.12 MER29 repetitive element.
9173	21750	34694	2.89	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
9173	21750	34695	2.89	3.0E-23	Z70684.1	NT	Human endogenous retroviral element HC2
10219	22714		1.23	3.0E-23	AW87927.1	EST_HUMAN	RC3-NN0096-270400-011-101 NN0066 Homo sapiens cDNA
10889	23503		1.54	3.0E-23	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
694	13317	25802	3.65	2.0E-23	AJ289980.1	NT	Homo sapiens KIAA0851 gene (partial). XT3 gene and LZTFL1 gene
1182	15351		4.01	2.0E-23	M55270.1	NT	Human matrix Gla protein (MGP) gene, complete cds
2821	15373	27942	1.47	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
2821	15373	27943	1.47	2.0E-23	P22105	SWISSPROT	TENASCIN-X PRECURSOR (TN-X) (HEXABRACHION-LIKE)
3418	16026		1.36	2.0E-23	AJ201458.1	EST_HUMAN	qs73f11.x1 NCLCGAP_P28 Homo sapiens cDNA clone IMAGE:1943757 3' similar to TR:Q13537 Q13537
3779	16379		3.93	2.0E-23	BE165980.1	EST_HUMAN	MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
4048	16845	29112	3.01	2.0E-23	H59831.1	EST_HUMAN	MR3-HT0487-150200-113-q01 HT0487 Homo sapiens cDNA
4048	16845	29113	3.01	2.0E-23	H59831.1	EST_HUMAN	Yr16a02.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Yr16a02.r1 Soares fetal liver spleen TNFLS Homo sapiens cDNA clone IMAGE:205418 5'
							Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450 polypeptide 5 (CYP3A5) gene, partial cds
7814	20357		4.59	2.0E-23	AF280107.1	NT	Homo sapiens chromosome 21 segment HS21C103
8777	21316	34238	1.05	2.0E-23	AL163303.2	NT	Human alcohol dehydrogenase gamma subunit (ADH3) gene, exon 1
11772	24161		3.5	2.0E-23	M32658.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12328	24512		4.44	2.0E-23	AF009860.1	NT	AU133931 OVARC1 Homo sapiens cDNA clone OVARC1000946 5'
12454	25017		1.35	2.0E-23	AU133931.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C052
4827	17210	29660	1.72	1.0E-23	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C010
4881	17456		5.35	1.0E-23	AL163210.2	NT	601238455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608653 5'
6821	19411		4.93	1.0E-23	BE378471.1	EST_HUMAN	zw62c06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782698 5' similar to contains PTR5.12 PTR repetitive element;
8297	20838	33759	4.53	1.0E-23	AA448097.1	EST_HUMAN	ab75a08.s1 Stralagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:852758 3' similar to
578	13208		1.48	9.0E-24	AA663213.1	EST_HUMAN	TR-E19822 E19822 CA PROTEIN.;
4753	17334	29777	1.16	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3
4753	17334	29778	1.10	8.0E-24	P23269	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN I3

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6578	19174	31973	1.06	8.0E-24	11422027	NT	Homo sapiens capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2), mRNA
3941	16539		1.23	7.0E-24	AW937854.1	EST_HUMAN	QV0-DT0047-170200-122-a08 DT0047 Homo sapiens cDNA
5345	17908		18.11	7.0E-24	AL039498.1	EST_HUMAN	DKFZp434A2311.1_1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434A2311.5'
10519	23057		2.8	7.0E-24	AW303317.1	EST_HUMAN	xx1703.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405.3' similar to contains Alu repetitive element; contains MER19.12 MER19 repetitive element;
735	13355		2.28	6.0E-24	AB001421.1	NT	Macaca fuscata mRNA for Testis-Specific Protein Y (TSPY), complete cds
871	13486	26001	12.95	6.0E-24	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
4042	16640	29107	9.12	5.0E-24	AJ229043.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
7735	20243	33134	0.9	5.0E-24	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
6087	18703	31451	3.17	4.0E-24	AA594178.1	EST_HUMAN	m31h05.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone IMAGE:1085529.3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN;
8815	21154	34068	1.37	4.0E-24	AW813711.1	EST_HUMAN	RC3-ST0197-130100-014-006 ST0197 Homo sapiens cDNA
11059	23571	36808	1.65	4.0E-24	BE544922.1	EST_HUMAN	601078812F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3464498.5'
12165	24405	30980	4.77	4.0E-24	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12428	24811	30989	1.37	4.0E-24	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
8362	20902		2.57	3.0E-24	AW614871.1	EST_HUMAN	h168c08.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2987950.3' similar to contains MER29.b2 MER29 repetitive element;
8414	20954		1.51	3.0E-24	AW962076.1	EST_HUMAN	EST374149 MAGE resequences, MAGG Homo sapiens cDNA
9386	21809	34760	3.79	3.0E-24	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C052
12247	24458	30959	2.85	3.0E-24	BF127762.1	EST_HUMAN	601810449F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053396.5'
2384	14953	27525	3.07	2.0E-24	AA167539.1	EST_HUMAN	zp1109.r1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609161.5'
3867	16485		0.82	2.0E-24	AW898189.1	EST_HUMAN	RC3-NH0088-080500-021-b03 NH0088 Homo sapiens cDNA
7490	20013	32878	1.14	2.0E-24	AF086824.1	NT	Mus musculus rho/rac-interacting citron kinase (Cik) mRNA, complete cds
8675	21214	34135	2.59	2.0E-24	AL119158.1	EST_HUMAN	DKFZp761L1712_r1_761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761L1712.5'
8712	21251		0.87	2.0E-24	H69214.1	EST_HUMAN	y92b09.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:212729.5' similar to contains MER28 repetitive element;
9768	22268	35250	0.82	2.0E-24	AI521759.1	EST_HUMAN	U77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008.3'
9768	22266	35251	0.82	2.0E-24	AI521759.1	EST_HUMAN	U77a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2138008.3'
12080	25082		13.88	2.0E-24	M28877.1	NT	Human O family dispersed repeat element
1734	14325	26867	3.18	1.0E-24	7706340	NT	Homo sapiens CGI-127 protein (LOC51646), mRNA
2897	15254		1.43	1.0E-24	AW820194.1	EST_HUMAN	QV0-ST0294-100400-185-c10 ST0294 Homo sapiens cDNA
3055	15671	28147	0.76	1.0E-24	D88423.1	NT	Mus musculus mRNA for HGT keratin, partial cds
4357	16944		1.97	1.0E-24	AF143313.1	NT	Homo sapiens PTEN (PTEN) gene, exon 2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7551	20070	32948	4.06	1.0E-24	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
7713	20222	33109	0.8	1.0E-24	BE144526.1	EST_HUMAN	MRO-HT0186-271199-005-409 HT0186 Homo sapiens cDNA
7885	20427	33335	1.38	1.0E-24	AW901164.1	EST_HUMAN	CMO-NN1010-130300-281-407 NN1010 Homo sapiens cDNA
11545	23993	37084	1.58	9.0E-25	7708707	NT	Homo sapiens putative secreted protein (SIG11), mRNA
5443	17998		2.05	8.0E-25	6138972	NT	Homo sapiens adrenergic, beta, receptor kinase 2 (ADRBK2), mRNA
5136	17708	30140	2.99	7.0E-25	AA483944.1	EST_HUMAN	ne92e10.s1 NCL CGAP_Kid1 Homo sapiens cDNA clone IMAGE:911754 similar to contains MER1.b2
8160	20701	33616	5.07	7.0E-25	AA468646.1	EST_HUMAN	ne06a09.s1 NCL CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR repetitive element;
11547	23995	37067	9.93	7.0E-25	AA583540.1	EST_HUMAN	nf25h06.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:914843 similar to SW.R14A_YEAST
7065	18084		4.4	6.0E-25	W87623.1	EST_HUMAN	p36105 PROBABLE 60S RIBOSOMAL PROTEIN L14EA;
7706	20215	33103	10.77	6.0E-25	7305360	NT	zh65h07.r1 Soares fetal liver spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:416989 5'
11196	23701	36762	4.55	5.0E-25	AW979107.1	EST_HUMAN	Mus musculus otogelin (Olog), mRNA
1496	14088	26628	2.75	4.0E-25	T98107.1	EST_HUMAN	EST391217 MAGE resequences, MAGP Homo sapiens cDNA
3449	16056		3.2	4.0E-25	AW887671.1	EST_HUMAN	ye6h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121783 5'
3974	16572	29042	1.42	4.0E-25	AF00368.1	NT	PM3-OT0093-280200-001-g07 OT0093 Homo sapiens cDNA
4407	16992		4.05	4.0E-25	BE170957.1	EST_HUMAN	Rattus norvegicus voltage-gated sodium channel mRNA, complete cds
3362	15970	28447	3.73	3.0E-25	8923321	NT	QV3-HT0543-140400-149-e11 HT0543 Homo sapiens cDNA
3362	15970	28448	3.73	3.0E-25	8923321	NT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
5022	17566	30039	0.69	3.0E-25	P26622	SWISSPROT	Homo sapiens hypothetical protein FLJ20344 (FLJ20344), mRNA
6728	19322	32127	0.84	3.0E-25	AA803590.1	EST_HUMAN	KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4)
8279	20820	33739	3.84	3.0E-25	AL163210.2	NT	np27b02.s1 NCL CGAP_P122 Homo sapiens cDNA clone IMAGE:1117515 3' similar to gb:M61866 ZINC FINGER PROTEIN 85 (HUMAN);
10911	23430	38450	2.02	3.0E-25	AA579013.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
1392	13986	26513	9.82	2.0E-25	5032158	NT	nf30h10.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:915331 similar to contains L1.L1 L1 repetitive element;
2347	14918	27492	7.6	2.0E-25	BE889016.1	EST_HUMAN	Homo sapiens transducin (beta)-like 1 (TBL1) mRNA
2858	15142	27711	3.84	2.0E-25	P17008	SWISSPROT	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
4268	18854	29301	2.04	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
4268	18854	29302	2.04	2.0E-25	P17008	SWISSPROT	40S RIBOSOMAL PROTEIN S16
9680	22179	35154	1.9	2.0E-25	AL449573.1	EST_HUMAN	40S RIBOSOMAL PROTEIN S16
387	13033	25522	0.71	1.0E-25	AL040229.1	EST_HUMAN	AL449573 Homo sapiens Testis (Stavrides GS) Homo sapiens cDNA
1291	13886		1.97	1.0E-25	9635487	NT	DKFZp434H0313_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0313 5'
							Human endogenous retrovirus, complete genome

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2478	15045	27813	1.13	1.0E-25	Q06055	SWISSPROT	ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (ATPASE PROTEIN 9) (SUBUNIT C)
4984	17558	30001	3.09	1.0E-25	BE162737.1	EST_HUMAN	PM1-HT0454-080100-002-h09 HT0454 Homo sapiens cDNA
6883	19279		0.85	1.0E-25	AA189080.1	EST_HUMAN	zq45b06.s1 Stragene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632827 3' similar to contains Alu repetitive element;
6890	24775	32460	3.08	1.0E-25	AA582690.1	EST_HUMAN	nm54h11.s1 NCL CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1087749 3'
7855	20397	33303	4.27	1.0E-25	AA709079.1	EST_HUMAN	z69g04.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:384822 3' similar to contains
9485	21990	34946	0.66	1.0E-25	X60960.1	NT	PTR5.13 PTR5 repetitive element;
9485	21990	34947	0.66	1.0E-25	X60960.1	NT	R rattus RY2G5 mRNA for a potential ligand-binding protein
10849	23370	36389	3.71	1.0E-25	U93163.1	NT	R rattus RY2G5 mRNA for a potential ligand-binding protein
11787	24171	36777	1.9	1.0E-25	D14547.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11787	24171	36778	1.9	1.0E-25	D14547.1	NT	Human DNA, SINE repetitive element
2523	15087	27660	1.57	9.0E-26	AL163218.2	NT	Human DNA, SINE repetitive element
11845	24828		1.69	9.0E-26	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C018
5872	18494		1.55	8.0E-26	D14547.1	NT	Homo sapiens chromosome 21 segment HS21C085
1621	14214	26745	0.92	7.0E-26	AF003528.1	NT	Human DNA, SINE repetitive element
4052	16849	29117	1.16	7.0E-26	X89211.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4239	16927	29276	2.04	7.0E-26	AW340153.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
5819	18443	31165	0.86	7.0E-26	AL163202.2	NT	hd02e12.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2808366 3'
11520	23988		8.46	7.0E-26	AA115895.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C002
12376	24544		3.49	7.0E-26	AW954559.1	EST_HUMAN	zq30d08.r1 Stragene neuroepithelium NT2RAM1 837234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb-M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
2287	14841	27418	2.32	6.0E-26	AF026308.1	NT	EST366329 MAGE resequences, MAGC Homo sapiens cDNA
3300	15998	28476	1.37	6.0E-26	AA206131.1	EST_HUMAN	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
10426	22920	35922	0.48	6.0E-26	AL163202.2	NT	zq52h04.r1 Stragene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:645271 5'
10426	22920	35923	0.48	6.0E-26	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
11531	23979	37049	5.92	6.0E-26	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1219	13819	26334	3.55	5.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;
1219	13819	26335	3.55	5.0E-26	A1708235.1	EST_HUMAN	as38h08.x1 Barstead aorta HPLRB8 Homo sapiens cDNA clone IMAGE:2319519 3' similar to WP:F49C12.11 CE03371;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1591	14184		2.25	4.0E-26	AA328548.1	EST_HUMAN	EST33446 Embryo, 12 week II Homo sapiens cDNA 5' end
9333	21847		3.53	4.0E-26	7657670	NT	Homo sapiens upstream binding transcription factor, RNA polymerase I (UBTF), mRNA
10539	23076	36090	3.69	4.0E-26	BE266187.1	EST_HUMAN	601191345F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535210 5'
1796	14388	26930	1.2	3.0E-26	D14547.1	NT	Human DNA, SINE repetitive element
2046	14628	27197	1	3.0E-26	AL045855.2	EST_HUMAN	DKFZp4341066_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4341066 5'
2077	14657		2.22	3.0E-26	AA115895.1	EST_HUMAN	z130d08.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone IMAGE:548943 5' similar to gb:MI14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
3846	16445	28906	1.48	3.0E-26	AA152484.1	EST_HUMAN	z303f10.r1 Stratagene cdon (#337204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
3846	16445	28907	1.48	3.0E-26	AA152484.1	EST_HUMAN	z303f10.r1 Stratagene cdon (#337204) Homo sapiens cDNA clone IMAGE:588427 5' similar to TR:G695374 G695374 THYROID RECEPTOR INTERACTOR ;
6991	19489	32311	6.04	3.0E-26	BE245458.1	EST_HUMAN	601684963F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4083278 5'
10604	23138		1.97	3.0E-26	AF036405.1	NT	Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds
11442	23892	36957	2.58	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11442	23892	36956	2.58	3.0E-26	AW875651.1	EST_HUMAN	QV2-PT0012-040400-124-e05 PT0012 Homo sapiens cDNA
11472	23922	36992	13.09	3.0E-26	AA593173.1	EST_HUMAN	nn37d05.s1 NCI_CGAP_GC5 Homo sapiens cDNA clone IMAGE:1086057 3' similar to contains OFR.11 OFR repetitive element ;
12566	24695		2.21	3.0E-26	AW073434.1	EST_HUMAN	xa57b09.x1 NCI_CGAP_HSC2 Homo sapiens cDNA clone IMAGE:2570873 3' similar to contains MER30.11 MER30 repetitive element ;
12661	24732	30857	1.46	3.0E-26	AF165520.1	NT	Homo sapiens phospholipase I protein (PBI) mRNA, complete cds
710	13331	25818	5.38	2.0E-26	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
1909	14494		2.42	2.0E-26	AL038099.2	EST_HUMAN	DKFZp566L171_s1 566 (synonym: hfk42) Homo sapiens cDNA clone DKFZp566L171 3'
3268	15890	28363	4.94	2.0E-26	X86994.1	NT	M.musculus mRNA for astrocytic phosphoprotein, PEA-15
10633	23166		3.35	2.0E-26	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
11096	23607	36647	5.24	2.0E-26	AB01412.1	EST_HUMAN	to89a01.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185416 3' similar to contains Alu repetitive element; contains element MER20 repetitive element ;
11296	23748		2.17	2.0E-26	AF055066.1	NT	Homo sapiens MHC class 1 region
11894	24237		1.65	2.0E-26	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
12101	25005	30612	3.03	2.0E-26	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
142	12807	25295	13.71	1.0E-26	BE170371.1	EST_HUMAN	QV4-HT0538-020300-123-e02 HT0538 Homo sapiens cDNA
2091	14671	27241	1.5	1.0E-26	AL039363.2	EST_HUMAN	DKFZp434H1910_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H1910 5'
2598	15160	27726	1.48	1.0E-26	BE814995.1	EST_HUMAN	MR2-BN0114-240500-030-g07 BN0114 Homo sapiens cDNA
2710	15287		6.31	1.0E-26	AF261085.1	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GADPH) mRNA, complete cds
6927	19586		2.52	1.0E-26	BE165980.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10772	23286		2.98	1.0E-26	AL038487.1	EST_HUMAN	DKFZp566C2146.1 566 (synonym: mfk2) Homo sapiens cDNA clone DKFZp566C2146 5'
12151	25084		2.79	1.0E-26	H55093.1	EST_HUMAN	CHR220032 Chromosome 22 exon Homo sapiens cDNA clone C22_45 5'
12625	24703		1.27	1.0E-26	AW408742.1	EST_HUMAN	UHF-BM0-adv-d-10-0-UI-1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063210 5'
7584	20099		1.17	8.0E-27	BF371227.1	EST_HUMAN	RC6-FN0138-110800-022-A02 FN0138 Homo sapiens cDNA
9227	21949		4	8.0E-27	U93163.1	NT	Homo sapiens IMAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
11648	24060		6.15	9.0E-27	BF445556.1	EST_HUMAN	nao3c07.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:3253644 3' similar to contains OFR.11 OFR repetitive element
11	12690	25146	3.07	8.0E-27	AI831462.1	EST_HUMAN	W49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element
583	13213		3.36	8.0E-27	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
1461	14053	26585	28.2	8.0E-27	AW162737.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
1461	14053	26586	28.2	8.0E-27	AW162737.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
2212	14787	27362	1.48	8.0E-27	AW964776.1	EST_HUMAN	au87h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783295 3' similar to gb:K00558 TUBULIN ALPHA-1 CHAIN (HUMAN);
3219	15831	28310	1.89	8.0E-27	P12236	SWISSPROT	PM2-SN0018-220300-002-a07 SN0018 Homo sapiens cDNA
3396	18004	28485	0.59	8.0E-27	AF181897.1	NT	ADP.ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
5873	18495	31221	1.14	8.0E-27	AV732214.1	EST_HUMAN	Homo sapiens WRN (WRN) gene, complete cds
7054	18073		2.9	8.0E-27	BE928560.1	EST_HUMAN	AV732214 HTF Homo sapiens cDNA clone HTFBCB06 5'
7111	19451	32267	2.49	8.0E-27	N84970.1	EST_HUMAN	MR4-BT0398-250800-204-d06 BT0398 Homo sapiens cDNA
9136	21671	34613	1.35	8.0E-27	AW857579.1	EST_HUMAN	J1751F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J1751 5' similar to REPETITIVE ELEMENT L1
9136	21671	34614	1.35	8.0E-27	AW857579.1	EST_HUMAN	GM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
712	13333		1.39	7.0E-27	Z70664.1	NT	GM1-CT0315-091289-063-d07 CT0315 Homo sapiens cDNA
5252	17815		2.66	7.0E-27	AW629172.1	EST_HUMAN	Human endogenous retroviral element HC2
8791	21330		0.77	7.0E-27	D86984.1	NT	h51h12.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975879 3' similar to TR:O76040 O76040 ORF2: FUNCTION UNKNOWN. ;
10628	23160		4.39	7.0E-27	AJ271735.1	NT	Human mRNA for KIAA0231 gene, partial cds
12298	24495		3.27	7.0E-27	AV723365.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region, segment 1/2
10605	23139	36151	11.92	6.0E-27	M26697.1	NT	AV723365 HTB Homo sapiens cDNA clone HTBAHE02 5'
11621	24063	37127	2.33	6.0E-27	U93163.1	NT	Human nucleolar protein (B23) mRNA, complete cds
							Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7752	20260		0.79	5.0E-27	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
10136	22631	35619	2.86	5.0E-27	BF668614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
10136	22631	35620	2.86	5.0E-27	BF668614.1	EST_HUMAN	602121491F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4278527 5'
2423	14991	27564	4.86	4.0E-27	D25303.1	NT	Human mRNA for Integrin alpha subunit, complete cds
6842	19432	32247	1.37	4.0E-27	9910589	NT	Mus musculus sperm tail associated protein (Stap), mRNA
7880	20422		1.14	4.0E-27	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
7925	20467		1.22	4.0E-27	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9859	22158	35130	0.8	4.0E-27	AW880859.1	EST_HUMAN	QV0-OT0033-070300-152-b10 OT0033 Homo sapiens cDNA
11473	23923	36993	2.38	4.0E-27	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2085	14866	27237	6.19	3.0E-27	X80658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
4358	16945	29387	1.56	3.0E-27	BE071924.1	EST_HUMAN	PM0-BT0527-090100-001-d11 BT0527 Homo sapiens cDNA
9549	18181	30596	6.22	3.0E-27	AA077705.1	EST_HUMAN	7B44C08 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B44C08
9229	21951	34900	3.67	3.0E-27	BF035327.1	EST_HUMAN	60145831F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3882086 5'
45	12724	25185	29.69	2.0E-27	AF054187.1	NT	Homo sapiens alpha NAC mRNA, complete cds
1940	14524		12.18	2.0E-27	AA565345.1	EST_HUMAN	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S
3143	15757		12.54	2.0E-27	AW 829172.1	EST_HUMAN	ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN); O76040 ORF2: FUNCTION UNKNOWN;
3261	15873	28353	1.74	2.0E-27	AF11187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
3261	15873	28354	1.74	2.0E-27	AF11187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
6779	19370	32185	0.88	2.0E-27	H02855.1	EST_HUMAN	Y366d1.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150840 5' similar to
8034	20576	33481	1.24	2.0E-27	A1896347.1	EST_HUMAN	SP-HMGC_MOUSE_Q02591 HOMEOBOX PROTEIN;
9193	21710		2.25	2.0E-27	AA551527.1	EST_HUMAN	w128p07.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2426268 3'
9707	22205	35178	1	2.0E-27	X06858.1	NT	nh08h05.s1 NCL_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943737 similar to contains L1.t3 L1 repetitive element;
9948	22443	35421	1.03	2.0E-27	M78590.1	EST_HUMAN	R. rattus RYA3 mRNA for a potential ligand-binding protein
9948	22443	35422	1.03	2.0E-27	M78590.1	EST_HUMAN	EST00738 Fetal brain, Stralagene (cat#836206) Homo sapiens cDNA clone HFBCF07
10834	23355	36370	3.38	2.0E-27	AU121685.1	EST_HUMAN	EST00738 Fetal brain, Stralagene (cat#836206) Homo sapiens cDNA clone HFBCF07
11360	14524		15.86	2.0E-27	AA565345.1	EST_HUMAN	AU121685 MAMMA1 Homo sapiens cDNA clone MAMMA1000746 5'
461	13095		1.17	1.0E-27	AL163248.2	NT	nk01b10.s1 NCL_CGAP_P111 Homo sapiens cDNA clone IMAGE:1000699 similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);
							Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
1034	13644	26157	1.25	1.0E-27	AB026898.1	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4155	16747		1.02	1.0E-27	BE350127.1	h009g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
6665	19261	32065	6.88	1.0E-27	6005855	MER29 repetitive element ;
6952	19529	32353	1.86	1.0E-27	F30158.1	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
6952	19529	32354	1.86	1.0E-27	F30158.1	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8546	21085	34008	0.7	1.0E-27	AB007923.1	HSPD20461 HM3 Homo sapiens cDNA clone s4000095C10
8916	21454		1.89	1.0E-27	BE079780.1	Homo sapiens mRNA for KIAA0454 protein, partial cds
8638	22138	35104	2.68	1.0E-27	D87449.1	RC6-BT0627-140200-011-E08 BT0627 Homo sapiens cDNA
11551	23999	37071	3.65	1.0E-27	AF111093.1	Human mRNA for KIAA0260 gene, partial cds
148	12810		2.02	9.0E-28	BE348399.1	Bos taurus latrophilin 3 splice variant bbah mRNA, complete cds
333	12985	25472	2.19	9.0E-28	AU128260.1	hwi7c11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183188 3' similar to TR:Q07314 Q07314
11732	24137		4.71	9.0E-28	BF377659.1	SECRETED NEUREXIN III-ALPHA-C PRECURSOR. [9] TR:Q07280 TR:Q07313 ;
12068	24923		4.41	8.0E-28	AW157574.1	AU126260 NT2RP1 Homo sapiens cDNA clone NT2RP1000443 5'
1223	13823	26338	16.9	7.0E-28	AU142750.1	CM2-TN0140-070900-372-q01 TN0140 Homo sapiens cDNA
11088	23578	36618	3.08	7.0E-28	11417868	au83108.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to
11688	24104		2.37	7.0E-28	AV735348.1	TR:O60302 O60302 KIAA0555 PROTEIN ; contains element MER22 repetitive element ;
8850	21389		1.04	6.0E-28	AF016052.1	AU142750 Y79AA1 Homo sapiens cDNA clone Y79AA1000824 5'
12346	24527		12.5	6.0E-28	AA504562.1	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
340	12992		2.28	5.0E-28	A021003.1	AV735348 CB Homo sapiens cDNA clone CBFAKA12 5'
4081	16677	28137	1.79	5.0E-28	R79762.1	Homo sapiens zinc finger protein ZNF191 (ZNF191) gene, complete cds
2654	15213	27786	1.12	4.0E-28	AW195066.1	aa80e03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825340 5' similar to contains Alu
3005	15821	28098	0.76	4.0E-28	4505316	repetitive element/contains element PTR5 repetitive element ;
3142	15756	28223	3.13	4.0E-28	BE409100.1	wo18c07.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2455892 3' similar to contains THR.b1
7368	19894	32757	1.79	4.0E-28	AI198941.1	THR repetitive element ;
10745	23269		4.9	4.0E-28	AF028308.1	y68f10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:146443 5'
						Q08379 GOLGIN-95 ;
						xa33c09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2695504 3' similar to SW:GG95_HUMAN
						Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
						601300703F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635305 5'
						q66f10.x1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1
						REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
						Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and bysinsogen gene families

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10885	23406		25.24	4.0E-28	AB038241.1	NT	Felis catus GAPDH mRNA for glyceraldehyde-3-phosphate dehydrogenase, complete cds
10904	19894	32757	3.33	4.0E-28	AI198941.1	EST_HUMAN	q166f10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755019 3' similar to gb:M19503 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (HUMAN);
12116	24375		1.71	4.0E-28	AW854244.1	EST_HUMAN	RC3-CT0254-240400-210-112 CT0254 Homo sapiens cDNA
12657	24728		72.51	4.0E-28	AW157571.1	EST_HUMAN	au83h08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2762911 3' similar to TR:O60302 O60302 KIA0555 PROTEIN; contains element MER22 repetitive element;
1328	13920		1.95	3.0E-28	AF155382.1	NT	Homo sapiens metalloprotease-like, disintegrin-like, cysteine-rich protein 2 epsilon (ADAM22) mRNA, complete cds
8761	21300	34221	3.77	3.0E-28	BF354030.1	EST_HUMAN	MR3-HT0713-280500-073-009 HT0713 Homo sapiens cDNA
10815	23336	36349	2.08	3.0E-28	U53588.1	NT	Homo sapiens MHC class 1 region
12147	24390		2.53	3.0E-28	AI831991.1	EST_HUMAN	w199f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2410885 3' similar to contains Alu repetitive element; contains element HGR repetitive element;
12284	24486		1.77	3.0E-28	BE082801.1	EST_HUMAN	RC2-BT0842-210200-073-003 BT0842 Homo sapiens cDNA
92	12768	25251	8.71	2.0E-28	BE082167.1	EST_HUMAN	RC1-BT0254-220300-019-c05 BT0254 Homo sapiens cDNA
1207	13807	26320	9.63	2.0E-28	Y11107.3	NT	Homo sapiens ITGB4 gene for Integrin beta 4 subunit, exons 3-41
2517	15081	27654	2.47	2.0E-28	AI348634.1	EST_HUMAN	q35b06.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1910483 3' similar to contains L1.b2 L1 repetitive element;
3407	16016	28495	0.64	2.0E-28	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8449	19050	31836	1.2	2.0E-28	BF224402.1	EST_HUMAN	hr76c03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134404 3' similar to contains LOR1.b1 LOR1 repetitive element;
6472	19073		5.22	2.0E-28	BF212905.1	EST_HUMAN	601814198F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4048751 5'
7988	20530	33437	0.77	2.0E-28	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
9505	22005		11	2.0E-28	AW972305.1	EST_HUMAN	EST384394 MAGe resequences, MAGL Homo sapiens cDNA
11481	23931	37002	1.91	2.0E-28	AF224689.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12127	24383		1.74	2.0E-28	H06376.1	EST_HUMAN	y76c09.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:44300 5'
1526	14118	26855	3.52	1.0E-28	D38044.1	NT	Human gene for Ahr-receptor, exon 7-9
2708	14835	27413	1.64	1.0E-28	BF333236.1	EST_HUMAN	QV1-BT0821-120800-360-b03 BT0821 Homo sapiens cDNA
2708	15265	27832	1.38	1.0E-28	AF000995.1	NT	Homo sapiens ubiquitously TPR motif, Y isoform (UTY) mRNA, alternative transcript 2, complete cds
4668	17250		0.96	1.0E-28	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
7801	20344		7.69	1.0E-28	11428885	NT	Homo sapiens similar to ribosomal protein L12 (H. sapiens) (LOC63091), mRNA
7981	20503		3.2	1.0E-28	8922793	NT	Homo sapiens hypothetical protein FLJ10968 (FLJ10968), mRNA
9202	21719	34683	4.72	1.0E-28	AA308744.1	EST_HUMAN	EST179615 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to similar to retroviral LTR

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9790	22288	35272	9.67	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
9790	22288	35273	9.67	1.0E-28	4758431	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLA1), mRNA
11693	24108		10.45	1.0E-28	AA054182.1	EST_HUMAN	zf51c01.r1 Soares retina N2b4-HR Homo sapiens cDNA clone IMAGE:380448 5'
12494	24811		1.56	1.0E-28	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12596	25034	30502	3.5	9.0E-29	AW663987.1	EST_HUMAN	h76g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978266 3'
12245	24456		5.36	8.0E-29	Q00130	SWISSPROT	HYPOPHYSICAL GENE 50 PROTEIN
1648	14238	26773	1.04	7.0E-29	AW966447.1	EST_HUMAN	EST1378521 IMAGE resequencing, MAGI Homo sapiens cDNA
3607	16211		0.91	7.0E-29	BE254708.1	EST_HUMAN	601114890F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355367 5'
12644	24718		13.85	7.0E-29	AJ132352.1	NT	Rattus norvegicus mRNA for 45 kDa secretory protein, partial
621	13248	25722	7.35	6.0E-29	A936748.1	EST_HUMAN	wp69b01.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475
12002	24307		9.29	6.0E-29	BE940436.1	EST_HUMAN	O15475 UNNAMED HERV-H PROTEIN :contains LTR7.b1 LTR7 repetitive element ;
5138	17710		1.02	5.0E-29	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
8666	21205		7.83	5.0E-29	AW887541.1	EST_HUMAN	RC3-OT0091-170300-011-c12 OT0091 Homo sapiens cDNA
12276	24480		1.32	5.0E-29	BE612449.1	EST_HUMAN	601451827F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3855726 5'
3269	15881		2.92	4.0E-29	A1752367.1	EST_HUMAN	cn15602.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn15c02 random
6190	18773		6.52	4.0E-29	BE164930.1	EST_HUMAN	QV1-HT0471-280300-121-a05 HT0471 Homo sapiens cDNA
8025	20587	33469	0.92	4.0E-29	A1878101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element ;
8025	20587	33470	0.92	4.0E-29	A1878101.1	EST_HUMAN	wd35g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element ;
8680	21219	34139	6.03	4.0E-29	J04888.1	NT	Human 90 kD heat shock protein gene, complete cds
4506	17090	29538	1.58	3.0E-29	AB042297.1	NT	Homo sapiens PTS gene for 6-pyruvyltetrahydropterin synthase, complete cds
4839	17417	29870	1.28	3.0E-29	BF333236.1	EST_HUMAN	QV1-BT0821-120900-360-b03 BT0821 Homo sapiens cDNA
6088	18704	31452	0.89	3.0E-29	BE314018.1	EST_HUMAN	601152657F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508527 5'
8668	21207	34124	2.6	3.0E-29	D38044.1	NT	Human gene for AII-receptor, exon 7-9
9224	21740	34683	1.93	3.0E-29	AW303317.1	EST_HUMAN	xv1703.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813405 3' similar to contains Alu repetitive element;contains MER19.12 MER19 repetitive element ;
9450	21976		2.01	3.0E-29	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9869	22366		0.76	3.0E-29	BE350127.1	EST_HUMAN	ht09g01.x1 NCI_CGAP_KidT3 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
11148	23656	36698	1.88	3.0E-29	AA403053.1	EST_HUMAN	z62b01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1333769 G1335769 GAG-POL POLYPYRROLINE ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11891	24234		2.61	3.0E-29	D83882.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
12553	25044		1.95	3.0E-29	D83882.1	NT	Human HsLIM15 mRNA for HsLIM15, complete cds
518	13150	25632	1.07	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
518	13150	25633	1.07	2.0E-29	AF084869.1	NT	Homo sapiens envelope protein RIC-6 (env) gene, complete cds
1580	14173	26703	7.26	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
1580	14173	26704	7.26	2.0E-29	AI963604.1	EST_HUMAN	wr65d10.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:2492563 3' similar to TR:O15546 O15546 HERV-E ENVELOPE GLYCOPROTEIN ;
4366	16953	29393	2.01	2.0E-29	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
5991	18611	31346	0.88	2.0E-29	AI082459.1	EST_HUMAN	cs71e04.x1 NCL_CGAP_GC2 Homo sapiens cDNA clone IMAGE:1610814 3' similar to contains L1.12 L1 repetitive element ;
6327	18933	31708	1.45	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7560	18933	31708	1.2	2.0E-29	AI806418.1	EST_HUMAN	wf27g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356860 3' similar to contains element MER6 repetitive element ;
7917	20459	33366	1.15	2.0E-29	BE867157.1	EST_HUMAN	601442206F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3946948 5'
8514	21053	33975	0.55	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
8514	21053	33976	0.55	2.0E-29	10567821	NT	Homo sapiens DNA-binding protein (LOC56242), mRNA
9427	21938	34894	3.74	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
9427	21936	34895	3.74	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10138	22633	35622	3.15	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
10138	22633	35623	3.15	2.0E-29	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11350	23805		2.03	2.0E-29	11425108	NT	Homo sapiens splicing factor similar to dnaJ (SPF31), mRNA
11390	23842		2.46	2.0E-29	AW880701.1	EST_HUMAN	QV0-OT0032-080300-155-d01 OT0032 Homo sapiens cDNA
11635	24075		1.93	2.0E-29	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
8727	21266	34186	7.44	1.0E-29	AW983980.1	EST_HUMAN	R1-HN0003-220300-021-b04 HN0003 Homo sapiens cDNA
10503	22997	36006	0.76	1.0E-29	X60658.1	NT	R. rattus RYA3 mRNA for a potential ligand-binding protein
6896	19292	32096	3.08	9.0E-30	AA761215.1	EST_HUMAN	nc26c07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1288332 3' similar to contains MER4.b1 MERA repetitive element ;
11773	24162		2.08	6.0E-30	11422745	NT	Homo sapiens zinc/iron regulated transporter-like (ZIRTL), mRNA
6481	19062		9.33	8.0E-30	F08688.1	EST_HUMAN	HSC23F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
8214	20755	33669	2.65	8.0E-30	AA383873.1	EST_HUMAN	EST97317 Thymus I Homo sapiens cDNA 5' end similar to EST containing O family repeat
8617	21166	34069	4.64	8.0E-30	AI557072.1	EST_HUMAN	PT2.1_13_B11.tumor2 Homo sapiens cDNA 3'
1562	14154		0.91	7.0E-30	BE081133.1	EST_HUMAN	PM4-BT0724-150400-004-d11 BT0724 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7779	20291	33190	1.28	7.0E-30	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862088 5'
1810	14400	28945	1.35	6.0E-30	D25303.1	NT	Human mRNA for integrin alpha subunit, complete cds
3224	15838	28314	2.38	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
4872	15838	28314	1.1	6.0E-30	BE008026.1	EST_HUMAN	QV0-BN0147-280400-214-f12 BN0147 Homo sapiens cDNA
10432	22826	35932	0.72	6.0E-30	AF177227.1	NT	Homo sapiens CTCL tumor antigen seq2-10 mRNA, partial cds
12615	18024		1.6	8.0E-30	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
4085	16681	29141	39.51	5.0E-30	AI399992.1	EST_HUMAN	igb2g03.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116276 3' similar to contains Alu repetitive element
5448	24850		4.03	5.0E-30	U87831.1	NT	Human aconitase hydratase (ACO2) gene, exon 7
10767	23291		3.31	5.0E-30	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
11034	23548	36583	6.29	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11034	23548	36584	6.29	5.0E-30	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2188	14764	27333	1.32	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
2188	14764	27334	1.32	4.0E-30	AW937471.1	EST_HUMAN	QV3-DT0043-090200-080-c06 DT0043 Homo sapiens cDNA
8936	21375	34289	3.16	4.0E-30	AW812488.1	EST_HUMAN	CM1-ST0181-091199-035-f08 ST0181 Homo sapiens cDNA
1191	13782		3.43	3.0E-30	AI338551.1	EST_HUMAN	qq83c05.x1 Soares_tetral_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1938920 3' similar to contains MER29 repetitive element
3821	16421	28883	0.87	3.0E-30	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
7893	20435		0.47	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
8423	20653		0.5	3.0E-30	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10330	22824	35820	1.69	3.0E-30	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
10460	22954	35964	0.53	3.0E-30	AB032969.1	NT	MER29 repetitive element
10460	22954	35965	0.53	3.0E-30	AB032969.1	NT	Homo sapiens mRNA for KIAA1143 protein, partial cds
11064	23596	36632	1.78	3.0E-30	P34056	SWISSPROT	Homo sapiens mRNA for KIAA1143 protein, partial cds
703	13324	25811	1.3	2.0E-30	AW857315.1	EST_HUMAN	TRANSCRIPTION FACTOR AP-2
1123	13726		2.35	2.0E-30	F06688.1	EST_HUMAN	CM0-CT0307-310100-158-h03 CT0307 Homo sapiens cDNA
1527	14119	26656	7.23	2.0E-30	BE175877.1	EST_HUMAN	HSC2F051 normalized infant brain cDNA Homo sapiens cDNA clone c-23f05
2740	15295	27862	9.08	2.0E-30	BE765232.1	EST_HUMAN	RC5-HT0582-110400-013-H08 HT0582 Homo sapiens cDNA
2944	15560	28034	6.74	2.0E-30	AF114156.1	NT	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
3857	16455	28919	2.18	2.0E-30	AW209581.1	EST_HUMAN	Homo sapiens Y-linked zinc finger protein (ZFY) gene, complete cds
4892	17467	29922	2.07	2.0E-30	BE298945.1	EST_HUMAN	UJ-HB1-af0-c-12-Q-UI st NCL_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722558 3'
4892	17467	29923	2.07	2.0E-30	BE298945.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'
6855	19443	32289	0.92	2.0E-30	BF306337.1	EST_HUMAN	601119860F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028438 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8412	20852	33871	0.81	2.0E-30	AA019103.1	EST_HUMAN	z658c10.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363186 5'
8474	21014	33830	5.63	2.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujliwara) Homo sapiens cDNA clone GEN-570C01 5'
8570	21109	34027	3.55	2.0E-30	BE070617.1	EST_HUMAN	7e37c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8570	21109	34028	3.55	2.0E-30	BE070617.1	EST_HUMAN	7e37c12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284662 3' similar to SW:DHSA_HUMAN P31040 SUCCINATE DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN SUBUNIT PRECURSOR ;
8908	22405	35380	3.21	2.0E-30	AW971588.1	EST_HUMAN	EST383657 MAGC resequences, MAGL Homo sapiens cDNA hs33406.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element ;
8994	22489	35477	6.11	2.0E-30	AW470791.1	EST_HUMAN	C18939 Human placenta cDNA (TFujliwara) Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element ;
308	12963	25452	12.31	1.0E-30	C18939.1	EST_HUMAN	C18939 Human placenta cDNA (TFujliwara) Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element ;
563	13194	25673	3.84	1.0E-30	AW468897.1	EST_HUMAN	hs30804.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2875489 3' similar to contains THR.b3 THR repetitive element ;
745	13385	25859	2.7	1.0E-30	AL163203.2	NT	MER1.13 MER1 MER1 repetitive element ;
2753	14827	27403	3.59	1.0E-30	AA664377.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003 ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
2502	15066	27640	1.84	1.0E-30	BF347728.1	EST_HUMAN	602022560.F1 NCL CGAP_Brd87 Homo sapiens cDNA clone IMAGE:4157991 5'
3035	15651	28129	1.36	1.0E-30	5803091	NT	Homo sapiens methionine aminopeptidase, eIF-2-associated p67 (MNPEP), mRNA
3090	15705	28177	1.06	1.0E-30	AA315045.1	EST_HUMAN	EST188868 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end
7708	20217	33105	16.59	1.0E-30	BF183230.1	EST_HUMAN	EST188868 HCC cell line (metastasis to liver in mouse) Homo sapiens cDNA 5' end
12288	25029		1.48	1.0E-30	AA289211.1	EST_HUMAN	EST11698 Uterus Homo sapiens cDNA 5' end
12411	24949		8.63	1.0E-30	H55593.1	EST_HUMAN	CHR220532 Chromosome 22 exon Homo sapiens cDNA clone C22_728 5'
3829	16429	28890	0.72	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
3829	16429	28891	0.72	9.0E-31	T73025.1	EST_HUMAN	yc65e06.r1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:85570 5'
8266	20807	33725	1.03	9.0E-31	R18214.1	EST_HUMAN	y99b08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:305566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8266	20807	33728	1.03	9.0E-31	R18214.1	EST_HUMAN	y99b08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:305566 5' similar to gb:X12953 RAS-RELATED PROTEIN RAB-2 (HUMAN);
8559	21098		1.84	9.0E-31	Z38293.1	EST_HUMAN	HSC05F032 normalized infant brain cDNA Homo sapiens cDNA clone c-05f03 3'
8561	21100	34020	0.52	9.0E-31	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
12840	24715	30887	1.89	9.0E-31	6755441	NT	Mus musculus syntenic 4 (Sdc4), mRNA
1115	13719	26230	6.84	8.0E-31	8923389	NT	Homo sapiens hypothetical protein FLJ20420 (FLJ20420), mRNA
2457	16024		4.22	8.0E-31	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
11801	24910		2.71	8.0E-31	AF012385.1	EST_HUMAN	AF012385 Human testis (C. De Smet) Homo sapiens cDNA clone TDP3.12b

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
740	13360		2.5	7.0E-31	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
2692	15249	27818	2.37	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
2692	15249	27819	2.37	7.0E-31	BE326517.1	EST_HUMAN	hw05a11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182012 3'
8340	20881	33800	0.82	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
8340	20881	33801	0.82	7.0E-31	AF208541.1	NT	Homo sapiens V1-vascular vasopressin receptor AVPR1A gene, promoter region and partial cds
9190	21707		1.62	7.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
12243	24455	30958	1.53	7.0E-31	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
							Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3742	16343		2.28	6.0E-31	AF223391.1	NT	
8094	20635		6.98	6.0E-31	AF055086.1	NT	Homo sapiens MHC class 1 region
							h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER28.b3
8273	20814	33736	0.78	6.0E-31	BE350127.1	EST_HUMAN	MER29 repetitive element ;
10617	23149	36161	1.69	6.0E-31	AU119105.1	EST_HUMAN	AU119105 HEMBA1 Homo sapiens cDNA clone HEMBA1005050 5'
11835	24189	31038	3.25	6.0E-31	AW372868.1	EST_HUMAN	RC5-BT0377-091289-031-D12 BT0377 Homo sapiens cDNA
11964	24868		2	6.0E-31	BE894488.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
206	12867	25352	3.89	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
206	12867	25353	3.89	5.0E-31	M60694.1	NT	Homo sapiens type I DNA topoisomerase gene, exon 8
8382	20922		0.75	5.0E-31	BF056540.1	EST_HUMAN	7k06f04.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:3443479 3' similar to TR.Q13537 Q13537
622	13249		2.67	4.0E-31	AJ271735.1	NT	SIMILAR TO POGO ELEMENT ; contains L1.t1 L1 repetitive element ;
1854	14442		2.42	4.0E-31	AL163280.2	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2815	15387		1.02	4.0E-31	5730038	NT	Homo sapiens chromosome 21 segment HS21C080
10427	22921	35924	0.65	4.0E-31	AF084484.1	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
12006	24309		1.65	4.0E-31	AJ230125.1	NT	Rattus norvegicus GTP-binding protein REM2 (Rem2) mRNA, complete cds
12399	24599		1.51	4.0E-31	AB008681.1	NT	Homo sapiens GGT1 gene, exon 1
							Homo sapiens gene for activin receptor type IIB, complete cds
7377	19903	32787	7.09	3.0E-31	4828853	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (NDUFB8) mRNA
7505	20627	32891	1.62	3.0E-31	11420328	NT	Homo sapiens hypothetical protein FLJ10842 (FLJ10842), mRNA
8102	20643		2.18	3.0E-31	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C008
9500	22000	34957	14.68	3.0E-31	D14523.1	NT	Horse mRNA for ferritin L-chain, complete cds
10488	22982	35990	0.64	3.0E-31	AA21242.1	EST_HUMAN	zu06d04.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731047 5'
10510	23048	36060	2.78	3.0E-31	P11174	SWISSPROT	40S RIBOSOMAL PROTEIN S15 (R1G PROTEIN)
11032	23546		6.94	3.0E-31	BF036327.1	EST_HUMAN	60145831F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1961	14545	27102	1.52	2.0E-31	AW838171.1	EST_HUMAN	QV2-LT0051-260300-111-403 LT0051 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2255	14829	27405	1.16	2.0E-31	AI393388.1	EST_HUMAN	ig44g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2111672 3'
2379	14948	27522	2.08	2.0E-31	AL119245.1	EST_HUMAN	DKFZp761G1513.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G1513 5'
2485	15050	27621	3.48	2.0E-31	AA458824.1	EST_HUMAN	aa88f11.s1 Stratagene fetal retina 837202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR:12 THR repetitive element;
5479	18113	30522	0.81	2.0E-31	AW444496.1	EST_HUMAN	UI-H-B13-akb-1-09-0-UJ.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733833 3'
5888	18511	31237	2.97	2.0E-31	BE350127.1	EST_HUMAN	h09g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3148256 3' similar to contains MER29 b3 MER29 repetitive element;
9009	21543		2.32	2.0E-31	AA877764.1	EST_HUMAN	nc06f04.s1 NCI_CGAP_Cot10 Homo sapiens cDNA clone IMAGE:1161055 3' similar to TR:Q13537 Q13537 MER37 TRANSPORTABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
9134	21689	34611	3.65	2.0E-31	7661535	NT	Homo sapiens B9 protein (B9), mRNA
9820	22318	35301	1.04	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9820	22318	35302	1.04	2.0E-31	AV710948.1	EST_HUMAN	AV710948 Cu Homo sapiens cDNA clone CuAALB07 5'
9987	22482	35467	1.73	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
9987	22482	35468	1.73	2.0E-31	BE408611.1	EST_HUMAN	601304125F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638310 5'
11934	24288		3.08	2.0E-31	AF148512.1	NT	Homo sapiens hexokinase II gene, promoter region
12078	25106		2.43	2.0E-31	AI114527.1	EST_HUMAN	HA1110 Human fetal liver cDNA library Homo sapiens cDNA
18	12697	25154	8.8	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
1703	14296	26831	3.28	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1703	14296	26832	3.28	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
1703	14296	26833	3.28	1.0E-31	O95371	SWISSPROT	OLFACTORY RECEPTOR 2C1
4742	17323	29763	1.19	1.0E-31	AL194376.1	EST_HUMAN	DKFZp947B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp947B235 5'
4742	17323	29764	1.19	1.0E-31	AL194376.1	EST_HUMAN	DKFZp947B235.1 547 (synonym: hibr1) Homo sapiens cDNA clone DKFZp947B235 5'
5406	18130	30538	3.47	1.0E-31	AW391879.1	EST_HUMAN	MR3-ST0220-151299-028-a08_1 ST0220 Homo sapiens cDNA
6282	18890	31658	1.84	1.0E-31	AF048727.1	NT	Homo sapiens minisatellite cab1 repeat region
7332	19859	32722	0.84	1.0E-31	AF126145.1	NT	Bos taurus xenobiotic/medium-chain fatty acid:CoA ligase form XL-III mRNA, nuclear mRNA encoding mitochondrial protein, complete cds
7772	20281	33178	0.68	1.0E-31	BE972818.1	EST_HUMAN	601652052F1 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:3835293 5'
10135	22630	35618	0.67	1.0E-31	U93163.1	NT	Homo sapiens MAGE-B2 (MAGE-B2), MAGE-B3 (MAGE-B3), MAGE-B4 (MAGE-B4), and MAGE-B1 (MAGE-B1) genes, complete cds
10796	23319	36329	2.94	1.0E-31	AI086434.1	EST_HUMAN	Q16595 FRATAXIN.;
6749	19342	32149	2.29	9.0E-32	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
7591	20108		1.07	9.0E-32	11430822	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2122	14700	27270	3.49	8.0E-32	AI058770.1	EST_HUMAN	oz15a09.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1675384 3'
5673	18300	30781	0.9	8.0E-32	AW997214.1	EST_HUMAN	RC2-BN0048-200300-015-s04 BN0048 Homo sapiens cDNA
4985	17559	30002	3.69	7.0E-32	P52591	SWISSPROT	NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PORE MEMBRANE PROTEIN OF 121 KD) (P145)
11909	24247		3.42	7.0E-32	X17283.1	NT	Human chromosome 22 immunoglobulin V(K) gene, part. with 5' breakpoint between orphion and neighbouring non-amplified region
2759	15314	27880	0.91	6.0E-32	AA78104.1	EST_HUMAN	tm34a10.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2159994 3' similar to contains MER29.13
7402	18927		1.37	6.0E-32	BE888016.1	EST_HUMAN	MER29 repetitive element;
12350	25086		1.51	6.0E-32	AA884653.1	EST_HUMAN	601511530F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913087 5'
1072	13677	26187	75.63	5.0E-32	AF116627.1	NT	ch37c03.s1 NCL_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1459972 3' similar to contains L1.13 L1 repetitive element;
966	13577		1.55	4.0E-32	AL163246.2	NT	Homo sapiens PRO1181 mRNA, complete cds
7599	20112	32987	3.11	4.0E-32	11432574	NT	Homo sapiens chromosome 21 segment HS21C046
7599	20112	32988	3.11	4.0E-32	11432574	NT	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
8300	20841		0.77	4.0E-32	BE064410.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
481	13114	25604	2.79	3.0E-32	Y17293.1	NT	RC4-BT0311-141199-011-h06 BT0311 Homo sapiens cDNA
1502	14094	26633	8.08	3.0E-32	AV731500.1	EST_HUMAN	Homo sapiens FL-1 gene, partial
2933	15549	28025	0.73	3.0E-32	5174574	NT	AV731500 HTF Homo sapiens cDNA clone HTFAK007 5'
2933	15549	28026	0.73	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9315	21829	34780	16.81	3.0E-32	AV758634.1	EST_HUMAN	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
9315	21829	34781	16.81	3.0E-32	AV758634.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
10805	23328	36339	7.7	3.0E-32	AA777621.1	EST_HUMAN	AV758634 BM Homo sapiens cDNA clone BMFBFBH12 5'
11093	23605		1.63	3.0E-32	BF035327.1	EST_HUMAN	z95a07.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448500 3' similar to contains THR.13 THR repetitive element;
11937	24270		6.37	3.0E-32	BE278086.1	EST_HUMAN	601458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
12325	15549	28025	6.26	3.0E-32	5174574	NT	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
12325	15549	28026	6.26	3.0E-32	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
12491	24670		5.38	3.0E-32	BE279086.1	EST_HUMAN	601156285F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139701 5'
5011	17584	30027	1.01	2.0E-32	BE296613.1	EST_HUMAN	601173631F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529159 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6400	19003	31781	0.9	2.0E-32	M35418.1	NT	Human cell 12-lipoxygenase mRNA, complete cds
6605	19202	32007	5.89	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
6605	19202	32008	5.89	2.0E-32	Z38133.1	NT	H. sapiens mRNA for myosin
8220	20761	33676	2.06	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
8220	20761	33677	2.06	2.0E-32	AA114294.1	EST_HUMAN	zn66c08.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:563150 5'
12610	24694	30859	1.41	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBF8IA08 5'
12610	24694	30860	1.41	2.0E-32	AV736449.1	EST_HUMAN	AV736449 CB Homo sapiens cDNA clone CBF8IA08 5'
7115	19455	32271	6.86	1.0E-32	11439789	NT	Homo sapiens chromosome 11 open reading frame 9 (C11ORF9), mRNA
8532	21071	33991	4.86	1.0E-32	AA720574.1	EST_HUMAN	hw21g02.s1 NCI_CGAP_GC80 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element:
3527	16132		5.7	9.0E-33	BE327112.1	EST_HUMAN	hw07c05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182216 3' similar to TR:O88539 O88539 WW DOMAIN BINDING PROTEIN 11:
6552	19150		4.1	9.0E-33	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8723	21262	34182	2.82	9.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156670 5'
10677	23209		6.39	9.0E-33	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
65	12744	25219	2.71	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
65	12744	25220	2.71	7.0E-33	5031738	NT	Homo sapiens short-chain alcohol dehydrogenase family member (HEP27) mRNA
2206	14782	27355	1.92	7.0E-33	AI580115.1	EST_HUMAN	to12b09.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2178809 3' similar to contains OFR.11 OFR repetitive element:
2675	15233		6.6	7.0E-33	AV730056.1	EST_HUMAN	AV730056 HTF Homo sapiens cDNA clone HTFAVE03 5'
3279	15890		15.76	7.0E-33	AW971307.1	EST_HUMAN	EST383396 MAGI resequences, MAGI Homo sapiens cDNA
8878	21415		1.06	7.0E-33	X54890.1	NT	Human NLRP mRNA for leukocyte common antigen-related peptide (protein-tyrosine phosphatase) (EC 3.1.3.49)
10708	23236	36249	4.73	7.0E-33	BF347229.1	EST_HUMAN	602021164F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156670 5'
11127	23635	36876	2.53	7.0E-33	AW971588.1	EST_HUMAN	EST383397 MAGI resequences, MAGI Homo sapiens cDNA
11915	24253	31009	7.43	7.0E-33	AA601416.1	EST_HUMAN	no16h01.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100881 3' similar to contains L1.1 L1 repetitive element:
3800	18400		0.79	6.0E-33	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
8217	18827	31569	1.11	6.0E-33	F30631.1	EST_HUMAN	HSPD21201 HM3 Homo sapiens cDNA clone s4000107H08
8217	18827	31600	1.11	6.0E-33	F30631.1	EST_HUMAN	HSPD21201-HM3 Homo sapiens cDNA clone s4000107H06
8515	21054	33977	7.9	6.0E-33	J04038.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) gene, complete cds
8636	21175	34094	4.14	6.0E-33	11429189	NT	Homo sapiens similar to RAD23 (S. cerevisiae) homolog B (H. sapiens) (LOC63277), mRNA
9923	22419	35393	1.73	6.0E-33	87556009	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9923	22419	35394	1.73	6.0E-33	6755609	NT	Mus musculus SRY-box containing gene 6 (Sox6), mRNA
1814	14404		1.48	5.0E-33	BF373515.1	EST_HUMAN	QV1-FT0169-100700-271-e02 FT0169 Homo sapiens cDNA
1925	14510		1.2	5.0E-33	1141884	NT	Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA
1943	14527	27082	1.32	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
1943	14527	27083	1.32	5.0E-33	4507208	NT	Homo sapiens spermidine synthase (SRM) mRNA
4132	16724	28178	0.8	5.0E-33	AB014599.1	NT	Homo sapiens mRNA for KIAA0699 protein, partial cds
10147	22842	35632	0.76	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
10147	22842	35633	0.76	5.0E-33	AW264679.1	EST_HUMAN	xq33f11.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2752461 3'
11720	24129		1.43	5.0E-33	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
1167	13769		1.82	4.0E-33	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
2170	14747	27316	1.67	4.0E-33	4758987	NT	Homo sapiens RAB11, member RAS oncogene family (RAB11) mRNA
2484	15031		2.24	4.0E-33	AA626621.1	EST_HUMAN	ab51b11.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844317 5' similar to contains Alu repetitive element; contains MER28.b2 MER28 repetitive element ;
2582	15145	27713	1.82	4.0E-33	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4581	17164	29807	1.39	4.0E-33	AW293349.1	EST_HUMAN	UI-H-B12-ah1-c-03-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727149 3'
5599	18229	30877	21.98	4.0E-33	AA053053.1	EST_HUMAN	217a08.r1 Stratagene cdon (#937204) Homo sapiens cDNA clone IMAGE:510038 5' similar to gb:X12671_ma1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
6526	19126	31919	0.76	4.0E-33	8383984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
6526	19126	31920	0.76	4.0E-33	8383984	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
1128	13731		5.55	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
1129	13731		3.84	3.0E-33	BE350127.1	EST_HUMAN	h109g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 MER29 repetitive element ;
2493	15468		1.01	3.0E-33	AV647851.1	EST_HUMAN	AV647851 GLC Homo sapiens cDNA clone GLCBCF09 3'
10336	22830	35824	1.19	3.0E-33	AA861510.1	EST_HUMAN	ak32b12.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1407847 3' similar to TR:Q13579 Q13579 MARINER TRANSPOSASE.;
19	12698		0.82	2.0E-33	A160189.1	EST_HUMAN	qb87g03.x1 Soares_fetal_hear NBHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
109	12698		2.24	2.0E-33	A160189.1	EST_HUMAN	qb87g03.x1 Soares_fetal_hear NBHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element ;
1415	14008	26536	2.48	2.0E-33	AA010242.1	EST_HUMAN	208a08.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430214 5'
1415	14008	26537	2.48	2.0E-33	AA010242.1	EST_HUMAN	208a08.r1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:430214 5'
4510	17094		4.41	2.0E-33	BE159039.1	EST_HUMAN	MRO-HT0405-160300-202-d08 HT0405 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5122	17694	30131	12.23	2.0E-33	AA626683.1	EST_HUMAN	ab51g11.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844386 5' similar to gb:X00734_cds1 TUBULIN BETA-5 CHAIN (HUMAN);
5255	17818	30242	1.93	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
5255	17818	30243	1.93	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
6555	19153	31949	1.5	2.0E-33	A127492.1	EST_HUMAN	q196d01.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880181 3'
9029	21568		2.63	2.0E-33	A1052256.1	EST_HUMAN	oz21d03.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1875973 3' similar to gb:M29538 TRANSLATIONAL INITIATION FACTOR 2 BETA SUBUNIT (HUMAN);
10497	22991	36000	0.65	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10497	22991	36001	0.65	2.0E-33	11421332	NT	Homo sapiens hypothetical protein SIRP-b2 (SIRP-b2), mRNA
10982	23496	36525	1.8	2.0E-33	AA43847.1	EST_HUMAN	zx48f05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795489 3' similar to TR:G1263081 G1263081 MARINER TRANSPOSASE.;
9	12688		1.08	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7437	19961	32827	1.21	1.0E-33	MT13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
9634	25126		0.62	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
11202	23707	36759	2.63	1.0E-33	AW968818.1	EST_HUMAN	QV3-BN0047-230200-102-b03 BN0047 Homo sapiens cDNA
11515	23963	37033	5.83	1.0E-33	U60822.1	NT	Human dystrophin (DMD) gene, exons 7, 8 and 9, and partial cds
12214	24437		1.6	1.0E-33	A1927191.1	EST_HUMAN	wc88c06.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462410 3'
12403	12688		2.81	1.0E-33	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
12434	24575	30913	2.55	1.0E-33	AV727809.1	EST_HUMAN	AV727809 HTC Homo sapiens cDNA clone HTCCNC12 5'
12628	24706		4.56	9.0E-34	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
1494	14086	26626	2.3	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
9911	14086	26626	0.66	7.0E-34	T70845.1	EST_HUMAN	yd15e05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108320 5'
11989	24299		1.75	7.0E-34	H12868.1	EST_HUMAN	y14c10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148722 5'
486	13128	25616	1.61	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
486	13128	25617	1.61	6.0E-34	U10991.1	NT	Human G2 protein mRNA, partial cds
11797	24177	31028	1.92	6.0E-34	U03886.1	NT	Mus musculus DAG/2J hair-specific (hac-1) gene
1923	14508		2.5	5.0E-34	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51729), mRNA
5218	17763	30201	5.85	5.0E-34	U30883.1	NT	Human splicing factor SRP55-1 (SRP-55) mRNA, complete cds
8800	21339	34268	1.18	5.0E-34	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10534	23071	36084	2.26	5.0E-34	AB037856.1	NT	Homo sapiens mRNA for KIAA1435 protein, partial cds
11133	23841		1.9	5.0E-34	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2041	14623	27192	3.42	4.0E-34	A1804667.1	EST_HUMAN	tt94c06.x1 NCI CGAP_Fr28 Homo sapiens cDNA clone IMAGE:2249194 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2745	15300	27866	1.06	4.0E-34	8922807	NT	Homo sapiens hypothetical protein FLJ10989 (FLJ10989), mRNA
8968	21506	34427	1.35	4.0E-34	BF209778.1	EST_HUMAN	601874950F1 NIH_MGC 54 Homo sapiens cDNA clone IMAGE:4102213 5'
6379	18983	31763	1.13	3.0E-34	M37277.1	NT	Human Ig germline H-chain D-region genes, partial cds
11031	23545		5.04	3.0E-34	BF035327.1	EST_HUMAN	601458331F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5'
8881	21419	34343	1.67	2.0E-34	A1678101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element:
8881	21419	34344	1.67	2.0E-34	A1678101.1	EST_HUMAN	w435g06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330170 3' similar to contains MER29.12 MER29 repetitive element:
1552	14144	26678	7.44	1.0E-34	P12236	SWISSPROT	ADP-ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3)
3736	16337	28802	1.24	1.0E-34	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4145	16737	29190	0.62	1.0E-34	AY006397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4145	16737	29191	0.62	1.0E-34	AY006397.1	NT	Homo sapiens WNT3 precursor (WNT3) mRNA, complete cds
4578	17161		8.22	1.0E-34	BE071414.1	EST_HUMAN	RC2-BT0506-240-400-016-h08 BT0506 Homo sapiens cDNA
6287	18895	31664	2.69	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3886999 5'
6287	18895	31665	2.69	1.0E-34	BE874052.1	EST_HUMAN	601484430F1 NIH_MGC 69 Homo sapiens cDNA clone IMAGE:3886999 5'
9613	22113	35076	17.45	1.0E-34	AL036635.1	EST_HUMAN	DKFZp564A1563_r1 564 (synonym: hfr2) Homo sapiens cDNA clone DKFZp564A1563 5'
11077	23589	36627	1.94	1.0E-34	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2), mRNA
12176	25037		3.1	1.0E-34	AA807097.1	EST_HUMAN	cc31c11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1351316 3' similar to gb:X68203 TYROSINE-PROTEIN KINASE RECEPTOR FLT4 PRECURSOR (HUMAN).
12423	24608		4.62	1.0E-34	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
3707	16308	28776	1.45	9.0E-35	AW663302.1	EST_HUMAN	h177806.y1 NCL_CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968787 5'
243	12902		10.67	8.0E-35	6031190	NT	Homo sapiens prohibitin (PHB) mRNA
1772	14362	26907	2.03	8.0E-35	BF589937.1	EST_HUMAN	nae33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 O75912 DIACYLGLYCEROL KINASE IOTA:
1772	14362	26908	2.03	8.0E-35	BF589937.1	EST_HUMAN	nae33a08.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258134 3' similar to TR:O75912 O75912 DIACYLGLYCEROL KINASE IOTA:
4891	17566	30010	3.45	8.0E-35	BF183195.1	EST_HUMAN	601809588F1 NIH_MGC 18 Homo sapiens cDNA clone IMAGE:4040324 5'
10570	23105	36120	1.8	8.0E-35	BE378480.1	EST_HUMAN	601236488F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3608513 5'
11907	24245		2.96	8.0E-35	BF569282.1	EST_HUMAN	602184624T1 NIH_MGC 42 Homo sapiens cDNA clone IMAGE:4300660 3'
6610	19207	32015	2	7.0E-35	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
1458	14050	26582	1.08	6.0E-35	AA757115.1	EST_HUMAN	ah53h03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1300397 3'
2010	14592	27152	1.29	6.0E-35	6005975	NT	Homo sapiens zinc finger protein 208 (ZNF208), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4127	16719	29174	0.67	6.0E-35	AW297191.1	EST_HUMAN	UI-HBW0-aid-4-09-0-UI.s1 NCL_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2731433 3'
7838	20380	33285	3.41	6.0E-35	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
8843	21182	34101	0.49	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
8843	21182	34102	0.49	6.0E-35	X94232.1	NT	H. sapiens mRNA for novel T-cell activation protein
9584	22084	35048	0.7	6.0E-35	AB002384.1	NT	Human mRNA for KIAA0366 gene, partial cds
9817	22315	35296	2.42	6.0E-35	AB037786.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds
152	12815	25303	37.67	5.0E-35	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase 1 mRNA, complete cds
1747	14337	26883	1.26	5.0E-35	XG3392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
3043	15859	28139	1.39	5.0E-35	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
							Homo sapiens cdk2 kinase (CLK2), propin1, cote1, glucocerebrosidase (GBA), and melanin genes, complete cds, melanin pseudogene and glucocerebrosidase pseudogene, and thrombospondin3 (THBS3) gene, partial cds
4499	17083	28533	1.81	5.0E-35	AF023288.1	NT	601431984F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917229 5'
8125	20688		3.51	5.0E-35	BE890992.1	EST_HUMAN	qg38c05.x1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to
8151	20692	33808	2.29	5.0E-35	A1208765.1	EST_HUMAN	SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
8151	20692	33607	2.29	5.0E-35	A1208765.1	EST_HUMAN	qg38c05.x1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1837448 3' similar to
11056	23588		3.53	5.0E-35	AA001786.1	EST_HUMAN	SW:Y249_HUMAN Q92539 HYPOTHETICAL PROTEIN KIAA0249. ;
1481	14074	26613	13.95	4.0E-35	BE257907.1	EST_HUMAN	zh84f12.r1 Soares fetal liver spleen, INFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
1855	14443	28999	4.12	4.0E-35	H91193.1	EST_HUMAN	601109719F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350405 5'
							yu98a07.r1 Soares fetal liver spleen, INFLS Homo sapiens cDNA clone IMAGE:241236 5' similar to contains PTR5 repetitive element ;
4927	17502		0.58	4.0E-35	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
7260	19788		2.06	4.0E-35	BE350127.1	EST_HUMAN	ht09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER28 b3
8455	20995	33913	6.68	4.0E-35	AL046596.1	EST_HUMAN	MER29 repetitive element ;
1623	14216	26748	31.49	3.0E-35	BE288182.1	EST_HUMAN	DKFZp434L148_r1_434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L148 5'
2369	14940		2.22	3.0E-35	AF224492.1	NT	601125260F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345063 5'
							Homo sapiens phospholipid scramblase 1 gene, complete cds
5543	18175	30589	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q8QZH7
							Q8QZH7 F-BOX PROTEIN FBL2 ;
5543	18175	30590	22.73	3.0E-35	BF433100.1	EST_HUMAN	7n25e09.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565361 3' similar to TR:Q8QZH7
							Q8QZH7 F-BOX PROTEIN FBL2 ;
9409	21918		1.72	3.0E-35	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10078	22573	35568	0.8	3.0E-35	AW003063.1	EST_HUMAN	wr03a05.x1 NCI CGAP GC8 Homo sapiens cDNA clone IMAGE:2480432 3' similar to SW:POL1_HUMAN P10268 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ; K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
113	15407	25269	1.18	2.0E-35	N88985.1	EST_HUMAN	A971F Heart Homo sapiens cDNA clone A971
1230	13829	26344	1.13	2.0E-35	T11909.1	EST_HUMAN	Homo sapiens mRNA for Gab2, complete cds
2259	14833	27411	4.88	2.0E-35	AB018413.1	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3353	15961	28437	0.79	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
3353	15961	28438	0.79	2.0E-35	6912459	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
3613	16216		0.85	2.0E-35	AB020702.1	NT	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3981	16579	28049	0.86	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
3981	16579	28050	0.86	2.0E-35	BE247575.1	EST_HUMAN	TCBAP2E4328 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4328
4777	17358		2.99	2.0E-35	H49239.1	EST_HUMAN	Y19a12.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:274079 5'
5770	18396	31110	1.48	2.0E-35	BF332417.1	EST_HUMAN	QV0-BT0701-210400-199-b04 BT0701 Homo sapiens cDNA
10675	23207	36219	4.14	2.0E-35	X69417.1	NT	H. sapiens PROS-27 mRNA
11663	15961	28437	1.34	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
11663	15961	28438	1.34	2.0E-35	6912459	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
12405	24563		42.99	2.0E-35	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
12525	15407	25269	1.4	2.0E-35	N88985.1	EST_HUMAN	K6932F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K6932 5' similar to REPETITIVE ELEMENT
50	12730	25194	5.95	1.0E-35	AA631949.1	EST_HUMAN	frf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
50	12730	25195	5.95	1.0E-35	AA631949.1	EST_HUMAN	frf16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
782	13401	25903	55.23	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131098-008-412 ST0162 Homo sapiens cDNA
782	13401	25904	55.23	1.0E-35	AW389473.1	EST_HUMAN	IL2-ST0162-131098-008-412 ST0162 Homo sapiens cDNA
942	13555		1.15	1.0E-35	T87947.1	EST_HUMAN	y03a01.1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to SP-A44282 A44282 RETROVIRUS-RELATED POL POLYPROTEIN - HUMAN ;
2579	15141	27710	1.96	1.0E-35	7705994	NT	Homo sapiens hypothetical protein (LOC51233), mRNA
2795	15348	27917	1.36	1.0E-35	BE350127.1	EST_HUMAN	Homo sapiens repetitive element ;
2795	15348	27918	1.36	1.0E-35	BE350127.1	EST_HUMAN	h109g01.x1 NCI CGAP K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
3177	15790	28262	1.03	1.0E-35	6006030	NT	h109g01.x1 NCI CGAP K1d13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3 Homo sapiens transcription elongation factor B (SII), polypeptide 1-like (TCBE1L) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3199	15811	28284	1.52	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
3198	15811	28285	1.52	1.0E-35	AV650422.1	EST_HUMAN	AV650422 GLC Homo sapiens cDNA clone GLCCE06 3'
4513	17097	29543	5.19	1.0E-35	7856905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
4513	17097	29544	5.19	1.0E-35	7856905	NT	Mus musculus activin receptor interacting protein 1 (Arip1-pending), mRNA
5701	18327	30831	1.31	1.0E-35	11528238	NT	Homo sapiens chromatin assembly factor 1, subunit B (p60) (CHAF1B), mRNA
7069	18088	30444	0.73	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
7069	18088	30445	0.73	1.0E-35	AW808665.1	EST_HUMAN	MR1-ST0111-111199-011-407 ST0111 Homo sapiens cDNA
7496	20019	32883	0.8	1.0E-35	AB033105.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
7637	20149	33033	0.98	1.0E-35	11418002	NT	Homo sapiens KIAA0645 gene product (KIAA0645), mRNA
9461	24794	34941	3.33	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
9461	24794	34942	3.33	1.0E-35	AU158595.1	EST_HUMAN	AU158595 PLACE3 Homo sapiens cDNA clone PLACE3000382 3'
10470	22984	35974	0.57	1.0E-35	BF589594.1	EST_HUMAN	nao06d06.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
10470	22984	35975	0.57	1.0E-35	BF589594.1	EST_HUMAN	nao06d06.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:3254051 3' similar to TR:O31341
11601	24044		4.48	1.0E-35	AI525119.1	EST_HUMAN	promina-7.D01.r bvtumor Homo sapiens cDNA 5'
11695	24998		1.3	1.0E-35	11418274	NT	Homo sapiens fibulin 1 (FBLN1), mRNA
12287	24489		1.87	1.0E-35	BE792832.1	EST_HUMAN	601584833F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3938985 5'
9166	21691	34635	0.51	8.0E-36	AA348480.1	EST_HUMAN	EST54938 Hippocampus II Homo sapiens cDNA 5' end similar to similar to endogenous retrovirus 9, 5' LTR
10080	22555		2.13	8.0E-36	7706259	NT	Homo sapiens CGI-09 protein (LOC51605), mRNA
2957	15573	28050	1.15	7.0E-36	AW857579.1	EST_HUMAN	CM1-CT0315-091289-063-407 CT0315 Homo sapiens cDNA
3152	15766		5.38	7.0E-36	4557498	NT	Homo sapiens C-terminal binding protein 2 (CTBP2), mRNA
7650	20162	33049	6.73	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12), gene, exons L and LN
7650	20162	33050	6.73	7.0E-36	U06672.1	NT	Human carcinoembryonic antigen gene family member 12 (CGM12), gene, exons L and LN
12070	24350	30965	5.15	7.0E-36	AF052051.1	NT	Homo sapiens glutathione transferase A4 gene, exon 1
2048	14830	27169	2.5	6.0E-36	7706622	NT	Homo sapiens nihjrh 2 (NINJ2), mRNA
2461	15028		5.35	6.0E-36	AB035346.1	NT	Homo sapiens TCL6 gene, exon 12
3701	16302	28770	0.98	6.0E-36	BF515101.1	EST_HUMAN	UIH-BW1-arc-c-12-0-JL.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083542 3'
5534	18166	30580	9.75	6.0E-36	AK435169.1	EST_HUMAN	th93b06.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2126195 3' similar to gb:M11948 PANCREATIC SECRETORY TRYPSIN INHIBITOR PRECURSOR (HUMAN);
7163	19695	32541	3.97	6.0E-36	AW780143.1	EST_HUMAN	h06h02.x1 NCL CGAP_Cot14 Homo sapiens cDNA clone IMAGE:3036627 3' similar to SW:IMA2_HUMAN
8586	21125	34045	2.54	6.0E-36	AF208181.1	NT	P52292 IMPORTIN ALPHA-2 SUBUNIT ; Homo sapiens synovial precursor, mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10125	22820		0.54	6.0E-36	C16927.1	EST_HUMAN	C16927 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA clone GEN-535C11 5'
11422	23873	36936	2.62	6.0E-36	A1380499.1	EST_HUMAN	tf85c09.x1 NCL CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107024.3 similar to contains MER9 b2
143	12808	25286	12.3	5.0E-36	AJ271735.1	NT	MER9 repetitive element ;
2779	15332	27901	15.02	5.0E-36	BE388436.1	EST_HUMAN	Homo sapiens Xq pseudautosomal region; segment 1/2
3672	16273	28739	1.07	5.0E-36	AL163209.2	NT	601285567F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607289 5'
4903	17478	29935	1.6	5.0E-36	5729729	NT	Homo sapiens chromosome 21 segment HS21C009
4903	17478	29936	1.6	5.0E-36	5729729	NT	Homo sapiens API5-like 1 (API5L1), mRNA
11661	12808	25286	4.05	5.0E-36	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
11963	24285	31024	2.88	5.0E-36	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1267	13864	26381	2.14	4.0E-36	BE010038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA
1491	14083	26824	1.88	4.0E-36	P10288	SWISSPROT	RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE ;
1687	14279	26813	1.35	4.0E-36	BE382574.1	EST_HUMAN	ENDONUCLEASE]
2264	14838		1.7	4.0E-36	AW247772.1	EST_HUMAN	601298674F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628396 5'
3397	18005	28486	0.83	4.0E-36	BE389299.1	EST_HUMAN	2820020.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820020 5'
3397	16005	28487	0.83	4.0E-36	BE389299.1	EST_HUMAN	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
4866	17442	28893	0.57	4.0E-36	AL163204.2	NT	601282266F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604168 5'
5310	17872	30294	0.58	4.0E-36	AA905361.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
5992	18515		0.94	4.0E-36	R64023.1	EST_HUMAN	ok05b1.1 s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1506909 3' similar to
6205	18816	31586	2.19	4.0E-36	11497041	NT	SW:D3HI_RAT P29268 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
7649	20161	33048	1.77	4.0E-36	M3320.1	NT	Y1905.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139713 5'
8490	21029	33947	1.15	4.0E-36	D87675.1	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), transcript variant 3, mRNA
8490	21029	33948	1.15	4.0E-36	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10867	23388	36403	2.36	4.0E-36	AA400370.1	EST_HUMAN	Homo sapiens DNA for amyloid precursor protein, complete cds
11981	24282		1.46	4.0E-36	11420516	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
12026	24872		6.32	4.0E-36	AV753628.1	EST_HUMAN	zu69c10.r1 Soares testis NHT Homo sapiens cDNA clone IMAGE:743250 5'
725	13345	25837	2.82	3.0E-36	AF09810.1	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
1545	14137	26671	1.01	3.0E-36	AF110239.1	NT	AV753629 TP Homo sapiens cDNA clone TPGABH01 5'
1545	14137	26672	1.01	3.0E-36	AF110239.1	NT	Homo sapiens neuraxin III-alpha gene, partial cds
2338	14909	27481	0.88	3.0E-36	7662401	NT	Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
							Homo sapiens calcium/calmodulin-stimulated cyclic nucleotide phosphodiesterase (PDE1A) gene, partial cds
							Homo sapiens KIAA0952 protein (KIAA0952), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4600	17184	29531	7.36	3.0E-36	10181139	NT	Mus musculus junctophilin 1 (Jp1-pending), mRNA
10895	23499	36529	2.06	3.0E-36	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:3862086 5'
3204	15816	28292	3.78	2.0E-36	BE259287.1	EST_HUMAN	601106343F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3342708 5'
5094	17687	30106	9.22	2.0E-36	AW880376.1	EST_HUMAN	QV0-OT0030-240300-174-h04 OT0030 Homo sapiens cDNA
5877	18304	30786	2.55	2.0E-36	AF287747.1	NT	Mus musculus p47-phox gene, complete cds
6012	18632	31367	4.22	2.0E-36	T08756.1	EST_HUMAN	EST08648 Infant Brain, Banto Soares Homo sapiens cDNA clone H188J28 5' end
6690	19286	32089	12.01	2.0E-36	T68629.1	EST_HUMAN	yc44a07.r1 Stragene liver (8937224) Homo sapiens cDNA clone IMAGE:83508 5'
9310	21824	34772	0.96	2.0E-36	BF512794.1	EST_HUMAN	UIH-BW1-emu-e-11-Q-UJ.a1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071132 3'
9468	21867	34817	0.6	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
9468	21867	34818	0.6	2.0E-36	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
918	13531	26049	2.35	1.0E-36	BE409310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
2190	14766	27337	0.91	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA
2190	14766	27338	0.91	1.0E-36	BE146523.1	EST_HUMAN	RC1-HT0217-131189-021-h07 HT0217 Homo sapiens cDNA
2243	14818	27392	1.34	1.0E-36	BF673781.1	EST_HUMAN	602136493F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272886 5'
2538	15102		1.75	1.0E-36	AW276898.1	EST_HUMAN	xp57a06.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2744434 3' similar to WP.C13F10.7 CE08148 ;
3388	15997		1.23	1.0E-36	AF156982.1	NT	Homo sapiens human endogenous retrovirus W proC8-19 protease (pro) gene, partial cds
5904	18526	31252	0.86	1.0E-36	AL044446.1	EST_HUMAN	DKFZp434G022_r1 434 (synonym: hles3) Homo sapiens cDNA clone DKFZp434G022 5'
5059	18878	31418	0.97	1.0E-36	4827064	NT	Homo sapiens zinc finger protein 147 (estrogen-responsive finger protein) (ZNF147) mRNA
6330	18936		3.97	1.0E-36	AB87714.1	EST_HUMAN	wb37c12.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2307862 3' similar to contains Alu repetitive element;
6524	19124	31916	1.13	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6524	19124	31917	1.13	1.0E-36	R25012.1	EST_HUMAN	yg36g10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34529 5' similar to SP:CAHP_HUMAN P35219 CARBONIC ANHYDRASE-RELATED PROTEIN ;
6783	19374	32190	0.7	1.0E-36	AL120542.1	EST_HUMAN	DKFZp761A228_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761A228 5'
7801	20443	33347	3.18	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7901	20443	33348	3.18	1.0E-36	AA148034.1	EST_HUMAN	zo51a12.r1 Stragene endothelial cell 937223 Homo sapiens cDNA clone IMAGE:590398 5'
7997	20539	33441	1.22	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
7997	20539	33442	1.22	1.0E-36	AA420467.1	EST_HUMAN	nc60e08.r1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:745670
8120	20681	33570	0.73	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8120	20681	33571	0.73	1.0E-36	AU141688.1	EST_HUMAN	AU141688 THYRO1 Homo sapiens cDNA clone THYRO1001033 5'
8859	21497	34420	2.88	1.0E-36	AW103658.1	EST_HUMAN	xs82b07.x1 NCI_CGAP_Bm35 Homo sapiens cDNA clone IMAGE:2614357 3'
10023	22518	35513	3.89	1.0E-36	BF364168.1	EST_HUMAN	QV3-NN1023-010900-199-h01 NN1023 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10231	22726	35717	0.71	1.0E-36	AW855688.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10231	22726	35718	0.71	1.0E-36	AW855688.1	EST_HUMAN	RC3-CT0279-040500-017-a10 CT0279 Homo sapiens cDNA
10826	23347	36363	3.55	1.0E-36	AW897636.1	EST_HUMAN	CM3-NN0061-140400-147-h12 NN0061 Homo sapiens cDNA
11258	23788	36844	4.94	1.0E-36	AW504143.1	EST_HUMAN	UI-HF-BNO-ale-c-03-Q.U1.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079277 5'
11848	24208		6.11	1.0E-36	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12316	24507		6.19	1.0E-36	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
12592	24683		3.59	1.0E-36	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
7415	19940	32804	1.94	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
7415	18940	32805	1.94	9.0E-37	AW009277.1	EST_HUMAN	ws80b07.x1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2504245 3'
12113	24374		1.63	9.0E-37	W22618.1	EST_HUMAN	73D4 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
3398	16006	28488	1.01	8.0E-37	4757079	NT	Homo sapiens chimerin (chimaerin) 2 (CHN2) mRNA
5456	18091		1.58	8.0E-37	BE698077.1	EST_HUMAN	CM0-UT0003-050800-503-409 UT0003 Homo sapiens cDNA
5994	18614	31348	4.02	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
5994	18614	31349	4.02	8.0E-37	BE350127.1	EST_HUMAN	h09g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
6037	18656	31398	6.7	8.0E-37	AW840840.1	EST_HUMAN	RC1-CN0008-210100-012-a09_1 CN0008 Homo sapiens cDNA
7825	20367	33275	6.31	8.0E-37	X87344.1	NT	H.sapiens DMA, DMB, HLA-Z1, IIP2, LMP2, TAP1, LMP7, DOB, DOB2 and RING8, 9, 13 and 14 genes
1328	13922		2.3	7.0E-37	AL042800.1	EST_HUMAN	DKFZp434E0422_11 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E0422 5'
1780	14370	26914	1.55	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
1780	14370	26915	1.55	7.0E-37	AF111167.2	NT	Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
10637	23169	36180	7.76	7.0E-37	AB17700.1	EST_HUMAN	wk25b11.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413341 3' similar to contains PTR5.t2 PTR5 repetitive element
10774	23288	36303	3.74	7.0E-37	AI536702.1	EST_HUMAN	bm87g03.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165140 3' similar to contains L1.b3 L1 repetitive element
5304	17866		2.5	6.0E-37	R10039.1	EST_HUMAN	y25a02.r1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:127850 5'
8377	20917	33837	0.54	6.0E-37	AF169688.1	NT	Homo sapiens protocadherin alpha 10 alternate isoform (PCDH-alpha10) mRNA, complete cds
12455	24568		3.85	6.0E-37	AF202723.1	NT	Homo sapiens Sad1 unc-84 domain protein 2 (SUN2) mRNA, partial cds
6243	18852	31622	4.92	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
6243	18852	31623	4.92	5.0E-37	AA307123.1	EST_HUMAN	EST178035 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
8691	21230	34150	0.85	5.0E-37	AV750211.1	EST_HUMAN	AV750211 NPC Homo sapiens cDNA clone NPCBGH09 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10800	23323		4.94	5.0E-37	7857117	NT	Homo sapiens glycine C-acetyltransferase (2-amino-3-ketobutyrate-CoA ligase) (GCAT), mRNA
11843	24205		5.21	5.0E-37	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
2468	15035	27602	1.7	4.0E-37	AA702784.1	EST_HUMAN	280b04.s1 Soares_fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
9278	21804	34755	0.68	4.0E-37	AA843806.1	EST_HUMAN	ak09c02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1405442 3'
10912	23431	36451	1.74	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10912	23431	36452	1.74	4.0E-37	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2061	14641	27215	2.58	3.0E-37	AL048986.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2061	14641	27216	2.58	3.0E-37	AL048986.1	EST_HUMAN	DKFZp434L2418_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L2418
2992	15608		3.5	3.0E-37	AW961150.1	EST_HUMAN	EST373222 MAGE resequences, MAGF Homo sapiens cDNA
5126	17698		0.79	3.0E-37	BF035327.1	EST_HUMAN	60145853.1F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862086 5'
							et34c05.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2373886 3' similar to TR.Q13537
7557	20075	32851	0.79	3.0E-37	A1749962.1	EST_HUMAN	Q13537 SIMILAR TO POGO ELEMENT.
404	13079	25571	0.9	2.0E-37	D88790.1	NT	Homo sapiens mRNA for AML1, complete cds
404	13079	25572	0.9	2.0E-37	D88790.1	NT	Homo sapiens mRNA for AML1, complete cds
1119	13722	26234	2.1	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002186 5'
1119	13722	26235	2.1	2.0E-37	AU131202.1	EST_HUMAN	AU131202 NT2RP3 Homo sapiens cDNA clone NT2RP3002186 5'
2006	14588	27148	1.45	2.0E-37	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
3962	16560	28029	6.99	2.0E-37		NT	Homo sapiens cytochrome P450, subfamily XXVIIA (steroid 27-hydroxylase, cerebrotendinous xanthomatosis), polypeptide 1 (CYP27A1b) mRNA
4330	16917	28360	0.59	2.0E-37	4826685	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
6765	19358	32167	3.94	2.0E-37	AA346720.1	EST_HUMAN	EST52931 Fetal heart II Homo sapiens cDNA 5' end
7938	20480	33390	0.53	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3453657 5'
7938	20480	33391	0.53	2.0E-37	BE537764.1	EST_HUMAN	601067534F1 NIH_MGC 10 Homo sapiens cDNA clone IMAGE:3453657 5'
7981	20523	33429	2.75	2.0E-37	BF204032.1	EST_HUMAN	601869157F1 NIH_MGC 17 Homo sapiens cDNA clone IMAGE:4111408 5'
11434	23884	36951	19.39	2.0E-37	AF176013.1	NT	Homo sapiens J domain containing protein 1 isoform b (JDP1) mRNA, complete cds
12633	24710		5.1	2.0E-37	11417872	NT	Homo sapiens pectadillo (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
2135	14713	27288	2.49	1.0E-37	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
3231	15843		0.98	1.0E-37	AW862082.1	EST_HUMAN	RC3-CT0347-210400-016-h03 CT0347 Homo sapiens cDNA
4243	16831	28282	0.96	1.0E-37	BE872865.1	EST_HUMAN	601448619F1 NIH_MGC 65 Homo sapiens cDNA clone IMAGE:3852652 5'
5075	17648	30089	3.67	1.0E-37	BF371719.1	EST_HUMAN	QV0-FN0180-280700-318-c10 FN0180 Homo sapiens cDNA
6155	18768		0.8	1.0E-37	7305360	NT	Mus musculus otogelin (Otog), mRNA
8156	20697	33610	0.84	1.0E-37	BE546032.1	EST_HUMAN	601072419F1 NIH_MGC 12 Homo sapiens cDNA clone IMAGE:3458308 5'
8670	21209	34127	3.03	1.0E-37	AA171408.1	EST_HUMAN	zp21b02.r1 Stratagene neuroepithelium (#937231) Homo sapiens cDNA clone IMAGE:610059 5' similar to contains L1:12 L1 repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10577	23112	36125	5.51	1.0E-37	M22878.1	NT	Human somatic cytochrome c (HC1) processed pseudogene, complete cds
12167	24406		3.8	1.0E-37	BE771814.1	EST_HUMAN	CM3-F10096-140700-243-q07 FT0096 Homo sapiens cDNA
5950	18571	31303	1.71	9.0E-38	10048482	NT	Rattus norvegicus multidomain presynaptic cytomatrix protein Piccolo (LOC66768), mRNA
1264	13861	26378	2.05	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
2543	15107	27680	1.49	8.0E-38	BF346221.1	EST_HUMAN	602018401F1 NCI_CGAP_Brrd7 Homo sapiens cDNA clone IMAGE:4153992 5'
12231	13861	26378	1.62	8.0E-38	11436955	NT	Homo sapiens Grb2-associated binder 2 (KIAA0571), mRNA
4307	16893	29336	0.63	7.0E-38	H10902.1	EST_HUMAN	yt5107.r1 Soares adult brain N258HB55 Homo sapiens cDNA clone IMAGE:171973 5'
3078	15693	28197	2.75	6.0E-38	BF030333.1	EST_HUMAN	601455722F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3859348 5'
5776	18401	31116	1.34	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
5776	18401	31117	1.34	6.0E-38	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
11698	24410	31117	10.47	6.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12201	24427	30952	14.11	6.0E-38	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12814	24837	30797	1.7	6.0E-38	11418184	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
756	13375	25870	1.26	5.0E-38	AW971819.1	EST_HUMAN	EST383908 MAGE resequences, MAGL Homo sapiens cDNA
2495	15059	27633	1.94	5.0E-38	AJ237740.1	NT	Homo sapiens RIBL1R gene (partial), exon 8
7096	19667	32506	2.15	5.0E-38	BE871610.1	EST_HUMAN	601450149F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:3854074 5'
124	12793	25277	3.63	4.0E-38	225466.1	NT	B. laurus mitochondrial aspartate aminotransferase mRNA, complete CDS
124	12793	25278	3.63	4.0E-38	225466.1	NT	B. laurus mitochondrial aspartate aminotransferase mRNA, complete CDS
1199	13800	26312	1.06	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
2148	14725		2.39	3.0E-38	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
3759	16360		1.37	3.0E-38	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaj-like) (HIRIP4), mRNA
3922	16520	28987	2.12	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
3922	16520	28988	2.12	3.0E-38	P53538	SWISSPROT	SSU72 PROTEIN
4721	17302		0.66	3.0E-38	BE278301.1	EST_HUMAN	601157633F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3504272 5'
6850	24772	32254	7.24	3.0E-38	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
7588	20103	32978	6.83	3.0E-38	BF373664.1	EST_HUMAN	CM3-F10181-140700-241-f07 FT0181 Homo sapiens cDNA
8584	21123	34043	2.01	3.0E-38	HB5494.1	EST_HUMAN	ya88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
8584	21123	34044	2.01	3.0E-38	HB5494.1	EST_HUMAN	ya88b04.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:249775 5'
9882	22379		1.7	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
11198	23703		1.54	3.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
12481	13800	26312	1.44	3.0E-38	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
54	12734	25202	1.84	2.0E-38	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
1422	14015	26544	2.23	2.0E-38	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	14280	26814	1.99	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
1688	14280	26815	1.99	2.0E-38	AA437353.1	EST_HUMAN	zw30d01.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:770785 5' similar to SW:MA12_RABIT P45701 MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ;
4681	17263	28714	2.98	2.0E-38	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
5283	17855	30280	0.63	2.0E-38	BE296224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
5283	17855	30281	0.63	2.0E-38	BE296224.1	EST_HUMAN	601177386F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532580 5'
5327	17937	30264	0.63	2.0E-38	AA437181.1	EST_HUMAN	z61d09.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:758129 5' similar to TR:G817957
7704	20213	33102	1.57	2.0E-38	AV721103.1	EST_HUMAN	G817957 GLYCINE RECEPTOR SUBUNIT ALPHA 4 ;
8420	20960	34289	5.5	2.0E-38	BE165980.1	EST_HUMAN	AV721103 HTB Homo sapiens cDNA clone HTBARH11 5'
8626	21365	34289	0.51	2.0E-38	F06450.1	EST_HUMAN	MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA
8685	21433	34356	1.37	2.0E-38	AF069755.1	NT	HSC16F031 normalized Infant brain cDNA Homo sapiens cDNA clone c-18f03
9148	21883		0.89	2.0E-38	BE222256.1	EST_HUMAN	Homo sapiens orphan G protein-coupled receptor HG20 (HG20) mRNA, complete cds
10345	22838	35835	1.98	2.0E-38	D63479.2	NT	hu09g02.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166130 3' similar to TR:O02710 O02710
							GAG POLYPEPTIDE ;
							Homo sapiens mRNA for KIAA0145 protein, partial cds
11114	23624	36665	3.38	2.0E-38	AA595480.1	EST_HUMAN	nc34g03.s1 NCI CGAP_P123 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
11114	23624	36666	3.38	2.0E-38	AA595480.1	EST_HUMAN	E212316 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE ;
11363	23815	36876	6.15	2.0E-38	BE712780.1	EST_HUMAN	nc34g03.s1 NCI CGAP_P123 Homo sapiens cDNA clone IMAGE:1102612 3' similar to TR:E212316
							E212316 NADP DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE ;
							QV2-HT0698-080800-283-e05 HT0698 Homo sapiens cDNA
11496	23945	37014	3.87	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11496	23945	37015	3.87	2.0E-38	AF190501.1	NT	Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA, partial cds
11753	24149		7.01	2.0E-38	AV726988.1	EST_HUMAN	AV726988 HTC Homo sapiens cDNA clone HTCAHX07 5'
11755	24150		1.88	2.0E-38	AB012723.1	NT	Homo sapiens gene for kinesin-like protein, complete cds
12050	24334		3.19	2.0E-38	M55630.1	NT	Human topoisomerase I pseudogene 2
12060	24343	31000	5.31	2.0E-38	H55641.1	EST_HUMAN	CHR220580 Chromosome 22 exon Homo sapiens cDNA clone C22_788 5'
12128	24384		2.87	2.0E-38	S74906.1	NT	E1 beta=pyruvate dehydrogenase beta [promoter] [human, placenta, Genomic, 1280 nt]
12624	24702		1.55	2.0E-38	11418248	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
							zu62b02.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:742539 5' similar to contains element
1132	13735		2.17	1.0E-38	AA401570.1	EST_HUMAN	MER19 repetitive element ;
2042	14624	27193	1.7	1.0E-38	4885288	NT	Homo sapiens guanine nucleotide binding protein-like 1 (GNL1), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2065	14845	27219	1.46	1.0E-38	7661069	NT	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
2539	15103	27876	1.71	1.0E-38	AF270831.1	NT	Homo sapiens cyclin K (CCNK) gene, exon 7
2645	15204	27777	14.26	1.0E-38	4758371	NT	Homo sapiens fibrinogen-like 1 (FGL1), mRNA
4235	16823	29274	1.03	1.0E-38	AB037863.1	NT	Homo sapiens mRNA for KIAA1442 protein, partial cds
4411	16996	29439	0.81	1.0E-38	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4416	17001	29444	1.52	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4416	17001	29445	1.52	1.0E-38	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4702	17284	29729	1.18	1.0E-38	8922543	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
5289	17851		29.49	1.0E-38	N46880.1	EST_HUMAN	Y58a01.r1 Soares, multiple sclerosis. 2Nbl-HMSP Homo sapiens cDNA clone IMAGE:277704 5' similar to SW:CA1H_MOUSE P36061 COLLAGEN ALPHA 1(XVII) CHAIN PRECURSOR ;
6178	18768	31556	4.28	1.0E-38	7305360	NT	Mus musculus obogelin (Obog), mRNA
6178	18768	31557	4.28	1.0E-38	7305360	NT	Mus musculus obogelin (Obog), mRNA
7435	19959	32824	3	1.0E-38	AB014512.1	NT	Homo sapiens mRNA for KIAA0512 protein, partial cds
9080	21816	34551	0.97	1.0E-38	11422250	NT	Homo sapiens hypothetical protein FLJ10600 (FLJ10600), mRNA
9331	21845	34795	6.34	1.0E-38	BE350127.1	EST_HUMAN	h08g01.x1 NCI_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11465	23915	36983	1.91	1.0E-38	7692109	NT	MER29 repetitive element ;
11906	24808		2.57	1.0E-38	AL163284.2	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
58	12738	25208	8.81	8.0E-39	4502312	NT	Homo sapiens chromosome 21 segment HS21C084
1438	14031	26559	1.49	8.0E-39	4758229	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) 16kD (ATP6C) mRNA
1669	14455		0.88	8.0E-39	AI823404.1	EST_HUMAN	Homo sapiens estrogen receptor-binding fragment-associated gene 9 (EBAG9) mRNA
2141	14719	27290	3.68	7.0E-39	AL163227.2	NT	wh53f10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384491 3' similar to TR:P87890 P87890
10688	23218	36230	2.32	6.0E-39	BF331829.1	EST_HUMAN	POL PROTEIN ;
11639	24078	37138	1.54	6.0E-39	11526372	NT	Homo sapiens chromosome 21 segment HS21C027
12532	24845		2.92	6.0E-39	BE670394.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1045	13653	26165	1.85	5.0E-39	AF003528.1	NT	QV1-BT0631-040900-357-02 BT0631 Homo sapiens cDNA
3014	15630	28108	7.14	5.0E-39	AI750154.1	EST_HUMAN	Homo sapiens hyaluronan-mediated motility receptor (RHAMM) (HMMR), mRNA
12219	24441		2.69	5.0E-39	11420289	NT	7634c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284356 3' similar to WP:R151.6
							CE00828 ;
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
							ai36504.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2374063 3' similar to TR:Q15408
							Q15408 NEUTRAL PROTEASE LARGE SUBUNIT ; contains LTR7.1 LTR7 repetitive element ;
							Homo sapiens hypothetical protein FLJ10803 (FLJ10803), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
576	13208	25686	35.11	4.0E-39	AB015810.1	NT	Chlorobacillus aethiops mRNA for ribosomal protein S4X, complete cds
3631	16234	28709	0.75	4.0E-39	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5895	18615	31350	0.73	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
5895	18615	31351	0.73	4.0E-39	11422113	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
8020	20562	33463	0.95	4.0E-39	AA682949.1	EST_HUMAN	ae92g04.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1020438 3' similar to contains OFR.b1 OFR repetitive element;
9252	21778	34728	0.82	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
9252	21778	34729	0.82	4.0E-39	D84116.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 2
12237	24452		4.45	4.0E-39	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12363	24536		5.52	4.0E-39	BE836452.1	EST_HUMAN	QV0-FN0063-260800-278-c08 FN0063 Homo sapiens cDNA
51	12731	25196	16.62	3.0E-39	AA631949.1	EST_HUMAN	fmf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
51	12731	25197	16.62	3.0E-39	AA631949.1	EST_HUMAN	fmf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
51	12731	25198	16.62	3.0E-39	AA631949.1	EST_HUMAN	fmf1c16 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR12-1
11744	24143	36764	6.46	3.0E-39	AJ084557.1	EST_HUMAN	ox63a10.s1 Soares, NHMPu, S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
11744	24143	36765	6.46	3.0E-39	AJ084557.1	EST_HUMAN	ox63a10.s1 Soares, NHMPu, S1 Homo sapiens cDNA clone IMAGE:1660986 3' similar to SW:GTR5_RAT P43427 GLUCOSE TRANSPORTER TYPE 5, SMALL INTESTINE ;
11791	24174		6.63	3.0E-39	H37903.1	EST_HUMAN	yp51c06.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:180954 3'
930	13543		9.84	2.0E-39	BE409203.1	EST_HUMAN	801301607F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636289 5'
945	13558		15.07	2.0E-39	AJ525119.1	EST_HUMAN	promina-7.D01.r bvtumor Homo sapiens cDNA 5'
1069	13874		3.85	2.0E-39	AF000573.1	NT	Homo sapiens homogenitase 1,2-dioxygenase gene, complete cds
1577	14170		41.87	2.0E-39	AW372318.1	EST_HUMAN	PMO-BT0340-211289-003-002 BT0340 Homo sapiens cDNA
2016	14598	27162	2.5	2.0E-39	AA720574.1	EST_HUMAN	nw21g02.s1 NCL_CGAP_CCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR.13 THR repetitive element ;
2657	15216	27788	1.56	2.0E-39	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C048
4492	17077	28527	1.7	2.0E-39	BF370207.1	EST_HUMAN	RC4-FN0037-280700-011-at0 FN0037 Homo sapiens cDNA
5882	18509	30804	3.89	2.0E-39	AA508880.1	EST_HUMAN	ng86f03.s1 NCL_CGAP_P16 Homo sapiens cDNA clone IMAGE:941693
7405	19930	32794	1.95	2.0E-39	AA080887.1	EST_HUMAN	zn06f02.r1 Stratagene HNT neuron (#937233) Homo sapiens cDNA clone IMAGE:546651 5'
8252	20793	33710	0.55	2.0E-39	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9415	21924		0.56	2.0E-39	AA984531.1	EST_HUMAN	am88c11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1630196 3'
9544	22044		0.54	2.0E-39	AJ686660.1	EST_HUMAN	tu35e03.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2253052 3'
11309	23802	36863	3.11	2.0E-39	D86964.1	NT	Human mRNA for KIAA0209 gene, partial cds
1560	14152	26884	2.33	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene
1560	14152	26885	2.33	1.0E-39	AJ006345.1	NT	Homo sapiens KVLQT1 gene

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1578	14171	26700	9.78	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
4719	17300	29745	0.87	1.0E-39	AW296073.1	EST_HUMAN	U-H-BWO-aii-h-06-D-U1 st NOI CGAP Sub6 Homo sapiens cDNA clone IMAGE:2730850 3'
4764	17345	29793	4.88	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4764	17345	29794	4.88	1.0E-39	AW951995.1	EST_HUMAN	EST364065 MAGE resequences, MAGB Homo sapiens cDNA
4812	17390	29841	10.18	1.0E-39	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
5561	18192	30638	0.86	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaaphorin) 5A (SEMA5A), mRNA
5581	18192	30639	0.86	1.0E-39	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaaphorin) 5A (SEMA5A), mRNA
5812	18436	31157	1.13	1.0E-39	T80876.1	EST_HUMAN	yd26g06.r1 Soares fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:109402 5' similar to contains Alu repetitive element; contains LTR1 repetitive element
5845	18469	31184	5.75	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
5845	18469	31195	5.75	1.0E-39	AJ278170.1	NT	Mus musculus mRNA for neuronal interacting factor X 1 (NIX1) (Nix1 gene)
6914	19573	32790	1.87	1.0E-39	11436736	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
7400	19925	32790	2.28	1.0E-39	D78132.1	NT	Homo sapiens mRNA for ras-related GTP-binding protein, complete cds
8498	21038	33959	0.85	1.0E-39	Q46530	SWISSPROT	RIBONUCLEASE K6 PRECURSOR (RNASE K6)
12181	24401		4.3	1.0E-39	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
581	13211	25689	2.07	9.0E-40	5803210	NT	Homo sapiens UDP-glucose pyrophosphorylase 2 (UGP2), mRNA
1278	13873	26392	20.54	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1278	13873	26393	20.54	9.0E-40	4755145	NT	Homo sapiens AE-binding protein 1 (AEBP1) mRNA
1498	14080	26630	1.54	9.0E-40	4507512	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
3853	16451	28914	0.68	9.0E-40	4503764	NT	Homo sapiens fragile X mental retardation 1 (FMR1) mRNA
4045	18004	29108	3.57	9.0E-40	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
3077	15892	28186	1	8.0E-40	AA078185.1	EST_HUMAN	7H15A04 Chromosome 7 HeLa cDNA Library Homo sapiens cDNA clone 7H15A04
3986	16594		1.74	8.0E-40	BE396541.1	EST_HUMAN	601288958F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3619186 5'
7702	20211	33098	2.01	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
7702	20211	33099	2.01	7.0E-40	U60325.1	NT	Human DNA polymerase gamma mRNA, nuclear gene encoding mitochondrial protein, complete cds
10776	23300	36308	2.48	7.0E-40	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
2753	15308	27873	5.43	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2753	15308	27874	5.43	6.0E-40	AA361275.1	EST_HUMAN	EST70527 T-cell lymphoma Homo sapiens cDNA 5' end similar to zinc finger protein family
6094	18710		2.11	6.0E-40	BE504766.1	EST_HUMAN	h240g01.x1 NCL_CGAP_GC8 Homo sapiens cDNA clone IMAGE:3210480 3'
6296	18904		1.42	6.0E-40	7661899	NT	Homo sapiens KIAA0211 gene product (KIAA0211), mRNA
7016	19513	32334	4.18	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
7015	19513	32335	4.18	6.0E-40	11439783	NT	Homo sapiens fatty acid desaturase 1 (FADS1), mRNA
9887	22384	35360	8.69	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
9887	22384	35361	8.69	6.0E-40	AV653028.1	EST_HUMAN	AV653028 GLC Homo sapiens cDNA clone GLCDGF04 3'
1919	14504	27061	1.42	4.0E-40	AI686005.1	EST_HUMAN	h91b01.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:2248873 3' similar to TR:O73505 O73505 POL PROTEIN.
2155	14732		1.38	4.0E-40	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
4478	17063	29513	9.28	4.0E-40	7662117	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7827	20369	33277	0.59	4.0E-40	AU127831	EST_HUMAN	AU127831 NT2RP2 Homo sapiens cDNA clone NT2RP2002172 5'
7833	20475	33384	4.44	4.0E-40	AA742809.1	EST_HUMAN	h34e10.r1 NCL_CGAP_Br4 Homo sapiens cDNA clone IMAGE:1222122
8985	21523	34451	3.91	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
8985	21523	34452	3.91	4.0E-40	BE009416.1	EST_HUMAN	PM0-BN0167-070500-002-h12 BN0167 Homo sapiens cDNA
10595	23129	36143	3.06	4.0E-40	AW841565.1	EST_HUMAN	RC1-CN0017-120200-012-e04 CN0017 Homo sapiens cDNA
4212	18801	29250	0.89	3.0E-40	AI925949.1	EST_HUMAN	wh1207.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2380549 3'
6750	19343	32150	7.27	3.0E-40	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
8321	20862	33787	3.69	3.0E-40	5454167	NT	Homo sapiens HBV associated factor (XAP4) mRNA
8899	21437	34380	1.28	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
9138	21673	34615	1.58	3.0E-40	AF078779.1	NT	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10541	23078	36092	1.79	3.0E-40	D88984.1	NT	Human mRNA for KIAA0209 gene, partial cds
10903	23423	36442	2.21	3.0E-40	BE350127.1	EST_HUMAN	h109g01.x1 NCL_CGAP_Kid13 Homo sapiens cDNA clone IMAGE:3146256 3' similar to contains MER29.b3
11145	23653	36695	13.89	3.0E-40	6005813	NT	MER29 repetitive element ; Homo sapiens serine threonine protein kinase (NDR), mRNA
11445	23895	36960	1.58	3.0E-40	AW118799.1	EST_HUMAN	xd96h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2605491 3' similar to TR:Q15804
347	12988		4.35	2.0E-40	AI223036.1	EST_HUMAN	Q15804 SIMILAR TO ENV OF TYPE A AND TYPE B RETROVIRUSES AND TO CLASS II HERV5 ; hg52h08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838847 3'
827	13444		22.71	2.0E-40	AW303868.1	EST_HUMAN	h24e10.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2761098 3' similar to SW:RS6_MOUSE P97461 40S RIBOSOMAL PROTEIN S6. ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1865	14451		1.38	2.0E-40	AV731601.1	EST_HUMAN	AV731601 HTF Homo sapiens cDNA clone HTFAZE05 5'
1978	14561	27119	1.39	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
1978	14561	27120	1.39	2.0E-40	4506188	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 7 (PSMA7) mRNA, and translated products
2116	14694	27262	0.95	2.0E-40	A1968862.1	EST_HUMAN	wf90a11.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2514716 3' similar to TR:Q91929 Q91929
2214	14769	27363	1.86	2.0E-40	5453592	NT	ZINC FINGER PROTEIN. ;
2714	15271		1.25	2.0E-40	BE275932.1	EST_HUMAN	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
3160	15774	28242	4.32	2.0E-40	5453592	NT	601121507F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345784 5'
5027	17601	30046	1.84	2.0E-40	AL163280.2	NT	Homo sapiens adenylyl cyclase-associated protein 2 (CAP2) mRNA
5027	17601	30047	1.84	2.0E-40	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5378	17938	30351	3.28	2.0E-40	4505880	NT	Homo sapiens chromosome 21 segment HS21C080
916	13529		1.05	1.0E-40	AA225989.1	EST_HUMAN	Homo sapiens plasminogen (PLG) mRNA
3337	15947		1.47	1.0E-40	4507142	NT	nc09a09.s1 NCL CGAP_P1 Homo sapiens cDNA clone IMAGE:1007608
4716	17297	29742	4.95	1.0E-40	4508012	NT	Homo sapiens sorting nexin 3 (SNX3) mRNA
6403	19006	31786	0.69	1.0E-40	W92708.1	EST_HUMAN	Homo sapiens zinc finger protein 200 (ZNF200) mRNA, and translated products
6403	19006	31787	0.69	1.0E-40	W92708.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7145	19678	32518	2.12	1.0E-40	AA573201.1	EST_HUMAN	zh79f11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418317 3'
7283	19811	32667	0.83	1.0E-40	P28008	SWISSPROT	h42f04.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
10797	23320	36330	4.13	1.0E-40	AJ149345.1	EST_HUMAN	h42f04.s1 NCL CGAP_AA1 Homo sapiens cDNA clone IMAGE:995167 3'
11615	24057		1.72	1.0E-40	AL163246.2	NT	POL POLYPROTEIN [CONTAINS: PROTEASE: REVERSE TRANSCRIPTASE; RIBONUCLEASE H]
12182	24956		7.52	1.0E-40	BF334112.1	EST_HUMAN	AU149345 NT2RM4 Homo sapiens cDNA clone NT2RM4002122 3'
3676	19474	28938	0.65	9.0E-41	W01596.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
7862	20404	33311	1.68	8.0E-41	AL163203.2	NT	MR2-CT0222-211099-002-e10 CT02222 Homo sapiens cDNA
861	15427	25990	1.58	7.0E-41	A1934394.1	EST_HUMAN	za36a02.11 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:294602 5'
861	15427	25991	1.58	7.0E-41	A1934394.1	EST_HUMAN	wp04h04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5411	17688	30377	0.95	7.0E-41	11431114	NT	wp04h04.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2463895 3'
5469	18103	30422	0.84	7.0E-41	11545770	NT	Homo sapiens hypothetical protein (FLJ10396) mRNA
6159	18772	31535	3.44	7.0E-41	11419208	NT	Homo sapiens hypothetical protein FLJ13188 (FLJ13188), mRNA
6494	19095	31879	0.8	7.0E-41	11433010	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7087	18086	30442	0.95	7.0E-41	U72335.1	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1), mRNA
							Human platelet activating factor acetylhydrolase, brain isoform, 45 kDa subunit (LIST1) gene, exons 3 and 4

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11311	23804	38864	1.98	7.0E-41	4758445	NT	Homo sapiens guanine nucleotide binding protein 10 (GNG10) mRNA
12631	24952		8.97	7.0E-41	11417972	NT	Homo sapiens pescedilla (zebrafish) homolog 1, containing BRCT domain (PES1), mRNA
302	12957	25447	1.42	6.0E-41	AB037183.1	NT	Homo sapiens DSCR5b mRNA, complete cds
2157	14734	27307	2.33	6.0E-41	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSOR1), mRNA
7912	20454	33360	1.58	6.0E-41	BF513783.1	EST_HUMAN	UIH-BW1-amp-b-03-0-UJ.st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070421 3'
12611	24873		1.61	6.0E-41	AW873637.1	EST_HUMAN	h06408.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3042183 3' similar to contains MER32.b3 MER32 repetitive element ;
1838	14426	26977	2.16	5.0E-41	T62628.1	EST_HUMAN	yc03e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:79826 3'
4184	16774		1.01	5.0E-41	4885636	NT	Homo sapiens target of myb1 (chicken) homolog (TOM1), mRNA
6667	19263		1.97	5.0E-41	BE067042.1	EST_HUMAN	PM4-BT0341-251199-002-F11 BT0341 Homo sapiens cDNA
414	13049		1.58	4.0E-41	BE156318.1	EST_HUMAN	QV0-HT0367-150200-114-g09 HT0367 Homo sapiens cDNA
1137	13740	26249	1.12	4.0E-41	AL119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
1455	14047	26577	9.23	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parethyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1455	14047	26578	9.23	4.0E-41	AI027117.1	EST_HUMAN	ow45e06.s1 Soares_parethyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1649794 3' similar to TR:O00597 O00597 CYTOCHROME C-LIKE POLYPEPTIDE ; contains LTR5.b1 LTR5 repetitive element ;
1469	14061	26596	1.87	4.0E-41	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
1677	14269	26802	8.43	4.0E-41	AI500406.1	EST_HUMAN	tm86c04.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165958 3' similar to contains OFR.b1 OFR repetitive element ;
2913	15530	28001	3.73	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
2913	15530	28002	3.73	4.0E-41	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4225	16813	29280	2.27	4.0E-41	X92685.1	NT	H sapiens DNase I hypersensitive site (HSS-3) enhancer element
6632	19228		1.36	4.0E-41	AV758295.1	EST_HUMAN	AV758295 BM Homo sapiens cDNA clone BMFBH06 5'
9610	22110	35072	6.75	4.0E-41	BF304683.1	EST_HUMAN	60188906F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
11522	23970		9.87	4.0E-41	AV710480.1	EST_HUMAN	AV710480 Cu Homo sapiens cDNA clone CuAAC07 5'
12375	24841		2.28	4.0E-41	AV708431.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
12570	24868	30875	4.65	4.0E-41	BE887118.1	EST_HUMAN	601508315F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910059 5'
983	13595	26109	1.84	3.0E-41	AB030176.1	NT	Homo sapiens PAD-H19 mRNA for peptidylarginine deiminase type II, complete cds
4428	17014	29456	2.7	3.0E-41	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5273	17834		1.03	3.0E-41	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
5683	18310	30805	9.55	3.0E-41	X87689.1	NT	H sapiens mRNA for putative p64 CLCP protein

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6518	19118	31909	1.73	3.0E-41	AB037808.1	NT	Homo sapiens mRNA for KIAA1387 protein, partial cds
7761	20269	33167	0.7	3.0E-41	R54765.1	EST_HUMAN	X75008.r1 Soares breast 2NDHbSt Homo sapiens cDNA clone IMAGE:154575 5'
11575	24021	37090	1.78	3.0E-41	AJ226041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
11703	24116		1.84	3.0E-41	AA609768.1	EST_HUMAN	af17110.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1031847 3'
1864	14200	26734	15.09	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
2001	14883	27142	1.76	2.0E-41	AA331940.1	EST_HUMAN	EST35818 Embryo, 8 week Homo sapiens cDNA 5' end
2260	14834	27412	1.13	2.0E-41	D86962.1	NT	Human mRNA for KIAA0207 gene, complete cds
2308	14880	27458	3.79	2.0E-41	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
2855	14200	26734	10.87	2.0E-41	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
4728	17309	29753	2.07	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
4728	17309	29754	2.07	2.0E-41	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C087
7668	20178	33065	6.67	2.0E-41	AF038404.1	NT	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds
8013	20555	33458	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8013	20555	33459	1.36	2.0E-41	M96944.1	NT	Human B-cell specific transcription factor (BSAP) mRNA, complete cds
8040	20582	33489	1.59	2.0E-41	AA328265.1	EST_HUMAN	EST31723 Embryo, 12 week Homo sapiens cDNA 5' end
8905	21443	34366	1.61	2.0E-41	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
9338	21852	34800	0.74	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9338	21852	34801	0.74	2.0E-41	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
11359	23813	36873	3.76	2.0E-41	AA372637.1	EST_HUMAN	EST84555 Colon adenocarcinoma IV Homo sapiens cDNA 5' end
3240	15852	28333	1.11	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
3240	15852	28334	1.11	1.0E-41	BE869735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
4666	17248	29701	11.21	1.0E-41	6678468	NT	Mus musculus tubulin alpha 6 (Tuba6), mRNA
9339	21853	34802	1.82	1.0E-41	AI217868.1	EST_HUMAN	q775c10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755858 3'
11039	23553	36588	2.41	1.0E-41	AW847812.1	EST_HUMAN	IL3-CT0213-180200-040-F08 CT0213 Homo sapiens cDNA
11842	24204		2.37	1.0E-41	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
8457	20997		1.34	9.0E-42	BE179191.1	EST_HUMAN	RC0-HT0613-210300-032-g01 HT0613 Homo sapiens cDNA
9101	21637	34575	2.43	8.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9101	21637	34576	2.43	9.0E-42	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
488	13121	25607	7.59	8.0E-42	AF003530.1	NT	Homo sapiens homeobox protein CDX4 (CDX4) gene, complete cds and flanking repeat regions
							rh07c02.s1 NCI CGAP Thy1 Homo sapiens cDNA clone IMAGE:943588 similar to TR:G434304 G434304
11881	24959		53.38	8.0E-42	AA493896.1	EST_HUMAN	387BP EXPRESSED SEQUENCE TAG MRNA;
11900	24830		2.62	8.0E-42	AW088062.1	EST_HUMAN	xc97a04.x1 NCI CGAP_Brn35 Homo sapiens cDNA clone IMAGE:2592174 3' similar to contains OFR.t2
987	13578		2.5	7.0E-42	AL163265.2	NT	OFR repetitive element;
							Homo sapiens chromosome 21 segment HS21C085

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8408	20948		0.82	7.0E-42	R10983.1	EST_HUMAN	y38g04.t1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129174 5'
9188	21745	34698	1.99	7.0E-42	A1204958.1	EST_HUMAN	qf58g12.x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754278 3'
23565	36800		1.59	7.0E-42	AA569592.1	EST_HUMAN	mf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
11052	23565	36601	1.59	7.0E-42	AA569592.1	EST_HUMAN	mf23g07.s1 NCI_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
1896	14481	27039	4.44	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
1896	14481	27040	4.44	6.0E-42	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2328	14899		3.36	6.0E-42	AW239656.1	EST_HUMAN	xp28f08.x1 NCI_CGAP_HN10 Homo sapiens cDNA clone IMAGE:2741799 3' similar to contains L1.11 L1 repetitive element;
5659	18286	30764	1.48	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
5893	18286	30764	1.5	6.0E-42	AB028990.1	NT	Homo sapiens mRNA for KIAA1067 protein, partial cds
141	12806		6.21	5.0E-42	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
463	13097	25588	1.39	5.0E-42	BE217813.1	EST_HUMAN	hiv31e11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175052 3'
512	13145		4.36	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
513	13146		2.72	5.0E-42	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6788	19379	32194	1.23	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6788	19379	32195	1.23	5.0E-42	11433063	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A), mRNA
6893	19827	32484	2.58	5.0E-42	11417957	NT	Homo sapiens myobulbin related protein 3 (MTMR3), mRNA
7253	19781	32837	1.84	5.0E-42	AF071569.1	NT	Homo sapiens multifunctional calcium/calmodulin-dependent protein kinase II delta2 isoform mRNA, complete cds
8713	21252	34174	2.85	5.0E-42	AB037715.1	NT	Homo sapiens mRNA for KIAA1284 protein, partial cds
10495	22889	35997	0.6	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10495	22889	35998	0.6	5.0E-42	11431168	NT	Homo sapiens 3-hydroxyanthranilate 3,4-dioxygenase (HAAO), mRNA
10877	23398	36415	1.82	5.0E-42	8923162	NT	Homo sapiens hypothetical protein FLJ20163 (FLJ20163), mRNA
783	13402	25905	7.93	4.0E-42	AF055096.1	NT	Homo sapiens MHC class I region
783	13402	25906	7.93	4.0E-42	AF055096.1	NT	Homo sapiens MHC class I region
1104	13708	28217	2.39	4.0E-42	AF055096.1	NT	Homo sapiens ribonuclease III (RN3), mRNA, complete cds
4272	18858	28307	1.46	4.0E-42	X59417.1	NT	H. sapiens PROS-27 mRNA
4335	16922	29364	5.27	4.0E-42	4506498	NT	Homo sapiens regulatory factor X, 4 (influences HLA class II expression) (RFX4) mRNA
4683	17265	29715	13.42	4.0E-42	4508008	NT	Homo sapiens zinc finger protein 177 (ZNF177) mRNA
5353	17913	30328	0.94	4.0E-42	7681635	NT	Homo sapiens DKFZP564O2082 protein (DKFZP564O2082), mRNA
10378	22872	35865	0.46	4.0E-42	AW371201.1	EST_HUMAN	CMD-BT0282-171299-127-b03 BT0282 Homo sapiens cDNA
10528	23065	36076	1.76	4.0E-42	AW618630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10528	23065	36077	1.78	4.0E-42	AW818630.1	EST_HUMAN	RC1-ST0278-040400-018-h11 ST0278 Homo sapiens cDNA
11290	23742	36789	3.45	4.0E-42	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:3862086 5'
1530	14122	26661	4.49	2.0E-42	BF376834.1	EST_HUMAN	RC0-TN0079-110900-024-g07 TN0079 Homo sapiens cDNA
2436	15003	27575	0.92	2.0E-42	AV690218.1	EST_HUMAN	AV690218 GKC Homo sapiens cDNA clone GKCCBB808 5'
2456	15023		2.69	2.0E-42	AW898344.1	EST_HUMAN	RC3-NN0070-270400-011-h10 NN0070 Homo sapiens cDNA
2489	15038	27603	2.41	2.0E-42	AW250059.1	EST_HUMAN	2819293.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819293 3'
5931	18553	31279	13.21	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGC resequences: MAGC Homo sapiens cDNA
5931	18553	31280	13.21	2.0E-42	AW955368.1	EST_HUMAN	EST367438 MAGC resequences: MAGC Homo sapiens cDNA
6849	19439	32253	0.84	2.0E-42	AI052586.1	EST_HUMAN	ow63d05.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1653417 3'
9755	22283	35235	1.1	2.0E-42	BE538919.1	EST_HUMAN	601061284F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447620 5'
9967	22462	35445	0.53	2.0E-42	P81849	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
9967	22462	35446	0.53	2.0E-42	P81849	SWISSPROT	RIBONUCLEASE K3 (RNAse K3)
11585	24030	37100	1.55	2.0E-42	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
763	13381	25880	1.52	1.0E-42	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
1080	13685	26197	0.84	1.0E-42	AW285809.1	EST_HUMAN	UI-H-B11-afn-e-04-0-UJ.s1 NC1_QGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721871 3'
1140	13743	26252	2.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1140	13743	26253	2.08	1.0E-42	AJ251818.1	NT	Homo sapiens partial C9 gene for complement component C9, exon 1
1285	15437	26404	10.72	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1285	15437	26405	10.72	1.0E-42	AF087166.1	NT	Homo sapiens NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog mRNA, nuclear gene encoding mitochondrial protein, complete cds
1738	14328	26872	1.86	1.0E-42	11423219	NT	Homo sapiens rec (LOC51201), mRNA
2581	15144	27712	5.25	1.0E-42	5174458	NT	Homo sapiens major histocompatibility complex, class II, DM alpha (HLA-DMA) mRNA
2991	15607	28087	6.58	1.0E-42	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
3770	16371	28836	2.85	1.0E-42	7602027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
3862	16460	28924	0.83	1.0E-42	5031610	NT	Homo sapiens Golgi vesicular membrane trafficking protein p18 (BET1) mRNA
3999	16597	29069	1.07	1.0E-42	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4331	16918	29361	1.92	1.0E-42	AL163260.2	NT	Homo sapiens chromosome 21 segment HS21C080
4697	17279	29725	0.86	1.0E-42	AW813617.1	EST_HUMAN	RC3-ST0197-161099-012-a03 ST0197 Homo sapiens cDNA
4856	17434	29885	2.65	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P131), mRNA
4856	17434	29886	2.65	1.0E-42	5803122	NT	Homo sapiens proteasome inhibitor (P131), mRNA
4893	17468	29924	6.23	1.0E-42	4508758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
5274	17835	30260	1.48	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5274	17835	30281	1.48	1.0E-42	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
9898	22493	35482	3.35	9.0E-43	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
10916	23435	36455	3.57	9.0E-43	AA435719.1	EST_HUMAN	279807.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:728532 3'
680	13304	25786	22.52	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
680	13304	25787	22.52	8.0E-43	AV736824.1	EST_HUMAN	AV736824 CB Homo sapiens cDNA clone CBLAKH08 5'
729	13349	25841	7.38	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
729	13349	25842	7.38	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
729	13349	25843	7.38	8.0E-43	8923276	NT	Homo sapiens hypothetical protein FLJ20297 (FLJ20297), mRNA
5877	18489	31225	0.82	8.0E-43	H13952.1	EST_HUMAN	308811.1 Soares_placenta Nb2HP Homo sapiens cDNA clone IMAGE:148172 5'
3703	16304	28772	7.6	7.0E-43	AW246442.1	EST_HUMAN	2822251.Sp1time NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2822251 5'
5414	17971	30381	1.1	7.0E-43	AA989045.1	EST_HUMAN	cr88a07.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602900 3' similar to contains LTR8 b3 LTR8 repetitive element
5414	17971	30382	1.1	7.0E-43	AA989045.1	EST_HUMAN	cr88a07.s1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1602900 3' similar to contains LTR8 b3 LTR8 repetitive element
8704	21243		3.4	7.0E-43	AI836748.1	EST_HUMAN	wp69b01.x1 NCL_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2466985 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;contains LTR7 b1 LTR7 repetitive element
1388	13982		9.98	6.0E-43	AA491890.1	EST_HUMAN	ns72d06.s1 NCL_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:908803 similar to gb.L05095 60S RIBOSOMAL PROTEIN L30 (HUMAN)
2628	15190		2.44	6.0E-43	AV708201.1	EST_HUMAN	AV708201 ADG Homo sapiens cDNA clone ADGACC10 5'
6453	19054	31839	2.54	6.0E-43	8955973	NT	Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (ABCC3), transcript variant MRP3B, mRNA
6988	19486	32308	2.15	6.0E-43	AW468897.1	EST_HUMAN	hd30b04.x1 Soares_NFL_T_GBC.S1 Homo sapiens cDNA clone IMAGE:2910991 3' similar to contains MER1.i3 MER1 MER1 repetitive element
9785	22263	35246	2.2	6.0E-43	AA195154.1	EST_HUMAN	2x35e06.r1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:665410 5' similar to TR:G529841 G529841 DB1, COMPLETE CDS, ;contains element PTR7 repetitive element
10980	23494		6.53	6.0E-43	AL119158.1	EST_HUMAN	DKFZp761L1712.r1 761 (synonym: hary2) Homo sapiens cDNA clone DKFZp761L1712 5'
149	12812		1.7	5.0E-43	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
528	13160	25841	3.37	5.0E-43	AA382780.1	EST_HUMAN	EST96033 Testis I Homo sapiens cDNA 5' end
2872	15490	27861	1.18	5.0E-43	AV732578.1	EST_HUMAN	AV732578 HTF Homo sapiens cDNA clone HITFANC06 5'
6447	19481	32302	1.23	5.0E-43	AI613509.1	EST_HUMAN	tw22e07.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
6983	19481	32302	0.77	5.0E-43	AI613509.1	EST_HUMAN	tw22e07.x1 NCL_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260452 3'
8812	21351		0.49	5.0E-43	H74277.1	EST_HUMAN	yu49g12.r1 Soares_fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:229510 5'
9286	21886	34831	3.67	5.0E-43	AA465288.1	EST_HUMAN	aa33d08.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 5'

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Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10297	22791	35781	2.17	5.0E-43	AI733244.1	EST_HUMAN	cc52c10.x5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1669810 3' similar to TR:P90591 P90591 PV14 GENE ;
10332	22826	35821	2.14	5.0E-43	AL049110.1	EST_HUMAN	DKFZp434D0119.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0119
10844	23178	36188	5.05	5.0E-43	AW863007.1	EST_HUMAN	MR2-SN0007-280-400-004-c02 SN0007 Homo sapiens cDNA
10850	23371	36390	4.1	5.0E-43	W29011.1	EST_HUMAN	5594 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11332	23030	36039	1.71	5.0E-43	X15904.1	NT	Human mRNA for alpha-actinin
1008	15390	26133	5.38	4.0E-43	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
5464	18099	30417	0.98	4.0E-43	AI056338.1	EST_HUMAN	cy47h03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:1669013 3'
6507	19107	31892	0.82	4.0E-43	6986009	NT	Homo sapiens glycyl-RNA synthetase (GARS), mRNA
7184	18716		2.22	4.0E-43	11416793	NT	Homo sapiens protocadherin beta 6 (PCDH6), mRNA
8118	20659	33568	4.54	4.0E-43	AI244341.1	EST_HUMAN	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
8118	20659	33569	4.54	4.0E-43	AI244341.1	EST_HUMAN	MER10 repetitive element ;
10217	22712	35704	1.33	4.0E-43	6005987	NT	q76a02.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1865354 3' similar to contains MER10.13
11184	23689	36736	1.68	4.0E-43	T77380.1	EST_HUMAN	MER10 repetitive element ;
11818	24189		4.47	4.0E-43	R20950.1	EST_HUMAN	Homo sapiens zinc finger protein 161 (ZNF161), mRNA
1255	13852		3.54	3.0E-43	AF223391.1	NT	y472h10.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113827 5'
1733	14324	26866	1.8	3.0E-43	X97869.1	NT	y906b05.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31363 5' similar to contains MER10 repetitive element ;
2176	14753	27323	1.15	3.0E-43	AJ276230.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3630	16233	28708	1.25	3.0E-43	S69002.1	NT	H. sapiens gene encoding La subantigen
4378	16965	29411	0.9	3.0E-43	AA548154.1	EST_HUMAN	Homo sapiens mRNA for partial phospholipase D1, splice variant PLD1a/b2
6498	18099	31853	2.08	3.0E-43	7305360	NT	Homo sapiens mRNA for partial phospholipase D1, splice variant PLD1a/b2
8498	18099	31854	2.08	3.0E-43	7305360	NT	AML1-EVI-1=AML1-EVI-1 fusion protein (rearranged translocation) [human, leukemic cell line SKH1, mRNA Mutant, 5938 nt]
8827	19417	32233	3.71	3.0E-43	U65487.1	NT	nk55d06.s1 NCI_CGAP_P17 Homo sapiens cDNA clone IMAGE:1017419
8104	20645		8.03	3.0E-43	AA458824.1	EST_HUMAN	Mus musculus otogelin (Otog), mRNA
8754	21293	34213	1.59	3.0E-43	7661721	NT	Mus musculus otogelin (Otog), mRNA
9778	22276	35261	0.77	3.0E-43	11420217	NT	Mus musculus otogelin (Otog), mRNA
11572	24019	37089	2.6	3.0E-43	5730038	NT	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds
							aa88f11.s1 Stragene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838413 3' similar to contains THR12 THR repetitive element ;
							Homo sapiens hypothetical protein (HSA011918), mRNA
							Homo sapiens similar to ornithine carbamoyltransferase (H. sapiens) (LOC63648), mRNA
							Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
196	12856		9.15	2.0E-43	AI190784.1	EST_HUMAN	qd51c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:173968 3' similar to contains PTR7.13
6601	19198	32003	0.95	2.0E-43	BE222778.1	EST_HUMAN	PTR7 PTR7 repetitive element;
6601	19198	32004	0.95	2.0E-43	BE222778.1	EST_HUMAN	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
7320	19847	32707	1.12	2.0E-43	AW207390.1	EST_HUMAN	MER40 repetitive element;
8250	20791		9.58	2.0E-43	U43701.1	NT	hu53a08.x1 NCI_CGAP_Brn41 Homo sapiens cDNA clone IMAGE:3173750 3' similar to contains element
11079	23591		3.66	2.0E-43	T03007.1	EST_HUMAN	MER40 repetitive element;
1690	14282	26817	2.54	1.0E-43	AF154836.1	NT	UI-H-B11-afi-a-09-0-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2721712 3'
1690	14282	26818	2.54	1.0E-43	AF154836.1	NT	Human ribosomal protein L23a mRNA, complete cds
1743	14333	26879	1.63	1.0E-43	AL163284.2	EST_HUMAN	FB1G5 Fetal brain, Stratagene Homo sapiens cDNA clone FB1G5 3' and similar to LINE-1
2750	15305	27863	4.08	1.0E-43	BF348283.1	EST_HUMAN	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
6723	19317	32121	9.22	1.0E-43	4507168	NT	Homo sapiens Ras-like GTP-binding protein (RAB27A) gene, exons 1b and 2
6723	19317	32121	9.22	1.0E-43	4507168	NT	Homo sapiens chromosome 21 segment HS21C084
7046	18068	30456	1.8	1.0E-43	R19751.1	EST_HUMAN	60202313F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157666 5'
7873	20415	33323	1.04	1.0E-43	AF152865.1	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
8010	20552		2.79	1.0E-43	AF198490.1	NT	Homo sapiens Sp4 transcription factor (SP4) mRNA
8771	21310	34233	26.95	1.0E-43	AW963676.1	EST_HUMAN	Homo sapiens Sp4 transcription factor (SP4) mRNA
10191	22686	35679	0.65	1.0E-43	AW953229.1	EST_HUMAN	Y94e01.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:34732 5' similar to
10843	23364	36380	8.02	1.0E-43	A1984961.1	EST_HUMAN	SP:BD38_MOUSE P28656 BRAIN PROTEIN DN38 :
11244	23774	36831	3.74	1.0E-43	11424378	NT	Homo sapiens vacuolar sorting protein 35 (VPS35) mRNA, complete cds
11757	24152		1.95	1.0E-43	AL137964.1	EST_HUMAN	EST375749 MAGe resequences, MAGH Homo sapiens cDNA
12054	24337	30998	3.9	1.0E-43	A1675416.1	EST_HUMAN	EST365299 MAGe resequences, MAGB Homo sapiens cDNA
12286	24488	30942	4.3	9.0E-44	A1222865.1	EST_HUMAN	wf87h01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2494705 3'
923	13536	26054	5.83	8.0E-44	A1222865.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
923	13536	26055	5.83	8.0E-44	A1222865.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E), mRNA
5424	17981	30388	0.89	8.0E-44	A1381520.1	EST_HUMAN	DKFZp761D1015_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761D1015 5'
8476	21015	33931	2.74	8.0E-44	X94354.1	NT	w89b04.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2313775 3'
11043	23557	36593	3.86	8.0E-44	Y10498.2	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
11536	23984	37056	1.86	8.0E-44	L29139.1	NT	qf23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
12008	24310	30892	2.76	8.0E-44	11527389	NT	qf23g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1845552 3'
							ts76c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2092822 3' similar to TR:P93107
							P93107 PF20 :
							H. sapiens DNA for Cone cGMP-PDE gene
							Homo sapiens mRNA for thymidine kinase, partial
							Homo sapiens myosin mRNA, partial cds
							Homo sapiens polymerase (RNA) II (DNA directed) polypeptide F (POLR2F), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12419	24859	30703	2.39	8.0E-44	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
687	13311		0.83	7.0E-44	R06035.1	EST_HUMAN	ye89d01.1 Scores fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:124920 5'
2276	14850	27428	1.12	7.0E-44	5031886	NT	Homo sapiens LIM domain-containing preferred translocation partner in lipoma (LPP) mRNA
2993	15609	28088	2.84	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
2993	15608	28089	2.84	7.0E-44	AF048729.1	NT	Homo sapiens minisatellite ms32 repeat region
3929	16527	28994	2.76	7.0E-44	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4328	16912	29354	0.96	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
4328	16912	29355	0.96	7.0E-44	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
6252	18861	31633	0.77	6.0E-44	Z20946.1	EST_HUMAN	AU159839 Y79AA1 Homo sapiens cDNA clone Y79AA1000496 3'
11611	24054	37118	2.92	6.0E-44	AW954050.1	EST_HUMAN	HSAAADEYU.P, Human fetal Brain Whole tissue Homo sapiens cDNA
325	12979		3.12	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
354	13003		1.75	5.0E-44	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
7829	20371	33278	3.5	5.0E-44	AF588523.1	EST_HUMAN	in40d02.x1 NCL_CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2170083 3' similar to contains OFR.t1
9306	21806		1.85	5.0E-44	AU124571.1	EST_HUMAN	AU124571 NT2RM4 Homo sapiens cDNA clone NT2RM4000218 5'
3481	16088	28541	2.18	4.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
5158	17727		1.16	4.0E-44	A435225.1	EST_HUMAN	ti1402.x1 NCL_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2130147 3'
8215	20766	33670	0.76	4.0E-44	L21948.1	NT	Human fibrillin (FBN1) locus polymorphism
8811	21350		0.54	4.0E-44	BE176618.1	EST_HUMAN	RC3-H10585-010400-023-008 HT0585 Homo sapiens cDNA
11117	23628	36668	7.04	4.0E-44	U90878.1	NT	Homo sapiens carboxyl terminal LIM domain protein (CLIM1) mRNA, complete cds
1821	14410		1.09	3.0E-44	6912477	NT	Homo sapiens karyopherin alpha 6 (importin alpha 7) (KPNA6), mRNA
3132	15746	28215	5.8	3.0E-44	AA169851.1	EST_HUMAN	zp18b05.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609777 5'
3959	16537	28028	2.94	3.0E-44	AA337234.1	EST_HUMAN	EST42299 Endometrial tumor Homo sapiens cDNA 5' end similar to similar to alpha-1-antitrypsinase F
5404	17962	30373	2.57	3.0E-44	BF691060.1	EST_HUMAN	602247109F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332195 5'
9438	21964	34913	0.56	3.0E-44	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
1087	13692	26201	2.13	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1087	13692	26202	2.13	2.0E-44	4826685	NT	Homo sapiens DEADH (Asp-Glu-Ala-Asp/His) box polypeptide 1 (DDX1) mRNA
1249	13846	26363	2.99	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1249	13846	26364	2.99	2.0E-44	5803200	NT	Homo sapiens transmembrane trafficking protein (TMP21), mRNA
1355	13949	26475	4.41	2.0E-44	AF133588.1	NT	Homo sapiens RAB36 (RAB36) mRNA, complete cds
1412	14005	26533	1.38	2.0E-44	BE465325.1	EST_HUMAN	hw14q06.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3182838 3' similar to SW:OXYB_HUMAN

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2106	14772	27346	1.71	2.0E-44	AF070651.1	NT	Homo sapiens tissue-type bone marrow zinc finger protein 4 mRNA, complete cds
2641	15200		2.07	2.0E-44	5901893	NT	Homo sapiens adaptor-related protein complex 4, sigma 1 subunit (CLAPS4), mRNA
3517	16122	28602	1.34	2.0E-44	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4669	17251	29703	1.86	2.0E-44	AW864379.1	EST_HUMAN	PM4-SN0016-120500-003-a04 SN0016 Homo sapiens cDNA
5441	17986	30401	1.08	2.0E-44	4506376	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
6245	18854	31625	1.71	2.0E-44	11448901	NT	Homo sapiens chemokine (C-C motif) receptor 9 (CCR9), mRNA
6941	18049	30471	1.05	2.0E-44	AF038968.1	NT	Homo sapiens general transcription factor 2-1 (GTF2I) mRNA, alternatively spliced product, complete cds
7444	19968	32835	4.03	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
7444	19968	32836	4.03	2.0E-44	11419226	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3), mRNA
8367	20907	33825	0.85	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0817), mRNA
8367	20907	33826	0.85	2.0E-44	7706370	NT	Homo sapiens vesicle transport-related protein (KIAA0817), mRNA
8554	21093	34013	1.47	2.0E-44	BE388058.1	EST_HUMAN	601286014F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613586 5'
11657	24084		1.8	2.0E-44	BE244902.1	EST_HUMAN	TCBAP1E2795 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2795
12608	24692		63.7	2.0E-44	11526283	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
56	12736	25205	5.03	1.0E-44	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
56	12736	25206	5.03	1.0E-44	7657334	NT	Homo sapiens Mischapen/NIK-related kinase (MINK), mRNA
606	13234	25708	2.28	1.0E-44	AW653132.1	EST_HUMAN	RC1-CT0249-030300-026-h12 CT0249 Homo sapiens cDNA
1239	13837		1.03	1.0E-44	AW994803.1	EST_HUMAN	RC1-BN0039-110300-012-b01 BN0039 Homo sapiens cDNA
1618	14211		4.77	1.0E-44	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
2266	14840	27416	3.03	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR 13 THR repetitive element;
2266	14840	27417	3.03	1.0E-44	AA434554.1	EST_HUMAN	zw53d02.r1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773763 5' similar to contains THR 13 THR repetitive element;
2321	15463	27468	1.21	1.0E-44	AA398099.1	EST_HUMAN	z88g11.r1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:729476 5'
2798	15341	27911	1.54	1.0E-44	AF196779.1	NT	Homo sapiens transcription factor (GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel a2
3788	16388		4.07	1.0E-44	AA455669.1	EST_HUMAN	8601c09.s1 Soares, NHHMPu_S1 Homo sapiens cDNA clone IMAGE:811984 3'
8209	20750	33663	1.33	1.0E-44	AW967073.1	EST_HUMAN	EST378147 MAGE resequences, MAG1 Homo sapiens cDNA
8209	20750	33664	1.33	1.0E-44	AW967073.1	EST_HUMAN	EST378147 MAGE resequences, MAG1 Homo sapiens cDNA
8580	21119	34040	0.94	1.0E-44	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8956	21494	34417	0.68	1.0E-44	AI1337183.1	EST_HUMAN	qx88g07.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2008628 3'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10892	23413		11.29	1.0E-44	AV714608.1	EST_HUMAN	AV714608.DCB Homo sapiens cDNA clone DCBBYE03 5'
11404	23855	36921	5.07	1.0E-44	10092684	NT	Homo sapiens Sushi domain (SCR repeat) containing (BK65A6.2), mRNA
11460	23910	36976	3.83	1.0E-44	AW846867.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
11460	23910	36977	3.83	1.0E-44	AW846867.1	EST_HUMAN	RC1-CT0198-150999-011-C08 CT0198 Homo sapiens cDNA
4678	17260	29711	1.31	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4678	17260	29712	1.31	9.0E-45	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
6757	19350	32159	1.34	9.0E-45	AB023212.1	NT	Homo sapiens mRNA for KIAA0995 protein, partial cds
2565	15129	27698	6.45	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
5241	17805	30228	7.14	8.0E-45	5174718	NT	Homo sapiens TRK-fused gene (NOTE: non-standard symbol and name) (TFG) mRNA
8051	20593	33501	0.84	8.0E-45	AA377985.1	EST_HUMAN	EST190893 Synovial sarcoma Homo sapiens cDNA 5' end
2984	15600		0.99	7.0E-45	AL160131.1	NT	Novel human gene mapping to chromosome 22
4050	16847		6.39	6.0E-45	AW157570.1	EST_HUMAN	au83h07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782809 3' similar to SW:R13A_HUMAN P40429 60S RIBOSOMAL PROTEIN L13A ;
12385	25063		2	6.0E-45	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
925	13538		1.34	5.0E-45	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
2045	14827	27198	12.03	5.0E-45	BF333627.1	EST_HUMAN	GM4-CN0044-180200-515-f01 CN0044 Homo sapiens cDNA
3246	15858	28341	2.25	5.0E-45	AI523786.1	EST_HUMAN	tg94f07.x1 NCLCGAP_CLL1 Homo sapiens cDNA clone IMAGE:2116453 3' similar to SW:PAX1_MOUSE P09084 PAIRED BOX PROTEIN PAX-1 ;
5703	18329	30832	8.34	5.0E-45	AA397781.1	EST_HUMAN	z72d03.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:727877 3' similar to contains element TAR1 repetitive element ;
6170	18782	31548	1.1	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6170	18782	31549	1.1	5.0E-45	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
6215	18825	31596	1.15	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6215	18825	31597	1.15	5.0E-45	AB022318.1	NT	Homo sapiens mRNA for inducible nitric oxide synthase, complete cds
6336	18942	31720	1.82	5.0E-45	11498268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6336	18942	31721	1.82	5.0E-45	11498268	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
8218	20759	33673	0.51	5.0E-45	11418704	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8971	21509	34431	1.79	5.0E-45	4759223	NT	Homo sapiens programmed cell death 5 (PDCD5), mRNA
11542	23980	37062	2.52	5.0E-45	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
1183	13784	26294	11.57	4.0E-45	X95826.1	NT	H. sapiens ART4 gene
2330	14901	27472	21.18	4.0E-45	BE285622.1	EST_HUMAN	601194440F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538425 5'
4605	17188	29635	0.68	4.0E-45	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
8896	21424		0.86	4.0E-45	AA226220.1	EST_HUMAN	nc28607.a1 NC1_CGAP_P1 Homo sapiens cDNA clone IMAGE:1009284 similar to contains element L1 repetitive element ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11629	24071		2.17	4.0E-45	BE044076.1	EST_HUMAN	h36h04.x1 NCL_CGAP_UH1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3 MER29 repetitive element ;
11673	25006	30613	1.66	4.0E-45	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
12278	24482		2.14	4.0E-45	BF676077.1	EST_HUMAN	602084052F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248253 5'
4161	15882		1.32	3.0E-45	T71480.1	EST_HUMAN	y43507.1 Soares fetal liver spleen 1NFILS Homo sapiens cDNA clone IMAGE:110245 5'
6383	18987	31767	1.29	3.0E-45	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahtc11), mRNA
6383	18987	31768	1.29	3.0E-45	6753651	NT	Mus musculus dynein, exon, heavy chain 11 (Dnahtc11), mRNA
8388	20928		1.29	3.0E-45	AV723976.1	EST_HUMAN	AV723976 HTB Homo sapiens cDNA clone HTBAAG01 5'
8726	21265	34185	3.78	3.0E-45	4758451	NT	Homo sapiens golgi autoantigen, golgin subfamily a, 2 (GOLGA2) mRNA
10209	22704	35696	11.34	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10209	22704	35697	11.34	3.0E-45	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
2547	15111		4.13	2.0E-45	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
3067	15882	28154	0.99	2.0E-45	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
6644	19240	32043	5.46	2.0E-45	L01665.1	NT	Human eosinophil Charcot-Leyden crystal (CLC) protein (lysophospholipase) gene, promoter and exon 1
7605	20118	32994	1.35	2.0E-45	BE782184.1	EST_HUMAN	501467793F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870838 5'
8354	20894	33815	0.75	2.0E-45	AW834834.1	EST_HUMAN	RC0-LT0001-150200-032-411 LT0001 Homo sapiens cDNA
10882	24798	36225	28.86	2.0E-45	BE934350.1	EST_HUMAN	MRO-HT0923-190800-201-a02 HT0923 Homo sapiens cDNA
11055	23567	36603	5.39	2.0E-45	AA458770.1	EST_HUMAN	aa87112.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838319 5' similar to TR:G1144569 G1144569 R-SLY1 ;
11378	23830	36692	2.33	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
11378	23830	36893	2.33	2.0E-45	AW270280.1	EST_HUMAN	xp72a03.x1 NCL_CGAP_Ov40 Homo sapiens cDNA clone IMAGE:2745868 3'
12548	24653		2.42	2.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
129	13067		2.71	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
434	13067		3.24	1.0E-45	BE389855.1	EST_HUMAN	601284360F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606183 5'
498	13130	25619	1.61	1.0E-45	4506412	NT	Homo sapiens RAP1A, member of RAS oncogene family (RAP1A), mRNA
1216	13816	28331	1.54	1.0E-45	7657290	NT	Homo sapiens Langerhans cell specific c-type lectin (LANGERIN), mRNA
3137	15751	28219	10.2	1.0E-45	U32169.1	NT	Human pro-a2 chain of collagen type XI (COL11A2) gene, complete cds
3539	16144	28627	0.88	1.0E-45	8659558	NT	Homo sapiens chromosome 21 open reading frame 1 (C21orf4), mRNA
3632	16235	28710	0.88	1.0E-45	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
4575	17158	29802	5.87	1.0E-45	BE386833.1	EST_HUMAN	601289116F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3618803 5'
5335	17896	30311	11.79	1.0E-45	7706128	NT	Homo sapiens oxysterol 7alpha-hydroxylase (CYP39A1), mRNA
7974	20516	33422	0.71	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA
7974	20516	33423	0.71	1.0E-45	11422236	NT	Homo sapiens peroxisomal biogenesis factor 14 (PEX14), mRNA

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8543	21082	34003	0.88	1.0E-45	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
9049	21586	34517	4.07	1.0E-45	BE887843.1	EST_HUMAN	601511226F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912535 5'
9441	21987	34916	0.88	1.0E-45	AB002287.1	NT	Humen mRNA for KIAA0289 gene, partial cds
11875	24225	31045	4.89	1.0E-45	11418099	NT	Homo sapiens protein kinase C, alpha binding protein (PRKCABP), mRNA
12063	24346		9.84	1.0E-45	11528291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
12068	24349		10.35	1.0E-45	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12513	24632	30895	3.48	1.0E-45	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1 subunit (CACNA1), mRNA
8170	20711	33628	1.87	9.0E-46	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krl2-6g), mRNA
8569	21108		6.51	9.0E-46	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10374	22868	35861	10.22	9.0E-46	AW246984.1	EST_HUMAN	2822449.5prime NIH_MGC_77 Homo sapiens cDNA clone IMAGE:2822449 5'
2486	15051	27622	9.69	8.0E-46	AI433261.1	EST_HUMAN	t32108.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2822449 5'
2486	15051	27623	9.69	8.0E-46	AI433261.1	EST_HUMAN	TUBULIN BETA-1 CHAIN (HUMAN);
7998	20540		6.07	8.0E-46	BE167244.1	EST_HUMAN	RC5-HT0508-280200-012-C12 HT0508 Homo sapiens cDNA
11513	23961		2.67	8.0E-46	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
2280	14834	27432	1.07	7.0E-46	U46007.1	NT	Rattus norvegicus espin mRNA, complete cds
4680	17262		6.38	7.0E-46	BE386165.1	EST_HUMAN	601277292F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618119 5'
4929	17604		0.88	7.0E-46	BE084386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
6193	18803	31572	3.72	7.0E-46	8922708	NT	Homo sapiens hypothetical protein FLJ10847 (FLJ10847), mRNA
6620	19217	32022	1.29	7.0E-46	BF105845.1	EST_HUMAN	601822835F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4042736 5'
12203	24428		1.6	7.0E-46	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2783	15336	27806	3.13	6.0E-46	AI884381.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
2783	15336	27807	3.13	6.0E-46	AI884381.1	EST_HUMAN	wm31108.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437575 3' similar to contains MER19.12
6278	18886	31655	9.32	6.0E-46	AI835448.1	EST_HUMAN	ts58h10.x1 NCI_CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2232835 3' similar to TR:O60363 O60363 SA GENE.
7269	19797	32653	0.83	6.0E-46	AW513244.1	EST_HUMAN	xc42e04.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2706654 3' similar to gb:1.08069 DNAJ
11288	23008		2.81	6.0E-46	BE784971.1	EST_HUMAN	PROTEIN HOMOLOG 2 (HUMAN);
218	12879		5.85	5.0E-46	AL163210.2	NT	601478409F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3880995 5'
3581	16185	28687	1.37	5.0E-46	BE677194.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
3581	16185	28688	1.37	5.0E-46	BE677194.1	EST_HUMAN	7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'
							7d81g01.x1 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:3279408 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6833	19423	32239	1.83	5.0E-46	BF580442.1	EST_HUMAN	naa38f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3258787 3' similar to TR:O75202
7021	19555	32380	3.81	5.0E-46	BF347229.1	EST_HUMAN	O75202 HOMOLOG OF RAT KIDNEY-SPECIFIC ;
7152	19884	32526	0.74	5.0E-46	AW582253.1	EST_HUMAN	602021184F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4156670 5'
9533	22033	34992	0.46	5.0E-46	AA398381.1	EST_HUMAN	QV4-ST0212-120100-075-009 ST0212 Homo sapiens cDNA
							z62c08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726926 3'
669	13283		1.73	4.0E-46	AA601143.1	EST_HUMAN	nc54a09.s1 NCI_CGAP_S51 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_ma1
							FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
1741	14331	26875	3.96	4.0E-46	AW770544.1	EST_HUMAN	h86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
							LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
1741	14331	26876	3.96	4.0E-46	AW770544.1	EST_HUMAN	h86c03.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3008836 3' similar to gb:X14008_ma1
2767	15321	27887	3.11	4.0E-46	M18048.1	NT	LYSOZYME C PRECURSOR (HUMAN);contains element MER37 repetitive element ;
5628	18257	30727	2.09	4.0E-46	M36852.1	NT	Human endogenous retrovirus RTVL-H2
5628	18257	30728	2.09	4.0E-46	M36852.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
12332	24516	30921	1.86	4.0E-46	AB002039.1	NT	Human Ig germline gamma-3 heavy-chain gene V region, partial cds
4482	17067	29517	0.81	3.0E-46	4506376	NT	Homo sapiens DNA for Human P2XM, complete cds
							Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4889	17464	29918	0.98	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
4889	17464	29919	0.98	3.0E-46	Z73660.1	NT	H. sapiens Ig lambda light chain variable region gene (7c.11.2) germline; Ig-Light-Lambda; VLambda
8684	21223	34143	7.65	3.0E-46	A1831462.1	EST_HUMAN	wf49c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2
8935	21473	34392	0.56	3.0E-46	L08850.1	NT	THR repetitive element ;
8935	21473	34393	0.56	3.0E-46	L08850.1	NT	Human AD amyloid mRNA, complete cds
11446	23896	36981	3.14	3.0E-46	D31765.1	NT	Human AD amyloid mRNA, complete cds
870	13485	26000	8.24	2.0E-46	AA488848.1	EST_HUMAN	Human mRNA for KIAA0061 gene, partial cds
1608	14201		1.41	2.0E-46	AA678246.1	EST_HUMAN	ne06a09.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:880408 3' similar to contains THR.b2 THR
							repetitive element ;
1683	14275	26808	2.17	2.0E-46	U78027.1	NT	z127a11.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:431998 3'
							Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
5110	17682	30119	1.2	2.0E-46	AA398286.1	EST_HUMAN	z159e02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726650 5' similar to SW:RSP1_MOUSE
							Q01730 RSP-1 PROTEIN. ;

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7497	20020	32884	6.85	2.0E-46	9910569	NT	Mus musculus sperm tail associated protein (Stap), mRNA
8014	20566		1.81	2.0E-46	BE869151.1	EST_HUMAN	601445137F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849297 5'
11125	23633		1.56	2.0E-46	7657233	NT	Homo sapiens small acidic protein (IMAGE145052), mRNA
11802	24963		1.74	2.0E-46	BF028854.1	EST_HUMAN	601765225F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3997326 5'
12094	24361		1.43	2.0E-46	AA001786.1	EST_HUMAN	zh84f12.r1 Soeires_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:428015 5'
12408	24846	30800	5.26	2.0E-46	AW27214.1	EST_HUMAN	zq78h03.x1 NCL_CGAP_Lu34 Homo sapiens cDNA clone IMAGE:2766789 3'
1276	13871	26391	5.79	1.0E-46	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10), mRNA
2320	14892	27487	4.58	1.0E-46	AW878516.1	EST_HUMAN	EST390825 MAGC resequences, MAGP Homo sapiens cDNA
2443	15010	27582	2.81	1.0E-46	H97330.1	EST_HUMAN	EST486095 WATM1 Homo sapiens cDNA clone 486095
3286	15897	28375	22.33	1.0E-46	AA631912.1	EST_HUMAN	np78b02.s1 NCL_CGAP_P22 Homo sapiens cDNA clone IMAGE:1132395 similar to gb:X76717 H. sapiens MT-11 mRNA. (HUMAN);
4999	17572		3.21	1.0E-46	AB023197.1	NT	Homo sapiens mRNA for KIAA0980 protein, partial cds
5878	18500	31226	11.77	1.0E-46	BF194707.1	EST_HUMAN	7c92b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
6131	24757	31500	4.79	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6131	24757	31501	4.79	1.0E-46	8923762	NT	Homo sapiens centaurin-alpha 2 protein (HSA272195), mRNA
6725	19319	32124	0.72	1.0E-46	BF196247.1	EST_HUMAN	7n48e07.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567852 3' similar to contains element MER22 repetitive element;
10742	18500	31226	4.43	1.0E-46	BF194707.1	EST_HUMAN	7c92b01.x1 NCL_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3643705 3'
11831	24196	31035	1.97	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4215398 5'
11831	24196	31036	1.97	1.0E-46	BF531102.1	EST_HUMAN	602072284F1 NCL_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4215398 5'
12626	24704		1.39	1.0E-46	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAIE03 5'
798	13415		3.52	9.0E-47	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5085	17638	30081	2.39	9.0E-47	AW770928.1	EST_HUMAN	h93e04.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3009534 3' similar to TR:O75703 O75703
6514	19114	31803	0.78	9.0E-47	11425439	NT	HYPOTHETICAL 12.4 KD PROTEIN;
12355	24951	30827	3.64	9.0E-47	11417968	NT	Homo sapiens zinc finger protein ZNF286 (ZNF286), mRNA
1844	14432	26985	16.42	8.0E-47	Y18536.1	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
1844	14432	26986	16.42	8.0E-47	Y18536.1	NT	Homo sapiens HLA-C gene, exon 5, individual 19323
2742	15297	27864	1.1	8.0E-47		NT	Homo sapiens HLA-C gene, exon 5, individual 19323
3058	15874	28150	2.05	8.0E-47	AJ228043.1	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), epsilon isoform (PPP2R5E) mRNA
3686	16287	28756	0.8	8.0E-47	AB041926.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 3/3
3686	16287	28757	0.8	8.0E-47	AB041926.1	NT	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
12436	24845		1.55	7.0E-47	AV683284.1	EST_HUMAN	Homo sapiens mRNA for GCK family kinase MINK-2, complete cds
							AV683284 GKC Homo sapiens cDNA clone GKCASH11 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9200	21717	34661	6.33	6.0E-47	AI085189.1	EST_HUMAN	t298h02.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2266659 3'
9628	22128	35091	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECOL5 beta mRNA for DNA helicase recQ5 beta, complete cds
9628	22128	35092	0.69	6.0E-47	AB042824.1	NT	Homo sapiens RECOL5 beta mRNA for DNA helicase recQ5 beta, complete cds
6691	19287	32090	5.97	5.0E-47	11423972	NT	Homo sapiens CDC37 (cell division cycle 37, S. cerevisiae, homolog) (CDC37), mRNA
10674	23206		4.92	5.0E-47	M78590.1	EST_HUMAN	EST00738 Fetal brain, Striatum (cat#636206) Homo sapiens cDNA clone HFB0F07
1445	14037	26567	3.92	4.0E-47	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
6920	19579	32408	0.94	4.0E-47	BE938806.1	EST_HUMAN	MIR4-TN0108-280800-201-404 TN0108 Homo sapiens cDNA
8417	20957	33874	2.47	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8417	20957	33875	2.47	4.0E-47	BE616483.1	EST_HUMAN	601280486F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622437 5'
8553	21092	34012	0.57	4.0E-47	AW993777.1	EST_HUMAN	RC3-BN0034-220300-015-105 BN0034 Homo sapiens cDNA
11494	23943		6.19	4.0E-47	AW515509.1	EST_HUMAN	x66b07.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2848597 3' similar to SW:INT6_MOUSE
570	13201	25682	3.11	3.0E-47	BE907634.1	EST_HUMAN	Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6, [1]
570	13201	25683	3.11	3.0E-47	BE907634.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
851	13467	25976	5.09	3.0E-47	N57483.1	EST_HUMAN	601497639F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899721 5'
981	13593	26108	9.88	3.0E-47	AL163264.2	NT	yf54b04.s1 Scores_multiple_sclerosis_2NblMSP Homo sapiens cDNA clone IMAGE:277327 3'
3343	15953	28429	0.77	3.0E-47	4504116	NT	Homo sapiens chromosome 21 segment HS21C084
4038	16636		5.04	3.0E-47	U63181.1	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
6163	18776	31538	4.81	3.0E-47	AW408800.1	EST_HUMAN	Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
6163	18776	31539	4.81	3.0E-47	AW408800.1	EST_HUMAN	UI-HF-BM0-adv-d-07-O-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
6880	19278		1.71	3.0E-47	AI22413.1	EST_HUMAN	UI-HF-BM0-adv-d-07-O-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063205 5'
7416	19941	32806	0.75	3.0E-47	AI819755.1	EST_HUMAN	qh04e07.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843716 3'
7416	19941	32807	0.75	3.0E-47	AI819755.1	EST_HUMAN	wj11h08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
8787	21306	34228	0.56	3.0E-47	AW963796.1	EST_HUMAN	wj11h08.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2402559 3'
8787	21306	34229	0.56	3.0E-47	AW963796.1	EST_HUMAN	EST375969 MAGE resequences, MAGH Homo sapiens cDNA
159	12822	25310	1.38	2.0E-47	4505318	NT	EST375969 MAGE resequences, MAGH Homo sapiens cDNA
1003	13614	26127	2.14	2.0E-47	AL183209.2	NT	EST375969 MAGE resequences, MAGH Homo sapiens cDNA
1003	13614	26128	2.14	2.0E-47	AL183209.2	NT	Homo sapiens myosin phosphatase, target subunit 2 (MYPT2), mRNA
1613	14206		1.1	2.0E-47	AI969279.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C009
1637	14229	26762	1.07	2.0E-47	7662109	NT	Homo sapiens chromosome 21 segment HS21C009
1717	14309	26848	3.75	2.0E-47	AA524514.1	EST_HUMAN	wq96b02.x1 NCL_CGAP_G06 Homo sapiens cDNA clone IMAGE:2479851 3'
4439	17025	29485	1.88	2.0E-47	4504866	NT	Homo sapiens KIAA0426 gene product (KIAA0426), mRNA
4473	17059	29506	1.91	2.0E-47	AA569592.1	EST_HUMAN	ng43h12.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937607 3'
4473	17059	29507	1.91	2.0E-47	AA569592.1	EST_HUMAN	Homo sapiens ring finger protein (C3HC4 type) 8 (RNF8), mRNA
							nf23g07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652
							nf23g07.s1 NCL_CGAP_P1 Homo sapiens cDNA clone IMAGE:914652

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4604	17187	29634	2.94	2.0E-47	5174648	NT	Homo sapiens RevRex activation domain binding protein-related (RAB-R) mRNA
4935	17510	29957	1.29	2.0E-47	AW965166.1	EST_HUMAN	EST1377239 IMAGE sequences, MAGI Homo sapiens cDNA
5956	18578	31312	0.93	2.0E-47	AF073921.1	NT	Homo sapiens regulator of G-protein signaling 6 variant form (RGSG6) mRNA, complete cds
6130	18745	31498	1.46	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
6130	18745	31498	1.46	2.0E-47	BE778475.1	EST_HUMAN	601463932F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3867487 5'
7696	24788		1.25	2.0E-47	L09731.1	NT	Homo sapiens 5-hydroxytryptamine 1D receptor pseudogene with an Alu repeat insertion
7905	20447	33353	1.74	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
7905	20447	33354	1.74	2.0E-47	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
8652	21191	34109	1.77	2.0E-47	AF071771.1	NT	Homo sapiens SPH-binding factor mRNA, partial cds
9410	21919	34867	1.33	2.0E-47	11528138	NT	Homo sapiens BTG family, member 3 (BTG3), mRNA
11863	24994	30608	2.82	2.0E-47	R42423.1	EST_HUMAN	y92508.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:29968 3' similar to contains OFR repetitive element;
1451	14043	26571	6.05	1.0E-47	A1333429.1	EST_HUMAN	qp99h03.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1931189 3'
3894	16493	28953	0.93	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
3894	16493	28954	0.93	1.0E-47	BE280477.1	EST_HUMAN	601155321F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138893 5'
5235	17799	30218	2.44	1.0E-47	AW813906.1	EST_HUMAN	RC3-ST0197-130400-017-002 ST0197 Homo sapiens cDNA
7109	19449	32265	5.59	1.0E-47	A1880888.1	EST_HUMAN	at19e06.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2355586 3' similar to gb:M222955
8802	21341		7.68	1.0E-47	AW664648.1	EST_HUMAN	RAS-RELATED PROTEIN RAP-1A (HUMAN);
10258	22753	35741	2.06	1.0E-47	L30115.1	NT	h184a11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2878972 3' similar to gb:M26326
1654	14246	26779	2.38	9.0E-48	AF223391.1	NT	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
3612	16215	28695	0.78	9.0E-48	BF359947.1	EST_HUMAN	Papio hamadryas alcohol dehydrogenase class I (ADH) gene, 5' region
5860	18482	31205	0.83	9.0E-48	BE888196.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
5860	18482	31206	0.83	9.0E-48	BE888196.1	EST_HUMAN	CM2-MT0100-310700-280-005 MT0100 Homo sapiens cDNA
6373	18977	31755	0.69	9.0E-48	AU123240.1	EST_HUMAN	60151714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
10995	23509	36542	3.37	9.0E-48	BE39813.1	EST_HUMAN	60151714F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913106 5'
1293	13888		2.34	8.0E-48	4501900	NT	AU123240 NT2RM1 Homo sapiens cDNA clone NT2RM1000978 5'
1294	13888		1.76	8.0E-48	4501900	NT	601310479F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632083 5'
3169	15783	28254	3.3	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
3169	15783	28255	3.3	8.0E-48	AW768477.1	EST_HUMAN	Homo sapiens aminocyclase 1 (ACY1), mRNA
							h161b03.x1 NCLCGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);
							h161b03.x1 NCLCGAP_Lym12 Homo sapiens cDNA clone IMAGE:3001133 3' similar to gb:X64707
							BREAST BASIC CONSERVED PROTEIN 1 (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4005	16803	29077	0.6	8.0E-48	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
516	13149		2.03	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
517	13149		20.88	7.0E-48	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
1544	14136	26870	1.08	7.0E-48	6912719	NT	Homo sapiens toubled-like kinase 1 (TLK1), mRNA
1679	14271	26804	3.49	7.0E-48	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
6672	19268	32072	21.95	7.0E-48	11416831	NT	Homo sapiens histidyl-RNA synthetase (HARS), mRNA
3658	18281	28733	1.19	6.0E-48	A176111.1	EST_HUMAN	w69h03.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398613 3'
6208	18818	31589	0.98	6.0E-48	AB006955.1	NT	Homo sapiens mRNA for AIE-76, complete cds
6881	19815	32450	0.87	6.0E-48	11420995	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX), mRNA
9051	21598	34520	2.17	6.0E-48	AF028816.1	NT	Homo sapiens putative oncogene protein mRNA, partial cds
9460	21986	34940	1.72	6.0E-48	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
9606	22108	35089	3.5	6.0E-48	AA189080.1	EST_HUMAN	zq45b06.s1 Stratagene hNT neuron (#637233) Homo sapiens cDNA clone IMAGE:632627 3' similar to contains Alu repetitive element;
2293	14967	27442	1.43	5.0E-48	4827059	NT	Homo sapiens xylulokinase (H. influenzae) homolog (XYLB) mRNA
2300	14873	27449	1.15	5.0E-48	4827059	NT	Homo sapiens xylulokinase (H. influenzae) homolog (XYLB) mRNA
3350	18002	28435	1.64	5.0E-48	4826891	NT	Homo sapiens phosphodiesterase 1A, calmodulin-dependent (PDE1A) mRNA
5418	17975	30383	1.13	5.0E-48	AF219936.1	NT	Homo sapiens diacylglycerol kinase iota (DGKI) gene, exon 32
8511	21050	33972	6.84	5.0E-48	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-H06 BT0311 Homo sapiens cDNA
10836	23957	36373	4.24	4.0E-48	A1620420.1	EST_HUMAN	tu47a02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2254154 3'
1428	14021	26549	1.75	3.0E-48	AV690964.1	EST_HUMAN	AV690964 GKC Homo sapiens cDNA clone GKCDRE12 5'
2019	14601	27165	9.63	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
2019	14601	27166	9.63	3.0E-48	4885170	NT	Homo sapiens chromosome X open reading frame 6 (CXORF6) mRNA
3465	16072	28545	0.98	3.0E-48	AF172453.1	NT	Homo sapiens oploid growth factor receptor mRNA, complete cds
3693	16294	28784	0.76	3.0E-48	AW664531.1	EST_HUMAN	h114b12.x1 NCL CGAP_GU1 Homo sapiens cDNA clone IMAGE:2872255 3' similar to SW:DCRB_HUMAN
4332	16919		0.67	3.0E-48	AA009541.1	EST_HUMAN	P56555 DOWN SYNDROME CRITICAL REGION PROTEIN B. ;
6053	18671	31410	2.98	3.0E-48	BE084571.1	EST_HUMAN	z04g03.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429844 5'
7087	19858	32497	1.01	3.0E-48	AF087913.1	NT	Human endogenous retrovirus HERV-P-T47D
8330	20871		3.02	3.0E-48	AA659930.1	EST_HUMAN	nv03f05.s1 NCL CGAP_P22 Homo sapiens cDNA clone IMAGE:1219137 3' similar to contains PTR5.b1 PTR5 repetitive element;
10753	23277	36280	8.32	3.0E-48	BF514170.1	EST_HUMAN	UI-H-BW1-aria-10-0-UI.s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082267 3'
5	12685	25142	2.18	2.0E-48	AA465007.1	EST_HUMAN	z680c03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:810052 5'
49	12729	25193	2.12	2.0E-48	AA631940.1	EST_HUMAN	fntfc7 Regional genomic DNA specific cDNA library Homo sapiens cDNA clone CR17-26

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4829	17212	29883	0.93	2.0E-48	BE248085.1	EST_HUMAN	TCBAP1D3842 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP3842
5095	17688	30107	1.8	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain, Stratagene Homo sapiens cDNA clone FB2E2 3' end
5095	17688	30108	1.8	2.0E-48	T03176.1	EST_HUMAN	FB2E2 Fetal brain, Stratagene Homo sapiens cDNA clone FB2E2 3' end
7528	20048	32919	4.15	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7528	20048	32920	4.15	2.0E-48	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
7539	20059	32893	3.51	2.0E-48	11498238	NT	Homo sapiens v-rel avian reticuloendotheliosis viral oncogene homolog A (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (p65)) (RELA), mRNA
8296	20837	33758	1.53	2.0E-48	AV743451.1	EST_HUMAN	AV743451 CB Homo sapiens cDNA clone CBCGGG10 5'
11828	12685	25142	4.4	2.0E-48	AA486007.1	EST_HUMAN	z680c03 r1 Soares ovary tumor NBH07 Homo sapiens cDNA clone IMAGE:810052 5'
60	12739	25210	3.22	1.0E-48	7706534	NT	Homo sapiens cisplatin resistance-associated overexpressed protein (LOC51747), mRNA
906	13520	26038	5.3	1.0E-48	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1114	13718	26228	2.58	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1114	13718	26229	2.58	1.0E-48	7657430	NT	Homo sapiens EBNA-2 co-activator (100kD) (p100), mRNA
1339	13934	26455	4.33	1.0E-48	5032032	NT	Homo sapiens RNA binding motif protein 8 (RBM8) mRNA
1682	14546	27103	19.18	1.0E-48	AL163302.2	NT	Homo sapiens chromosome 21 segment HS21C102
3535	16140	28622	0.81	1.0E-48	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
5312	17874	30296	1.37	1.0E-48	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
6431	19034	31818	1.14	1.0E-48	AB889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14589 SIMILARITY TO U73941;
6431	19034	31819	1.14	1.0E-48	AB889077.1	EST_HUMAN	td17c01.x1 NCI_CGAP_Co18 Homo sapiens cDNA clone IMAGE:2075904 3' similar to TR:O14588 O14589 SIMILARITY TO U73941;
6625	19222		0.94	1.0E-48	Y18000.1	NT	Homo sapiens NF2 gene
7303	19831	32690	2.58	1.0E-48	4755137	NT	Homo sapiens huntingtin (Huntington disease) (HD) mRNA
8765	21304	34225	0.52	1.0E-48	4758895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8765	21304	34226	0.52	1.0E-48	4758895	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
9140	21675	34818	0.84	1.0E-48	4502838	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1) mRNA
9192	21709	34653	6	1.0E-48	AB033071.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
9485	21942	34889	0.73	1.0E-48	BE168410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
9502	22002	34959	3.86	1.0E-48	BF304693.1	EST_HUMAN	601888096F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122119 5'
10272	22767	35734	3.54	1.0E-48	11428808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
10272	22767	35755	3.54	1.0E-48	11428808	NT	Homo sapiens B cell linker protein (SLP65), mRNA
11789	24937		1.62	1.0E-48	W26785.1	EST_HUMAN	15d8 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2052	14633	27204	0.96	8.0E-49	AB028497.1	NT	Mus musculus MysPDZ mRNA for myosin containing PDZ domain, complete cds
6204	18814	31584	3.44	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
6204	18814	31585	3.44	8.0E-49	10048417	NT	Mus musculus T-box 20 (Tbx20), mRNA
8236	20777	33698	3.22	8.0E-49	U23850.1	NT	Human Inositol 1,4,5 trisphosphate receptor type 1 mRNA, partial cds
9900	22397	35372	1.23	8.0E-49	AB008981.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
10736	23281	36276	1.6	8.0E-49	AI623722.1	EST_HUMAN	ts38d12.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2230871 3' similar to contains Alu repetitive element; contains element PTR5 repetitive element;
145	13052	25542	2.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
145	13052	25543	2.62	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
417	13052	25542	2.38	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
417	13052	25543	2.38	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
418	13052	25542	2.59	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
418	13052	25543	2.59	7.0E-49	5729990	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, ATPase, 4 (PSMC4) mRNA
1263	13860	26377	3.49	7.0E-49	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5651	18278	30755	1.97	7.0E-49	AI807191.1	EST_HUMAN	wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
5651	18288	30766	1.11	7.0E-49	AL120937.1	EST_HUMAN	O54923 RSEC15
5973	18278	30755	1.14	7.0E-49	AI807191.1	EST_HUMAN	DKFp762C033_s1 762 (synonym: hmd2) Homo sapiens cDNA clone DKFp762C033 3'
							wf25h04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2356663 3' similar to TR:O54923
							complete (MOUSE);
211	12872	25358	57.13	6.0E-49	AW1731740.1	EST_HUMAN	be55g05.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900504 3' similar to gb:X17206.40S
4193	16782	28231	0.59	6.0E-49	AL162091.1	EST_HUMAN	RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element,
6571	19169	31966	0.69	6.0E-49	AL140742.1	EST_HUMAN	complete (MOUSE);
11159	23666	36711	3.66	6.0E-49	AW452218.1	EST_HUMAN	DKFp761A138_s1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFp761A138 3'
11514	23962	37031	3.9	6.0E-49	AA366556.1	EST_HUMAN	AU140742 PLACE4 Homo sapiens cDNA clone PLACE4000148 5'
11514	23962	37032	3.9	6.0E-49	AA366556.1	EST_HUMAN	UHH-B13-ab-a-05-0-U1 s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3066048 3'
12166	24825	25854	7.5	6.0E-49	AA707567.1	EST_HUMAN	EST17525 Pancreas tumor III Homo sapiens cDNA 5' end
741	13361	25854	6.61	5.0E-49	AL163210.2	NT	EST17525 Pancreas tumor III Homo sapiens cDNA 5' end
741	13361	25855	6.61	5.0E-49	AL163210.2	NT	z28c08.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:451694 3'
							Homo sapiens chromosome 21 segment HS21C010
							Homo sapiens chromosome 21 segment HS21C010
1830	14419	26868	3.16	5.0E-49	AA172121.1	EST_HUMAN	z029c07.r1 Stralagene neuroepithelium (#637231) Homo sapiens cDNA clone IMAGE:610800 5' similar to
2776	15331	27900	4.95	5.0E-49	U17714.1	NT	TR:G233226 RTVL-H PROTEIN; contains LTR7.13 LTR7 repetitive element;
							Homo sapiens putative tumor suppressor ST13 (ST13) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3311	15022	28398	6.09	5.0E-49	11436355	NT	Homo sapiens similar to ribosomal protein S27 (metalloproteinin 1) (H. sapiens) (LOC63362), mRNA x08601.x1 NCL_CGAP_U14 Homo sapiens cDNA clone IMAGE:2675593 3' similar to WP:B0350.2B CE06703 ;
551	13182	25659	26.48	4.0E-49	AW189533.1	EST_HUMAN	
7316	19843	32704	0.79	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
7316	19843	32705	0.79	4.0E-49	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
8798	21337	34263	0.46	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
8798	21337	34264	0.46	4.0E-49	11425374	NT	Homo sapiens copine III (CPNE3), mRNA
12021	25056		4.9	4.0E-48	AA210798.1	EST_HUMAN	z6005.r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:682977 5'
12110	24371		3.14	4.0E-48	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
586	13216	25693	1.08	3.0E-49	XG8968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
2674	15232		1.43	3.0E-49	AA016131.1	EST_HUMAN	z631c05.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.13 L1 repetitive element ;
5120	17892	30130	2.33	3.0E-49	U46999.1	NT	Human type IV collagen (COL4A6) gene, exon 40
7448	19872	32839	9.89	3.0E-49	H39479.1	EST_HUMAN	EST25e12 WATM1 Homo sapiens cDNA clone 25e12
11181	23887	36734	1.98	3.0E-49	AA337561.1	EST_HUMAN	EST42572 Endometrial tumor Homo sapiens cDNA 5' end
689	13313		1.57	2.0E-49	BE165980.1	EST_HUMAN	MR3-HIT0487-150200-113-g01 HIT0487 Homo sapiens cDNA
3259	15871	28351	1.3	2.0E-49	N28446.1	EST_HUMAN	y23d08.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:262571 5'
3627	16230	28706	0.67	2.0E-49	AF026564.1	NT	Homo sapiens RNA binding protein II (RBMII) gene, complete cds
4918	17493	29945	0.67	2.0E-49	AI167357.1	EST_HUMAN	oz88d02.x1 Soares_senescent_fibroblasts_NBHSF Homo sapiens cDNA clone IMAGE:1682403 3' similar to gb-M31470 RAS-LIKE PROTEIN TC10 (HUMAN); contains Alu repetitive element; contains element MER22 repetitive element ;
4932	17507	26954	0.61	2.0E-49	BF511846.1	EST_HUMAN	UIH-B14-aps-d-02-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3088538 3'
6834	19424	32240	1.13	2.0E-49	AV717898.1	EST_HUMAN	AV717898 DCB Homo sapiens cDNA clone DCBALB01 5'
8043	20585		1.71	2.0E-49	M66033.1	EST_HUMAN	EST02558 Fetal brain, Striatum (cat#936206) Homo sapiens cDNA clone HFB CY50
12121	24929		1.81	2.0E-49	AF163864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
932	13545		9.12	1.0E-49	BF035327.1	EST_HUMAN	601458531 F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
1600	14192	28723	14.26	1.0E-49	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
1837	14425	26976	4.07	1.0E-49	BE255216.1	EST_HUMAN	601115769 F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3356273 5'
5562	18193	30840	8.31	1.0E-49	BF131007.1	EST_HUMAN	601820053 F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4052052 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6228	18837	31610	0.95	1.0E-49	H18291.1	EST_HUMAN	yn48h04.r1 Soares adult brain N2b5H1B55Y Homo sapiens cDNA clone IMAGE:171703 5' similar to SP:GBG1_HUMAN Q08447 GUANINE NUCLEOTIDE-BINDING PROTEIN G(T) GAMMA-1 SUBUNIT ;
6234	18843	31615	0.94	1.0E-49	AW964640.1	EST_HUMAN	EST376713 MAGC resequences, MAGH Homo sapiens cDNA
7275	19803	32661	3.31	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7275	19803	32662	3.31	1.0E-49	BE398110.1	EST_HUMAN	601290330F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620863 5'
7342	19869	32733	2.3	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta_8to9weeks_2Nbl-HP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
7342	19869	32734	2.3	1.0E-49	N25884.1	EST_HUMAN	yw78g12.s1 Soares placenta_8to9weeks_2Nbl-HP8to9W Homo sapiens cDNA clone IMAGE:258406 3' similar to gb:X65873 KINESIN HEAVY CHAIN (HUMAN);
8023	20565	33467	1.23	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8023	20565	33468	1.23	1.0E-49	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
8609	21148	34378	0.93	1.0E-49	8694184	NT	Homo sapiens RNA binding motif protein 7 (LOC51120), mRNA
8923	21461	34378	1.26	1.0E-49	BE409340.1	EST_HUMAN	60130092F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635398 5'
10033	22526	35523	1.26	1.0E-49	AL043129.2	EST_HUMAN	DKFZp343D2423_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp343D2423 5'
10927	23445	36466	2.28	1.0E-49	AV751477.1	EST_HUMAN	AV751477 NPD Homo sapiens cDNA clone NPDAWE04 5'
11190	23695	36744	3.48	1.0E-49	11427366	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11653	24081		1.39	1.0E-49	BE159343.1	EST_HUMAN	MR0-HT0407-010200-006-f02 HT0407 Homo sapiens cDNA
12015	24314		2.46	1.0E-49	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CERSR1), mRNA
6536	25117		0.88	9.0E-50	BE295758.1	EST_HUMAN	601176250F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531588 5'
181	12843	25927	2.91	8.0E-50	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
748	13368	25862	1.7	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
748	13368	25863	1.7	8.0E-50	X95097.2	NT	Homo sapiens mRNA for VIP receptor 2
1070	13675		6.91	8.0E-50	AF000573.1	NT	Homo sapiens homogenisate 1,2-dioxygenase gene, complete cds
1800	14390	26935	2.81	8.0E-50	4501890	NT	Homo sapiens actinin, alpha 1 (ACTN1) mRNA
2522	15086	27658	1	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2522	15086	27659	1	8.0E-50	7706394	NT	Homo sapiens p47 (LOC51874), mRNA
2723	15278	27645	0.98	8.0E-50	4826658	NT	Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA
4182	16772	29221	0.99	8.0E-50	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
647	13270	25748	0.97	7.0E-50	BE089591.1	EST_HUMAN	QV0-BT0703-280400-211-e08 BT0703 Homo sapiens cDNA
8880	19614	32448	0.94	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
6880	19614	32449	0.94	7.0E-50	BF091922.1	EST_HUMAN	RC8-TN0073-150900-011-A12 TN0073 Homo sapiens cDNA
7346	19672	32736	1.25	7.0E-50	AA627822.1	EST_HUMAN	nc95ae12.s1 NCI CGAP C99 Homo sapiens cDNA clone IMAGE:1148206 3' similar to gb:X66391 60S
10636	23168	36179	22.7	7.0E-50	AI872131.1	EST_HUMAN	RIBOSOMAL PROTEIN L6 (HUMAN);
							wm55g11.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4435	17021		0.62	6.0E-50	BE794381.1	EST_HUMAN	601589565F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
8155	20696		6.9	6.0E-50	BE044076.1	EST_HUMAN	h38h04.x1 NCL_CGAP_U1 Homo sapiens cDNA clone IMAGE:3039511 3' similar to contains MER29.b3
10694	23224	36237	5.53	6.0E-50	AA312079.1	EST_HUMAN	MER29 repetitive element ;
10694	23224	36238	5.53	6.0E-50	AA312079.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1829	14418	26966	0.98	5.0E-50	BF332938.1	EST_HUMAN	EST182775 Jurkat T-cells VI Homo sapiens cDNA 5' end
1829	14418	26967	0.98	5.0E-50	BF332938.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
9022	21559		4.65	5.0E-50	AA557683.1	EST_HUMAN	CM0-BT0792-300500-398-b05 BT0792 Homo sapiens cDNA
11619	24081	37125	1.57	5.0E-50	AA403053.1	EST_HUMAN	h45h10.s1 NCL_CGAP_P4 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.13 PTR5 repetitive element ;
950	13582		1.74	4.0E-50	AA601143.1	EST_HUMAN	262601.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726889 5' similar to TR:G1335769
7285	19813	32669	1.04	4.0E-50	BE087536.1	EST_HUMAN	G1335769 GAG-POL POLYPROTEIN ;
1982	14585		2.4	3.0E-50	M18048.1	NT	h54e09.s1 NCL_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1104520 3' similar to gb:X53741_mel
3338	15948	28424	0.78	3.0E-50	AA746142.1	EST_HUMAN	FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
3815	16415	28879	0.93	3.0E-50	AW755264.1	EST_HUMAN	QV1-BT0681-280300-127-112 BT0681 Homo sapiens cDNA
6862	19596	32427	1.45	3.0E-50		NT	Human endogenous retrovirus RTVL-H2
7640	20152	33036	4.41	3.0E-50	AF233436.2	NT	ab03f06.s1 NCL_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1322627 3'
7640	20152	33037	4.41	3.0E-50	AF233436.2	NT	CMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5 Cardiomyopathy associated gene 5
8518	21037	33980	0.73	3.0E-50	6601589	NT	Homo sapiens similar to serpin domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC63232), mRNA
9732	22230	35207	1.32	3.0E-50	AB046818.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
9741	22239	35220	0.98	3.0E-50	11418514	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP1a mRNA, complete cds
10412	22806	35903	0.67	3.0E-50	AB002297.1	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
10981	23495	38524	1.76	3.0E-50	11436955	NT	Homo sapiens mRNA for KIAA1598 protein, partial cds
11339	23037	36046	5.96	3.0E-50	AJ245621.1	NT	Homo sapiens t-complex 10 (a murine tcp homolog) (TCP10), mRNA
810	13427		9.29	2.0E-50	AF059086.1	NT	Human mRNA for KIAA0299 gene, partial cds
1118	13721	26233	4.82	2.0E-50	4557752	NT	Homo sapiens Gtb2-associated binder 2 (KIAA0571), mRNA
1492	14084	26825	3.56	2.0E-50	AF198303.1	NT	Homo sapiens CTL2 gene
3326	15936	28412	0.61	2.0E-50	AF111168.2	NT	Homo sapiens MHC class 1 region
						NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1) mRNA
						NT	Homo sapiens decorin D mRNA, complete cds, alternatively spliced
						NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds, and unknown genes

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4347	16934	29375	0.6	2.0E-50	D88424.1	NT	Mus musculus mRNA for high-sulfur keratin protein, partial cds
8258	20799	33716	1.24	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8258	20799	33717	1.24	2.0E-50	AB038162.1	NT	Homo sapiens TFF gene cluster for trefoil factor, complete cds
8393	20933	33854	9.32	2.0E-50	X08956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
8393	20933	33855	9.32	2.0E-50	X08956.1	NT	Human HALPHA44 gene for alpha-tubulin, exons 1-3
9799	22297	35281	2.89	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9799	22297	35282	2.89	2.0E-50	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
11512	23960		2.09	2.0E-50	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
487	13120	25606	1.56	1.0E-50	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
2403	14971		6.87	1.0E-50	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
10095	22690	35583	0.77	1.0E-50	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
6136	18750	31507	0.89	9.0E-51	AW511225.1	EST_HUMAN	hcd4e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912378 3' similar to TR:Q95636
6372	18976	31754	0.69	9.0E-51	AA744837.1	EST_HUMAN	Q95636 CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II.; ny87h03.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1283381 3'
8606	21145	34060	0.7	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
9248	21774	34725	1.16	9.0E-51	AA043738.1	EST_HUMAN	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
9420	21929	34875	0.52	9.0E-51	A1791154.1	EST_HUMAN	z651c09.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486352 5'
9420	21929	34876	0.52	9.0E-51	A1791154.1	EST_HUMAN	ab23g04.x5 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:841686 3' similar to
4532	17116	29581	2.81	8.0E-51	4503932	NT	SW:PSM_HUMAN Q04609 PROSTATE-SPECIFIC MEMBRANE ANTIGEN ;
4532	17116	29582	2.81	8.0E-51	4503932	NT	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
4687	17249	29702	13.1	8.0E-51	AA610842.1	EST_HUMAN	Homo sapiens glycine amidinotransferase (L-arginine:glycine amidinotransferase) (GATM) mRNA
5319	17881	30300	1.68	8.0E-51	AF092132.1	NT	np88e09.s1 NCI CGAP Lu11 Homo sapiens cDNA clone IMAGE:1142440 3' similar to gb:X12671_ma1
7648	20160	33047	2.06	8.0E-51	AU138590.1	EST_HUMAN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HUMAN);
9385	21808		0.99	8.0E-51	AU138590.1	EST_HUMAN	Homo sapiens PAK2 mRNA, complete cds
3051	15687	28145	0.72	7.0E-51	AW274720.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73/NY-CO-38) mRNA
3321	15931	28408	1.51	7.0E-51	AW889219.1	EST_HUMAN	AU138590 PLACE1 Homo sapiens cDNA clone PLACE1008887 5'
3408	16017	28496	0.76	7.0E-51	AW274720.1	EST_HUMAN	xn34e03.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340
4247	16835	29286	2.14	7.0E-51	AL079628.1	EST_HUMAN	QV4-NT0028-200400-160-405 NT0028 Homo sapiens cDNA xn34e03.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2695564 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN ;
							DKFZp434B2229_r1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434B2229 5'

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4247	16835	29287	2.14	7.0E-51	AL079628.1	EST_HUMAN	DKFZp434B2229_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2229 5'
4443	17029	29469	1.69	7.0E-51	AW295603.1	EST_HUMAN	U1-H-BW0-aiip-b-05-o-U1.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2729817 3'
11534	23982	37053	1.65	7.0E-51	AF161449.1	NT	Homo sapiens HSPC331 mRNA, partial cds
1575	14168	26699	17.64	6.0E-51	6878763	NT	Homo sapiens putative DNA binding protein (M96), mRNA
2022	14604	27169	5.19	6.0E-51	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
3520	16125	28605	17.1	6.0E-51	7657266	NT	Homo sapiens KIAA0928 protein Mx2 interacting nuclear target (MINT) homolog (KIAA0928), mRNA
4397	16982	29426	1.09	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
4397	16982	29427	1.09	6.0E-51	9910553	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
6142	18768	31514	57.08	6.0E-51	X01788.1	NT	Human hemoglobin related (Hpr) gene exon 3
6152	18765	31527	11.76	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
8152	18765	31528	11.76	6.0E-51	AF070083.1	NT	Homo sapiens mitogen-activated protein kinase kinase 1 (MKK4) gene, exon 4
8558	19592	32424	1.05	6.0E-51	4508736	NT	Homo sapiens ribosomal protein S8 kinase, 70kD, polypeptide 1 (RPS8KB1) mRNA
6972	19549	32373	0.71	6.0E-51	11416751	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
7044	18064	30454	2.22	6.0E-51	11429665	NT	Homo sapiens non-kinase Cdc42 effector protein SPEC2 (LOC56990), mRNA
9064	21801	34530	0.68	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9064	21801	34531	0.68	6.0E-51	11428525	NT	Homo sapiens hypothetical protein FLJ11042 (FLJ11042), mRNA
9601	22101	35064	1.79	6.0E-51	7661535	NT	Homo sapiens B9 protein (B9), mRNA
9677	22176	35151	1.35	6.0E-51	U50093.1	NT	Human ankyrin (ANK1) gene, exon 2
11136	23644	36684	1.83	6.0E-51	11528289	NT	Homo sapiens interleukin 17 receptor (IL17R), mRNA
11403	23854	36919	1.58	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
11403	23854	36920	1.58	6.0E-51	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
824	13441	25948	6.74	5.0E-51	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
836	13452	25962	1.36	5.0E-51	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
1028	15431	26153	1.01	5.0E-51	AL133204.1	NT	Novel human gene mapping to chromosome X
1651	14243	26777	0.99	5.0E-51	5031980	NT	Homo sapiens 26S proteasome-associated peptidyl homologue (POH1) mRNA
2629	15191	27759	9.09	5.0E-51	AJ007558.1	NT	Homo sapiens mRNA for nucleoporin 155
4017	16615	29088	1.21	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4017	16615	29089	1.21	5.0E-51	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5231	17795	30214	1.66	5.0E-51	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
11069	23581	36621	2.02	5.0E-51	BE01320.1	EST_HUMAN	7a41a02.x1 NCI_CGAP_G06 Homo sapiens cDNA clone IMAGE:3221258 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11160	23687	36712	4.75	5.0E-51	5803136	NT	Homo sapiens RNA binding motif protein 3 (RBM3), mRNA
140	12805	25294	15.49	3.0E-51	AI587348.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
1218	13818	26333	34.32	3.0E-51	AI587348.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
4420	17005	29448	2.04	3.0E-51	AL159142.1	NT	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2224720 3' similar to gb:M26326
							KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
							Novel human gene mapping to chromosome 22
7579	20095	32972	1.16	3.0E-51	R15914.1	EST_HUMAN	y647c08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:53233 5' similar to gb:M14123_cds4
8773	21312		6.15	3.0E-51	M29083.1	NT	RETROVIRUS-RELATED POL POLYPROTEIN (HUMAN); contains LTR5 repetitive element ;
8998	25124		0.6	3.0E-51	AW593777.1	EST_HUMAN	Human hnRNP C2 protein mRNA
12348	24529		2.15	3.0E-51	AF003528.1	NT	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA 5'
							Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat
							regions
389	13035	25524	2.03	2.0E-51	4507798	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman
717	13338	25824	0.94	2.0E-51	BE391063.1	EST_HUMAN	syndrome) (UBE3A) mRNA
717	13338	25825	0.94	2.0E-51	BE391063.1	EST_HUMAN	601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
							601285694F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607463 5'
1726	14317	26860	5.61	2.0E-51	AA233352.1	EST_HUMAN	z30a05.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:664880 5' similar
3795	16395	28860	2.71	2.0E-51	AI492415.1	EST_HUMAN	to TR:G233226 G233226 RTVL-H PROTEIN, contains LTR7 t3 LTR7 repetitive element ;
4592	17175	29621	1.73	2.0E-51	AW137828.1	EST_HUMAN	tr81c09.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2131732 3'
							U1H.B11-adj-4-02-0-J1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716851 3'
5630	18259	30730	0.76	2.0E-51	AI732851.1	EST_HUMAN	q334f08.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
							P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
5630	18259	30731	0.76	2.0E-51	AI732851.1	EST_HUMAN	q334f08.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE
6166	18778	31542	3.29	2.0E-51	BE782015.1	EST_HUMAN	P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
7350	19876		0.77	2.0E-51	AF216927.1	NT	601470448F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3873563 5'
7480	20002	32867	1	2.0E-51	7662349	NT	Homo sapiens diacylglycerol kinase (dGKI) gene, exon 23
8632	21171	34088	2.08	2.0E-51	BE901994.1	EST_HUMAN	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
8632	21171	34089	2.08	2.0E-51	BE901994.1	EST_HUMAN	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958613 5'
8964	21502	34424	0.95	2.0E-51	11037064	NT	601676787F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958613 5'
							Homo sapiens disrupted in schizophrenia 1 (DISC1), mRNA
9431	21957	34905	1.48	2.0E-51	AI917078.1	EST_HUMAN	ts74807.x1 NCI_CGAP_G08 Homo sapiens cDNA clone IMAGE:2236980 3' similar to SW:TRKC_HUMAN
9521	22021	34978	5.22	2.0E-51	BE165980.1	EST_HUMAN	Q16288 NT-3 GROWTH FACTOR RECEPTOR PRECURSOR ;
							MR3-HT0487-150200-113-g01 HT0487 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9537	22037	34997	0.61	2.0E-51	AB007926.1	NT	Homo sapiens mRNA for KIAA0457 protein, partial cds
10329	22823	35819	1.73	2.0E-51	AV682474.1	EST_HUMAN	AV682474 GKB Homo sapiens cDNA clone GKBAGF05 5'
10368	22862	35855	1.03	2.0E-51	AA378559.1	EST_HUMAN	EST91296 Synovial sarcoma Homo sapiens cDNA 5' end
11207	18259	30730	11.47	2.0E-51	A1732851.1	EST_HUMAN	ab34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
11207	18259	30731	11.47	2.0E-51	A1732851.1	EST_HUMAN	ab34f09.x5 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325609 3' similar to SW:NME1_MOUSE P35436 GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 1 PRECURSOR ;
12343	24524	30824	2.6	2.0E-51	11419159	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4), mRNA
119	12780	25272	27.93	1.0E-51	4503528	NT	Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1) mRNA
1541	14133		28.47	1.0E-51	AV742248.1	EST_HUMAN	AV742248 CB Homo sapiens cDNA clone GBFBGC12 5'
4498	17082	29531	1	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
4498	17082	29532	1	1.0E-51	4759071	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 15 (SCYA15) mRNA
5588	18219	30969	2.68	1.0E-51	T18962.1	EST_HUMAN	bt2056t Testis 1 Homo sapiens cDNA clone bt2056
7645	20157	33044	0.85	1.0E-51	A1572532.1	EST_HUMAN	tc39g02.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2089106 3'
7644	20386	33289	7	1.0E-51	BF434359.1	EST_HUMAN	766b02.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3544091 3' similar to TR:P87892 P87892 PROTEASE ;
11813	25129		3.01	1.0E-51	AV760590.1	EST_HUMAN	AV760590 MDS Homo sapiens cDNA clone MDSGBB02 5'
10568	23104	36118	1.71	9.0E-52	R91638.1	EST_HUMAN	yq10h04.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
10568	23104	36119	1.71	9.0E-52	R91638.1	EST_HUMAN	SP:YGAF_ECOLI_P37339 HYPOTHETICAL PROTEIN IN GABP 3'REGION ;
12105	24367		6.53	9.0E-52	AA777821.1	EST_HUMAN	z185a07.e1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196567 5' similar to contains THR13 THR repetitive element ;
163	12826	25313	8	8.0E-52	AA720574.1	EST_HUMAN	rw21g02.s1 NCI_CGAP_GCB0 Homo sapiens cDNA clone IMAGE:1241138 3' similar to contains THR13 THR repetitive element ;
1543	14135	26669	1.32	8.0E-52	X84900.1	NT	H. sapiens mRNA for laminin-5, alpha3b chain
1694	14286	26821	2.12	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
1694	14286	26822	2.12	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
4066	14286	26821	6.96	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4066	14286	26822	6.98	8.0E-52	11968028	NT	Homo sapiens hypothetical protein FLJ13556 similar to N-myc downstream regulated 3 (FLJ13556), mRNA
7526	20046	32815	1.8	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
7526	20046	32816	1.8	8.0E-52	11416585	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
8943	21481	34403	1.39	7.0E-52	W56471.1	EST_HUMAN	z559a06.t1 Soares_papillary_thyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:326578 5' similar to contains Alu repetitive element
1229	13828		0.85	6.0E-52	BE072409.1	EST_HUMAN	QV3-BT0537-271289-049-407 BT0537 Homo sapiens cDNA
1732	14323	26865	2.63	6.0E-52	AF109607.1	NT	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds
5902	18524	31249	2.12	6.0E-52	AI208794.1	EST_HUMAN	qg44f04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838047 3'
11086	23598	36635	1.83	6.0E-52	BE048172.1	EST_HUMAN	tz46h04.y1 NCL_CGAP_Bm52 Homo sapiens cDNA clone IMAGE:2291671 5' similar to SW:PGBM_MOUSE_Q05783 BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR;
4535	17119	29566	1.77	5.0E-52	Z77898.1	NT	H. sapiens flow-sorted chromosome 8 HindIII fragment, SC6pA18H7
1702	14295	26830	1.27	4.0E-52	AF257318.1	NT	Homo sapiens SH3-containing protein SH3GLB1 mRNA, complete cds
1823	14412	26957	1.35	4.0E-52	47588.43	NT	Homo sapiens nucleoporin 155kD (NUP155) mRNA
4000	16598	29070	0.62	4.0E-52	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4849	17427	29879	0.77	4.0E-52	AI766814.1	EST_HUMAN	wf89b02.x1 NCL_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400459 3'
5490	18124	30531	1.2	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
5490	18124	30532	1.2	4.0E-52	4506132	NT	Homo sapiens phosphoribosyl pyrophosphate synthetase-associated protein 2 (PRPSAP2) mRNA
7882	20524	33430	1.63	4.0E-52	BE622032.1	EST_HUMAN	601440687F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3915638 5'
8471	21011	33928	5.51	4.0E-52	11417035	NT	Homo sapiens hydroxysteroid (17-beta) dehydrogenase 4 (HSD17B4), mRNA
11933	24267		5.12	4.0E-52	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12458	24599		13.98	4.0E-52	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12601	24687		1.57	4.0E-52	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
4168	16767		12.28	3.0E-52	11437042	NT	Homo sapiens hypothetical protein FLJ10875 (FLJ10875), mRNA
588	13218	25694	4.18	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
588	13218	25695	4.18	2.0E-52	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1793	14383	26928	2.64	2.0E-52	AB007899.1	NT	Homo sapiens KIAA0439 mRNA, partial cds
2544	15108	27681	1.1	2.0E-52	BE207575.1	EST_HUMAN	bb66b07.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030421 5' similar to gb-X16493 M.musculus mRNA for Zpf-1 zinc finger protein (MOUSE);
2784	15318		5.55	2.0E-52	BF677892.1	EST_HUMAN	602084710F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248891 5'
5113	17685	30121	3.51	2.0E-52	AL137188.3	NT	Novel human gene mapping to chromosome 20, similar to membrane transporters
5881	18503	31228	3.32	2.0E-52	AW848041.1	EST_HUMAN	IL3-CT0214-231289-053-E12 CT0214 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6505	19105	31850	1.85	2.0E-52	11141868	NT	Homo sapiens interleukin 21 receptor (IL21R), mRNA
6814	19405	32221	0.89	2.0E-52	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7022	19556	32381	0.68	2.0E-52	AI792146.1	EST_HUMAN	os45d12.y6 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1608311 5'
8587	21126		10.89	2.0E-52	AF147880.1	NT	Macaca mulatta beta-tubulin mRNA, complete cds
8866	21405	34329	0.82	2.0E-52	AA778795.1	EST_HUMAN	z145g05.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453272 3'
9400	21823		1.25	2.0E-52	4758789	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme Q reductase) (NDUFS5) mRNA
10024	22519	35514	5.62	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10024	22519	35515	5.62	2.0E-52	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
11083	23595	36830	6.08	2.0E-52	AI831462.1	EST_HUMAN	w148c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11083	23595	36831	6.08	2.0E-52	AI831462.1	EST_HUMAN	w148c04.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2406150 3' similar to contains THR.b2 THR repetitive element;
11094	23606	36846	3.85	2.0E-52	AV715377.1	EST_HUMAN	AV715377 DCB Homo sapiens cDNA clone DCBAE03 5'
11231	23762		1.87	2.0E-52	W70260.1	EST_HUMAN	z149g12.11 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:344038 5'
11484	23933		3.4	2.0E-52	11417990	NT	Homo sapiens LIM domain kinase 2 (LIMK2), mRNA
11741	25099	30500	14.03	2.0E-52	AW236297.1	EST_HUMAN	xn72e07.x1 NCI_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2700036 3' similar to contains Alu repetitive element; contains element LTR2 repetitive element;
12154	24396		3.83	2.0E-52	AI808885.1	EST_HUMAN	w167d05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360649 3' similar to TR:Q16859
558	13189	25698	1.59	1.0E-52	AA634445.1	EST_HUMAN	Q16859 CARBOXYLESTERASE;
1414	14007	28535	11.81	1.0E-52	4504026	NT	z175h12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743879 3'
2573	15136		1.75	1.0E-52	4502238	NT	Homo sapiens glutamate-ammonia ligase (glutamine synthase) (GLUL) mRNA
3095	15710	28181	1.65	1.0E-52	S61070.1	NT	Homo sapiens arylsulfatase D (ARSD), transcript variant 1, mRNA
5538	18168	30582	4.84	1.0E-52	M29428.1	NT	pd=reverse transcriptase homodog (retroviral element) [human, endogenous retroviral element RTVL-Hp1, Genomic, 660 nt]
6527	19127	31921	2.18	1.0E-52	U38964.1	NT	Human P-glycoprotein (MDR1) gene, exon 4
7488	19981	32846	2.21	1.0E-52	X07292.1	NT	Human PMS2 related (hPMSR2) gene, complete cds
8401	20941		1.24	1.0E-52	AL163227.2	NT	Human aldolase C gene for fructose-1,6-bisphosphate aldolase
9116	21652	34583	0.61	1.0E-52	AF078779.1	NT	Homo sapiens chromosome 21 segment HS21C027
10469	22963		1.13	1.0E-52	AW020370.1	EST_HUMAN	Rattus norvegicus putative four repeat ion channel mRNA, complete cds
10479	22973		0.78	1.0E-52	AL163202.2	NT	d108g05.y1 Morton_Fetal_Cochlea Homo sapiens cDNA clone IMAGE:2483145 5'
10646	23178	38191	10.04	1.0E-52	U48296.1	NT	Homo sapiens protein tyrosine phosphatase PTPCAAX1 (hPTPCAAX1) mRNA, complete cds
10716	23244		2.37	1.0E-52	11426321	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 2 (PSMB2), mRNA

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Single Exon Probes Expressed in Fetal Liver

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3859	16457	28920	1.13	9.0E-53	4506064	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B) mRNA
5188	17751	30182	0.91	9.0E-53	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
11987	24297		3.79	7.0E-53	BF238465.1	EST_HUMAN	601904771F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4132793 5'
12432	24969		5.2	7.0E-53	AI421782.1	EST_HUMAN	t44f07.x1 NCL_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2096077 3' similar to contains THR.11 THR repetitive element;
4174	16765	29213	4.45	5.0E-53	4758543	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2) (HNRPC) mRNA
5364	17924	30338	1	5.0E-53	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
12035	24324		1.58	5.0E-53	AW813563.1	EST_HUMAN	RC3-ST0197-151099-011-g10 ST0197 Homo sapiens cDNA
53	12733	25200	1.15	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
53	12733	25201	1.15	4.0E-53	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
4947	17522	29964	0.99	4.0E-53	7705414	NT	Homo sapiens hook1 protein (HOOK1), mRNA
9337	21851		0.66	4.0E-53	AI613037.1	EST_HUMAN	906f04.x1 NCL_CGAP_UK3 Homo sapiens cDNA clone IMAGE:2278327 3'
9671	22170		0.71	4.0E-53	F13080.1	EST_HUMAN	HSC3D041 normalized infant brain cDNA Homo sapiens cDNA clone c-3id04
11091	23603	36842	3.98	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053977 5'
11091	23603	36843	3.98	4.0E-53	BF128701.1	EST_HUMAN	601810969F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4053977 5'
2684	15242	27810	2.09	3.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
3794	16394	28859	1.19	3.0E-53	AW050836.1	EST_HUMAN	w22c07.x1 Soares Dieckgraefe_colon_NHCD Homo sapiens cDNA clone IMAGE:2558796 3'
4691	17273	29721	0.85	3.0E-53	AW803563.1	EST_HUMAN	IL2-UM0081-240300-055-D03 UM0081 Homo sapiens cDNA
5616	18247	30698	0.99	3.0E-53	AF001212.1	NT	Homo sapiens 28S proteasome subunit 9 mRNA, complete cds
5808	18433	31154	0.91	3.0E-53	11526297	NT	Homo sapiens MIL1 protein (MIL1), mRNA
6341	18947	31724	0.89	3.0E-53	BE160025.1	EST_HUMAN	QV1-HT0412-280300-123-c04 HT0412 Homo sapiens cDNA
7155	19687	32530	0.92	3.0E-53	Y10388.3	NT	H. sapiens graf gene
7155	19687	32531	0.92	3.0E-53	Y10388.3	NT	H. sapiens graf gene
8246	20787	33706	10.03	3.0E-53	S72043.1	NT	GIF-growth inhibitory factor [human, brain, Genomic, 2015 nt]
8793	21332	34256	0.51	3.0E-53	10835090	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
8987	21525		7.06	3.0E-53	5901953	NT	Homo sapiens FGFR1 oncogene partner (FOP), mRNA
11867	24221		1.27	3.0E-53	11426423	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
483	13116		32.68	2.0E-53	AA366556.1	EST_HUMAN	EST77525 Pancreas tumor III Homo sapiens cDNA 5' end
2365	14936	27508	5.15	2.0E-53	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2574	15137		12.23	2.0E-53	4502316	NT	Homo sapiens ATPase, H ⁺ transporting, lysosomal (vacuolar proton pump) 31kD; Vacuolar proton-ATPase, subunit E; V-ATPase, subunit E (ATP6E), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2752	15307	27871	0.9	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1, cyclin D-related (CBFA2T1) mRNA
2752	15307	27872	0.9	2.0E-53	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1, cyclin D-related (CBFA2T1) mRNA
3255	15867	28347	0.85	2.0E-53	7705687	NT	Homo sapiens leucine aminopeptidase (LOC51056), mRNA
3282	15893	28372	0.67	2.0E-53	AF083822.1	NT	Homo sapiens dihydropyridine receptor alpha 2 subunit (CACNA2D1) gene, exon 6
4133	16725	29179	2.15	2.0E-53	M61873.1	NT	Human Krueppel-related DNA-binding protein (TF34) gene, partial cds
5619	18248	30699	3.27	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
5619	18248	30700	3.27	2.0E-53	BF334740.1	EST_HUMAN	PM1-CT0396-170800-001-g03 CT0396 Homo sapiens cDNA
7812	20355	33263	0.84	2.0E-53	AW975598.1	EST_HUMAN	EST387707 MAGE resequences, MAGN Homo sapiens cDNA
7949	20491		0.83	2.0E-53	AA085652.1	EST_HUMAN	IS429.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9326	21843		17.91	2.0E-53	AW245676.1	EST_HUMAN	2822665.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822665 5'
1495	14087	26627	1.88	1.0E-53	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
3456	16063	28538	1.4	1.0E-53	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region; section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
4220	16808	29256	0.67	1.0E-53	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
5099	17671	30110	1.08	1.0E-53	BE280386.1	EST_HUMAN	601176726F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531919 5'
6764	19385	32201	1.34	1.0E-53	BF364201.1	EST_HUMAN	CM4-NN1029-150800-543-e02 NN1029 Homo sapiens cDNA
7295	19823	32692	0.93	1.0E-53	BE012071.1	EST_HUMAN	RC5-BN1058-270400-031-D01 BN1058 Homo sapiens cDNA
7876	20418	33326	0.5	1.0E-53	AA249072.1	EST_HUMAN	II9571.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9018	21555	34483	15.04	1.0E-53	X78536.1	NT	H. sapiens mRNA for hnRNPcore protein A1
3290	15901	28381	0.57	9.0E-54	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5505	24743	30549	5.34	9.0E-54	4506788	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
221	12882	25367	3.54	8.0E-54	BE386785.1	EST_HUMAN	601272663F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614031 5'
1875	14461	27018	1.62	8.0E-54	4504610	NT	Homo sapiens insulin-like growth factor 2 receptor (IGF2R) mRNA
4841	17419	29871	0.6	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
4841	17419	29872	0.6	8.0E-54	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
6092	18708	31456	20.41	8.0E-54	6005700	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 8 (ABCAB8), mRNA
407	13082	25574	1.55	7.0E-54	AA812537.1	EST_HUMAN	ai79c12.s1 Soares_testes_NHT Homo sapiens cDNA clone 1377046 3' similar to contains MER30.13 MER30 repetitive element.
1870	14456	27013	2.37	7.0E-54	Y16845.1	NT	Homo sapiens mRNA for monocyte chemotactic protein-2
2246	14820	27395	5.06	7.0E-54	N27177.1	EST_HUMAN	yw68d12.a1 Soares_placenta_8to9weeks_ZNblHP8td9W Homo sapiens cDNA clone IMAGE:257399 3' similar to contains LTR7.b3 LTR7 repetitive element;
4694	17276		23.4	7.0E-54	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10034	22528	35524	2.32	7.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC63182), mRNA qb67g03.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1705204 3' similar to contains OFR.11 OFR repetitive element;
11171	23878		7.41	7.0E-54	AI160189.1	EST_HUMAN	Homo sapiens DNA for MICB, exon 4, 5 and partial cds
26	12705	25163	2.31	6.0E-54	AB003618.1	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
408	13083	25575	1.14	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
408	13083	25576	1.14	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
1917	14502	27058	1.44	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
1917	14502	27059	1.44	6.0E-54	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3322	15932	28409	1.06	6.0E-54	8922148	NT	Homo sapiens hypothetical protein DKFZp434M035 (DKFZp434M035), mRNA
4076	16672	29133	35.06	6.0E-54	4502872	NT	Homo sapiens chloride channel 6 (CLCN6) mRNA
4561	17144	29591	0.88	6.0E-54	AV754746.1	EST_HUMAN	AV754746 TP Homo sapiens cDNA clone TPGAAC10 5'
4989	17543	29885	1.07	6.0E-54	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5001	17574		1.81	6.0E-54	Y08846.1	NT	H. sapiens shc pseudogene, p86 isoform
5140	17574		2.28	6.0E-54	Y08846.1	NT	H. sapiens shc pseudogene, p86 isoform
11329	23027	36036	3.33	6.0E-54	AWB13567.1	EST_HUMAN	RC3-ST0197-151099-011-408 ST0197 Homo sapiens cDNA
2195	14771	27345	2.41	5.0E-54	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
195	12855		111.77	4.0E-54	AF110103.1	NT	Tupala belangeri beta-actin mRNA, partial cds
							EST1177696 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to glyceraldehyde-3-phosphate dehydrogenase
991	13603	26117	69.58	4.0E-54	AA306784.1	EST_HUMAN	Human mRNA for KIAA0077 gene, partial cds
1841	14429	26981	2.97	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
1841	14429	26982	2.97	4.0E-54	D38521.1	NT	Human mRNA for KIAA0077 gene, partial cds
							w428d11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2329269 3' similar to TR:O02711
3238	15850		1.45	4.0E-54	A1935086.1	EST_HUMAN	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
87	12773	25255	9.57	3.0E-54	AA313487.1	EST_HUMAN	EST185371 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
2804	15166	27733	0.97	3.0E-54	AL110383.1	EST_HUMAN	DKFZp434E0731_r1_434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434E0731 5'
6063	18680	31422	1.44	3.0E-54	4502434	NT	Homo sapiens BMX non-receptor tyrosine kinase (BMX) mRNA
7422	18946	32811	1.54	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
7422	18946	32812	1.54	3.0E-54	AA844061.1	EST_HUMAN	ai92c08.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1388270 3'
10964	23478	36504	4.52	3.0E-54	BF345600.1	EST_HUMAN	602019408F1 NCJ_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4155121 5'
							z70f12.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:72727 5' similar to TR:G191315
							G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN ;
11247	23777	36834	4.44	3.0E-54	AA393362.1	EST_HUMAN	EST366628 MAGC resequences, MAGC Homo sapiens cDNA
11844	24208	31040	2.75	3.0E-54	AW954559.1	EST_HUMAN	RC1-BT0313-131199-011-b09 BT0313 Homo sapiens cDNA
11855	25059		4.05	3.0E-54	AW748985.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
670	13284	25774	29.57	2.0E-54	5031900	NT	Homo sapiens killer cell lectin-like receptor subfamily G, member 1 (KLRG1), mRNA
1409	14002	28530	1.59	2.0E-54	4507164	NT	Homo sapiens nuclear antigen Sp100 (SP100) mRNA
1595	14188	28719	1.03	2.0E-54	AA555008.1	EST_HUMAN	nt78a09.s1 NCL CGAP_P-3 Homo sapiens cDNA clone IMAGE:1204600 similar to contains element L1 repetitive element
2577	15139	27709	0.88	2.0E-54	AW163175.1	EST_HUMAN	ai92903.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2763764 5' similar to SW: CUL1_HUMAN Q13616 CULLIN HOMOLOG 1
2635	15195	27768	1.29	2.0E-54	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2920	15537	28012	1.26	2.0E-54	AW057524.1	EST_HUMAN	wa00b12.x1 Soares NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2552927 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING
3602	16206		5.09	2.0E-54	AA532925.1	EST_HUMAN	nt45g09.s1 NCL CGAP_P-8 Homo sapiens cDNA clone IMAGE:995488 similar to gb:X53777 60S RIBOSOMAL PROTEIN L23 (HUMAN);
3915	16513	28975	0.82	2.0E-54	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
3915	16513	28976	0.82	2.0E-54	4506378	NT	Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP4K3), mRNA
4283	16869		2.42	2.0E-54	4502642	NT	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA
4536	17120		1.11	2.0E-54	AF208161.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4541	17125		3.09	2.0E-54	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5666	18293	30773	2.15	2.0E-54	4759089	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 14 (SCYA14) mRNA
5788	18413	31130	0.88	2.0E-54	BE047864.1	EST_HUMAN	tz43c11.y1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291348 5'
5935	18556	31284	3.66	2.0E-54	11426857	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
6022	18641	31381	11.65	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6022	18641	31382	11.65	2.0E-54	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6763	19356	32165	0.88	2.0E-54	AF008915.1	NT	Homo sapiens EVIS homolog mRNA, complete cds
7177	19709	32557	8.13	2.0E-54	11426544	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1), mRNA
9547	22047	35008	3.27	2.0E-54	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
9822	22418	35392	1.45	2.0E-54	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10028	22523	35519	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
10028	22523	35520	0.88	2.0E-54	11416762	NT	Homo sapiens serologically defined colon cancer antigen 10 (SDCCAG10), mRNA
11573	24020		3.33	2.0E-54	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
12368	24539	30903	2.87	2.0E-54	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
4564	17147		1.23	1.0E-54	BF315418.1	EST_HUMAN	601889230F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128535 5'
8964	21203	34121	0.64	1.0E-54	11417222	NT	Homo sapiens similar to nuclear factor related to kappa B binding protein (H. sapiens) (LOC83182), mRNA
10152	22647	35640	0.56	1.0E-54	AA412409.1	EST_HUMAN	zu10e09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10152	22647	35641	0.58	1.0E-54	AA412409.1	EST_HUMAN	zu10c09.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:731464 5'
12547	24652		3.58	1.0E-54	AU077341.1	EST_HUMAN	AU077341 Sugano cDNA library Homo sapiens cDNA clone Zv6C880 similar to 5'-end region of Human gamma-glutamyl transpeptidase mRNA, 5 end
10262	22757	35744	0.81	8.0E-55	BE081489.1	EST_HUMAN	QV2-BT0835-160400-143-h12 BT0835 Homo sapiens cDNA
1359	13953		0.91	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1362	13958		2.21	8.0E-55	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
11075	23587		2.49	8.0E-55	AW409714.1	EST_HUMAN	fr02a02.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960907 5'
1120	13723	26236	1.55	7.0E-55	R09348.1	EST_HUMAN	Y26e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127998 5' similar to SP:C561 BOVIN P10897 CYTOCHROME
8739	21278		1.75	7.0E-55	AW103839.1	EST_HUMAN	xd76c02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603522 3' similar to TR:060365 O60365 FOS39554 1.
9109	21645	34585	1.34	7.0E-55	AA889581.1	EST_HUMAN	ak28a11.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1407280 3'
9142	21677	34620	1.89	7.0E-55	AU139609.1	EST_HUMAN	AU139609 PLACE1 Homo sapiens cDNA clone PLACE1011576 5'
11087	23589	36636	14.07	7.0E-55	AI661056.1	EST_HUMAN	iq28f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
11087	23599	36637	14.07	7.0E-55	AI661056.1	EST_HUMAN	iq28f09.x1 NCL_CGAP_U11 Homo sapiens cDNA clone IMAGE:2210249 3'
12516	24885		9.8	7.0E-55	H23396.1	EST_HUMAN	ym57g07.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:52444 5'
11389	23841	36906	2.37	6.0E-55	AB040934.1	NT	Homo sapiens mRNA for KIAA1501 protein, partial cds
1806	14396	26940	1.13	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
1806	14396	26941	1.13	5.0E-55	AA704971.1	EST_HUMAN	z95b09.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462617 3'
6681	19257	32080	1.88	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6681	19257	32081	1.88	5.0E-55	4502240	NT	Homo sapiens arylsulfatase E (chondrodysplasia punctata 1) (ARSE), mRNA
6772	24769	32174	2.24	5.0E-55	4505952	NT	Homo sapiens paroxonase 2 (PON2) mRNA, and translated products
6772	24769	32175	2.24	5.0E-55	4505952	NT	Homo sapiens paroxonase 2 (PON2) mRNA, and translated products
7337	19864	32728	0.79	5.0E-55	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
7936	20478	33398	0.65	5.0E-55	11528491	NT	Homo sapiens BCL2-associated athanogene (BAG1), mRNA
8974	21512	34435	2.35	5.0E-55	4506302	NT	Homo sapiens protein tyrosine phosphatase, receptor type, alpha polypeptide (PTPRA) mRNA
9243	21769		1.89	5.0E-55	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
9950	22445	35425	1.55	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
9950	22445	35426	1.55	5.0E-55	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10122	22617	35608	0.93	5.0E-55	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
11925	24260		2.15	5.0E-55	11417972	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
59	15408	25209	1.97	4.0E-55	AW957994.1	EST_HUMAN	EST370064 IMAGE sequences, IMAGE Homo sapiens cDNA
700	13322	25809	41.63	4.0E-55	4826973	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1489	14082	26621	1.12	4.0E-55	7661713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1489	14082	26622	1.12	4.0E-55	7681713	NT	Homo sapiens predicted osteoblast protein (GS3786), mRNA
1561	14153		1.02	4.0E-55	BF061411.1	EST_HUMAN	7152b10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3390043 3' similar to contains L1.13 L1 repetitive element;
2071	14651	27222	1.47	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2071	14651	27223	1.47	4.0E-55	4506180	NT	Homo sapiens proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2) mRNA
2132	14710	27281	8.27	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG) mRNA
2132	14710	27282	8.27	4.0E-55	4503314	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG) mRNA
2349	14920	27495	1.84	4.0E-55	4507794	NT	Homo sapiens ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1) mRNA
3318	15928	28405	1.01	4.0E-55	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
8285	20826		7.61	4.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
11108	23618		4.93	4.0E-55	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
11845	24207		1.88	4.0E-55	BF303941.1	EST_HUMAN	60188657F2 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4120338 5'
6710	19304	32108	0.83	3.0E-55	AA077156.1	EST_HUMAN	7509A09 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7509A09
10224	22719	35709	0.48	3.0E-55	AF005273.1	NT	Sus scrofa domestica submaxillary apomucin mRNA, complete cds
11780	24167		6.76	3.0E-55	BE178519.1	EST_HUMAN	PM1-HT0603-090300-001-g08 HT0603 Homo sapiens cDNA
12563	24663		1.93	3.0E-55	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
400	13044	25535	2.16	2.0E-55	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
577	13207		2.15	2.0E-55	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
677	13301	25783	3.11	2.0E-55	4507206	NT	Homo sapiens syntaxin-binding protein 1 (STXBP1) mRNA, and translated products
2986	15602	28082	0.93	2.0E-55			Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
4888	17463	28917	2.37	2.0E-55	BE179888.1	EST_HUMAN	CM1-HT0876-150800-357-g03 HT0876 Homo sapiens cDNA
7515	24785	32802	0.67	2.0E-55	AW501988.1	EST_HUMAN	UI-HF-BN0-aks-f-06-0-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078275 5'
8995	21533	34462	0.46	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
8995	21533	34463	0.46	2.0E-55	BF224452.1	EST_HUMAN	hr76h08.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134463 3'
9087	21623		3.77	2.0E-55	A1002836.1	EST_HUMAN	am98h06.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684185 3' similar to contains THR b2 THR repetitive element;
9165	21700		0.7	2.0E-55	BE007859.1	EST_HUMAN	QV0-BN0147-280400-213-g08 BN0147 Homo sapiens cDNA
10144	22639	35620	0.47	2.0E-55	A439401.1	EST_HUMAN	q3h08.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2140479 3'
10828	23349	39365	2.22	2.0E-55	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
100	12776	25258	1.25	1.0E-55	4505080	NT	Homo sapiens mannose-6-phosphate receptor (cation dependent) (M6PR) mRNA
203	12864	25348	84.41	1.0E-55	U09823.1	NT	Oryzotegus cuniculus New Zealand white elongation factor 1 alpha (Rabelfa2) mRNA, complete cds
600	13228	25702	0.86	1.0E-55	AI026718.1	EST_HUMAN	ov65g09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1644160 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1189	13760	26301	6.18	1.0E-55	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1983	14575	27134	1.21	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
1993	14575	27135	1.21	1.0E-55	BE277861.1	EST_HUMAN	601120116F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967027 5'
2363	14834		2.58	1.0E-55	5803174	NT	Homo sapiens SMA3 (SMA3), mRNA
2376	15399	27519	1.04	1.0E-55	AF000990.1	NT	Homo sapiens testis-specific Testis Transcript Y 1 (TTY1) mRNA, partial cds
2568	15122	27691	10.31	1.0E-55	X13111.1	NT	Human mRNA for HLA-A11E, a MHC class I molecule (major histocompatibility complex)
2590	15152	27718	4.82	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2590	15152	27719	4.82	1.0E-55	AB007866.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
2642	15201	27774	1.88	1.0E-55	L54057.1	NT	Homo sapiens CLP mRNA, partial cds
4061	16658	29120	4.09	1.0E-55	AL163267.2	NT	Homo sapiens chromosome 21 segment HS21C067
4382	16996	29417	1.24	1.0E-55	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4837	17415		1.17	1.0E-55	N77261.1	EST_HUMAN	Y44G03.r1 Soares fetal liver spleen 1NF5 Homo sapiens cDNA clone IMAGE:245620 5'
4954	17529	29970	1.61	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
4954	17529	29971	1.61	1.0E-55	AB037163.1	NT	Homo sapiens DSCR5b mRNA, complete cds
5311	17873	30295	1.03	1.0E-55	8923125	NT	Homo sapiens hypothetical protein FLJ20126 (FLJ20126), mRNA
5689	18315	30814	8.13	1.0E-55	AF119856.1	NT	Homo sapiens PRO1851 mRNA, complete cds
6417	18020	31804	7.22	1.0E-55	11433046	NT	Homo sapiens PRO1851 mRNA, complete cds
6417	18020	31805	7.22	1.0E-55	11433046	NT	Homo sapiens PRO1851 mRNA, complete cds
7930	20472	33381	2.11	1.0E-55	11432994	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7930	20472	33382	2.11	1.0E-55	11432994	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
8026	20568	33471	0.97	1.0E-55	AF224492.1	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
8026	20568	33472	0.97	1.0E-55	AF224492.1	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
10791	23314	36322	4.95	1.0E-55	AL163210.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
10791	23314	36323	4.95	1.0E-55	AL163210.2	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11322	23020	36029	2.23	1.0E-55	U50950.1	NT	Homo sapiens phospholipid scramblase 1 gene, complete cds
11342	23040	36049	1.68	1.0E-55	T10045.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C010
11448	23898	36964	1.81	1.0E-55	10567821	NT	Human infant brain unknown product mRNA, complete cds
7401	19926	32791	1.97	9.0E-56	BE378074.1	EST_HUMAN	seq1575 b4HB3MA Cdb-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-F61 5' similar to similar to Chinese Hamster DHFR-coamplified protein mRNA
2761	15316	27882	3.95	7.0E-56	H10934.1	EST_HUMAN	Homo sapiens DNA-binding protein (LOC56242), mRNA
7636	20148	33031	2.11	7.0E-56	AW361213.1	EST_HUMAN	Homo sapiens DNA-binding protein (LOC56242), mRNA
7636	20148	33032	2.11	7.0E-56	AW361213.1	EST_HUMAN	Homo sapiens DNA-binding protein (LOC56242), mRNA
1730	14321	26863	1.59	5.0E-56	AW897712.1	EST_HUMAN	Y62903.r1 Soares adult brain N2b5HB55Y Homo sapiens cDNA clone IMAGE:173044 5' similar to contains THR repetitive element

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9088	21624	34559	0.8	5.0E-56	AW015507.1	EST_HUMAN	UI-H-B10p-eau-e-05-0-J1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2710544 3'
10289	22784		1.35	5.0E-56	W28189.1	EST_HUMAN	43c5 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
12020	25048	30509	3.74	5.0E-56	H55099.1	EST_HUMAN	CHR220038 Chromosome 22 exon Homo sapiens cDNA clone C22_55 5'
30	12709	25166	22.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
30	12709	25167	22.23	4.0E-56	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
2733	15288	27855	7.6	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2733	15288	27856	7.6	4.0E-56	4507728	NT	Homo sapiens tubulin, beta polypeptide (TUBB) mRNA
2838	13183	25861	3.4	4.0E-56	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
8405	19008	31789	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BMD31 mRNA, complete cds
8405	19008	31790	5.85	4.0E-56	AF217508.1	NT	Homo sapiens uncharacterized bone marrow protein BMD31 mRNA, complete cds
10400	22894	35889	1.2	4.0E-56	AF043349.1	EST_HUMAN	Homo sapiens lymphocyte-specific protein 1 (LSP1) gene, LSP1-7 allele, partial cds
10803	23326	36335	8.31	4.0E-56	A1498068.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
10803	23326	36336	8.31	4.0E-56	A1498068.1	EST_HUMAN	tm65g12.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2163048 3'
1386	13880	26507	2.12	3.0E-56	8824023	NT	Homo sapiens hypothetical protein PRO1304 (PRO1304), mRNA
1801	14391	26936	4.33	3.0E-56	6912743	NT	Homo sapiens 5'-3' exonuclease 2 (XRN2), mRNA
3159	15773	28240	1.88	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3159	15773	28241	1.88	3.0E-56	AA325826.1	EST_HUMAN	EST28889 Cerebellum II Homo sapiens cDNA 5' end
3803	16502	29061	2.38	3.0E-56	AF050066.1	NT	Homo sapiens VHC class 1 region
3803	16502	29061	2.38	3.0E-56	AF050066.1	NT	Homo sapiens VHC class 1 region
4477	17062	29512	0.82	3.0E-56	7657042	EST_HUMAN	601310203F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631848 5'
4515	17089	29546	5.15	3.0E-56	AL163268.2	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
4873	17255	29707	2.57	3.0E-56	5902085	NT	Homo sapiens chromosome 21 segment HS21C068
4925	17500		1.14	3.0E-56	BE893572.1	EST_HUMAN	Homo sapiens superkiller viralicidic activity 2 (S. cerevisiae homolog)-like (SKIV2L), mRNA
5280	17842	30269	0.6	3.0E-56	6912593	NT	601438154F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3923100 5'
5346	17842	30269	0.59	3.0E-56	6912593	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
5863	18485	31208	1.4	3.0E-56	4759163	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
5863	18485	31209	1.4	3.0E-56	4759163	NT	Homo sapiens phosphatidylinositol transfer protein, beta (PITPNB), mRNA
6956	19533	32358	6.22	3.0E-56	11421124	NT	Homo sapiens sparc/osteonectin, cvcv and kazal-like domains proteoglycan (testican) (SPOCK) mRNA
8750	21289	34209	5.2	3.0E-56	11418704	NT	Homo sapiens lysosomal-associated membrane protein 2 (LAMP2), mRNA
9727	22225	35202	0.86	3.0E-56	D63479.2	NT	Homo sapiens bone morphogenetic protein 5 (BMP5), mRNA
10375	22869	35862	1.63	3.0E-56	11434956	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
							Homo sapiens KIAA0317 gene product (KIAA0317), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11194	23699	36749	6.31	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11194	23699	36750	6.31	3.0E-56	5902013	NT	Homo sapiens nuclear pore complex interacting protein (NPIP), mRNA
11883	24230	31002	1.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
11883	24230	31003	1.3	3.0E-56	11434876	NT	Homo sapiens caveolin 3 (CAV3), mRNA
550	13181		2.35	2.0E-56	AA198818.1	EST_HUMAN	zq52a08.s1 Stratiene neuroepithelium (#37231) Homo sapiens cDNA clone IMAGE:645208 3'
762	15424	25878	1.37	2.0E-56	BE064396.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
762	15424	25879	1.37	2.0E-56	BE064396.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
2426	14994	27567	1.32	2.0E-56	M26081.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
2426	14994	27568	1.32	2.0E-56	M26081.1	NT	Human cGMP phosphodiesterase alpha subunit (CGPR-A) mRNA, complete cds
3017	15633	28110	1.33	2.0E-56	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3358	15966		1.2	2.0E-56	AB009681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3566	16190	28674	1.34	2.0E-56	AV703184.1	EST_HUMAN	AV703184 ADB Homo sapiens cDNA clone ADBCFG10 5'
7147	19680	32521	1.9	2.0E-56	5730038	NT	Homo sapiens SET domain and mannan transposase fusion gene (SETMAR) mRNA
1016	13626		12.77	1.0E-56	AF190930.1	NT	Macaca fascicularis protein tyrosine phosphatase (PRL-1) mRNA, complete cds
3737	16338	28803	1.67	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
3737	16338	28804	1.67	1.0E-56	AW589833.1	EST_HUMAN	hg23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2946452 3'
9886	22363		0.71	1.0E-56	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
9961	22456	35439	1.57	1.0E-56	AW845987.1	EST_HUMAN	RC2-CT0163-220999-001-E02 CT0163 Homo sapiens cDNA
653	13276		1.74	9.0E-57	AW860885.1	EST_HUMAN	QV0-OT0033-070300-152-h03 OT0033 Homo sapiens cDNA
11099	23609	36649	1.92	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11099	23609	36650	1.92	9.0E-57	AF228497.1	NT	Homo sapiens serine protease 17 (KLK4) gene, complete cds
11397	23849	36915	2.01	9.0E-57	AB020981.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
15	12694	25150	0.98	8.0E-57	8923349	NT	Homo sapiens mRNA for cyclin B2, complete cds
319	12973	25482	2.71	8.0E-57	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
917	13530	26048	8.64	8.0E-57	AW264599.1	EST_HUMAN	xt05d10.x1 NCI_CGAP_Bm63 Homo sapiens cDNA clone IMAGE:2759251 3' similar to gb:U05875
1852	14440	26997	1.52	8.0E-57	AA496109.1	EST_HUMAN	INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (HUMAN);
3428	16036	28516	1	8.0E-57	4758279	NT	z51b12.r1 Soares_testis NHT Homo sapiens cDNA clone IMAGE:757161 5'
3428	16036	28517	1	8.0E-57	4758279	NT	Homo sapiens EPHA4 (EPHA4) mRNA
5187	17762	30183	0.6	8.0E-57	BE296916.1	EST_HUMAN	Homo sapiens EPHA4 (EPHA4) mRNA
5450	24958	30631	3.17	8.0E-57	11418185	NT	60094440F-1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960864 5'
6590	19187	31989	12.5	8.0E-57	AB023177.1	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
6590	19187	31990	12.5	8.0E-57	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7729	20237	33128	2.72	8.0E-57	AB020644.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7728	20237	33128	2.72	8.0E-57	AB020844.1	NT	Homo sapiens mRNA for KIAA0837 protein, partial cds
11351	12684	25150	3.59	8.0E-57	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
12271	24477	30896	1.41	8.0E-57	11545732	NT	Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
1261	13858	26375	1.16	7.0E-57	AJ003100.1	NT	Homo sapiens GYS2 gene, exon 14
3287	15898	28376	1.08	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3287	15898	28377	1.08	7.0E-57	7242158	NT	Homo sapiens NME7 (NME7), mRNA
3309	15920	28397	1	7.0E-57	6005978	NT	Homo sapiens Kruppel-like factor 8 (KLF8), mRNA
3946	16544	29011	2.3	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
3946	16544	29012	2.3	7.0E-57	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
4524	17108		1.08	7.0E-57	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHIT) gene, exon 5
12634	24092		5.12	5.0E-57	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region, segment 1/2
3817	16417	28880	1.68	4.0E-57	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
837	13453	25983	1.03	3.0E-57	4507768	NT	Homo sapiens ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome) (UBE3A) mRNA
1376	13969		39.52	3.0E-57	AA230279.1	EST_HUMAN	nc1307.s1 NCJ_CGAP_P1 Homo sapiens cDNA clone IMAGE:1008037 similar to SW:RS10_HUMAN
2434	15001	27573	1.01	3.0E-57	AA348335.1	EST_HUMAN	P46783.40S RIBOSOMAL PROTEIN S10.
2727	15282	27849	0.93	3.0E-57	BE676822.1	EST_HUMAN	EST54770 Hippocampus II Homo sapiens cDNA 5' end
							783b10.x1 NCJ_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
							CE20263
							783b10.x1 NCJ_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3296443 3' similar to WP:Y47H9C.2
							CE20263
2727	15282	27850	0.93	3.0E-57	BE676822.1	EST_HUMAN	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cln) gene, complete cds
3618	16221	28699	0.93	3.0E-57	AF232708.1	NT	
3760	16381		60.31	3.0E-57	AW853984.1	EST_HUMAN	RC3-CT0254-110300-027-d10 CT0254 Homo sapiens cDNA
6180	16790	31559	1.34	3.0E-57	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6272	18880	31848	3.17	3.0E-57	BE786537.1	EST_HUMAN	80158989F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
8087	20628	33542	3.09	3.0E-57	W28130.1	EST_HUMAN	4268 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
8111	20652	33560	2.27	3.0E-57	11545768	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8111	20652	33561	2.27	3.0E-57	11545768	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
8223	20784	33681	0.61	3.0E-57	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
8368	20908	33827	1.18	3.0E-57	J05262.1	NT	Human farnesyl pyrophosphate synthetase mRNA, complete cds
8792	21331	34255	4.05	3.0E-57	AU117659.1	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
9174	21751	34698	0.63	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor.
9174	21751	34697	0.63	3.0E-57	11545798	NT	Homo sapiens hypothetical protein FLJ11656 (FLJ11656), mRNA
10787	23311	36318	3.02	3.0E-57	AW248374.1	EST_HUMAN	2820473.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820473 5'
11890	25066	30513	7.99	3.0E-57	W23871.1	EST_HUMAN	zb45d11.r1 Soares, fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306549 5'
12272	24962		1.69	3.0E-57	AW178575.1	EST_HUMAN	RC0-HT0112-080969-001-C06 HT0112 Homo sapiens cDNA
1480	14073	26612	0.88	2.0E-57	AI478904.1	EST_HUMAN	tm25c10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157618 3' similar to contains Alu repetitive element;
1548	14140	26673	0.86	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1548	14140	26674	0.86	2.0E-57	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
2444	15011	27583	1.15	2.0E-57	BE172526.1	EST_HUMAN	MIR0-HT0559-010400-009-h10 HT0559 Homo sapiens cDNA
2756	15311	27877	4.79	2.0E-57	AA845419.1	EST_HUMAN	ak02b02.s1 Soares_parathyroid_tumor_NbHPA Homo sapiens cDNA clone IMAGE:1404747 3' similar to contains Alu repetitive element; contains element MER22 repetitive element;
3486	16091		2.28	2.0E-57	AL183204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3605	16209	28688	0.71	2.0E-57	R07702.1	EST_HUMAN	ye8h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
3605	16209	28689	0.71	2.0E-57	R07702.1	EST_HUMAN	ye8h01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125809 5'
4004	16602	29076	0.62	2.0E-57	BE073264.1	EST_HUMAN	MIR0-BT0551-060300-103-b03 BT0551 Homo sapiens cDNA
4608	17191	29637	8.02	2.0E-57	AL183283.2	NT	Homo sapiens chromosome 21 segment HS21C083
5849	18473		1.57	2.0E-57	AA016131.1	EST_HUMAN	za31c06.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360584 5' similar to contains L1.t3 L1 repetitive element;
6184	18794		29.73	2.0E-57	BF115266.1	EST_HUMAN	7n80f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3570986 3' similar to contains TAR1.t1
6307	18914	31688	0.73	2.0E-57	11431281	NT	MER22 repetitive element;
8566	21105	34024	1.22	2.0E-57	AF045452.1	NT	Homo sapiens small inducible cytokine subfamily A (Cys-Cys), member 22 (SCYA22), mRNA
9760	22258	35241	2.55	2.0E-57	AF057722.1	NT	Homo sapiens cell-line KG1 transcriptional regulatory protein p54 mRNA, complete cds
11150	23658	36701	2.05	2.0E-57	11424084	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exons 3 and 4
11150	23658	36702	2.05	2.0E-57	11424084	NT	Homo sapiens hypothetical protein FLJ20041 (FLJ20041), mRNA
11192	23697	36746	1.84	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
11192	23697	36747	1.84	2.0E-57	AJ245503.1	NT	Homo sapiens partial mRNA for PEX5 related protein
8626	21165		3.5	1.0E-57	BE043031.1	EST_HUMAN	hc32a08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3039062 3' similar to TR:000246 O00246 HYPOTHETICAL 9.3 KD PROTEIN;
12049	24333		6.35	1.0E-57	AW470791.1	EST_HUMAN	ha33d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875499 3' similar to contains THR.b3 THR repetitive element;
5857	18480	31203	1.02	9.0E-58	AA297847.1	EST_HUMAN	EST11348 Uterus Homo sapiens cDNA 5' end
12335	24518	30922	2.62	9.0E-58	BE395081.1	EST_HUMAN	601309465F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631000 5'
615	13242		3.87	8.0E-58	BE868715.1	EST_HUMAN	601445948F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850211 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
682	13306	25789	3.77	8.0E-58	AI798376.1	EST_HUMAN	t34507.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
682	13306	25790	3.77	8.0E-58	AI798376.1	EST_HUMAN	t34507.x1 NCL CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2220181 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ;
1897	14482	27041	2.82	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
1897	14482	27042	2.82	8.0E-58	11434921	NT	Homo sapiens putative protein O-mannosyltransferase (POMT2), mRNA
3003	15619		2.94	8.0E-58	7706132	NT	Homo sapiens DHHC1 protein (LOC51304), mRNA
10735	23260		6.42	7.0E-58	6174542	NT	Homo sapiens MADS box transcription enhancer factor 2, polypeptide B (myocyte enhancer factor 2B) (MEF2B) mRNA
10809	23332	36344	3.77	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-all-g-10-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
10809	23332	36345	3.77	7.0E-58	AW504109.1	EST_HUMAN	UI-HF-BNO-all-g-10-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079867 5'
2414	14982	27558	3.39	6.0E-58	AU130689.1	EST_HUMAN	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
2926	15542	28017	1.26	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
2926	15542	28018	1.26	6.0E-58	BE242150.1	EST_HUMAN	TCAAP1E1219 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1219
6318	18925	31702	1.15	6.0E-58	AF106911.1	NT	Homo sapiens chemokine MIP-2 gamma (MIP-2 gamma) mRNA, complete cds
10211	22706	35700	0.99	6.0E-58	11434746	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type 21 (PTPN21), mRNA
12150	24393		1.87	6.0E-58	11526291	NT	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
322	12978	25484	3.26	5.0E-58	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
739	13359	25853	5.81	5.0E-58	BE763984.1	EST_HUMAN	RC4-NT0057-160600-016-b05 NT0057 Homo sapiens cDNA
1236	13835	26350	3.59	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1236	13835	26351	3.59	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1237	13835	26350	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
1237	13835	26351	2.7	5.0E-58	AW797948.1	EST_HUMAN	CM3-UM0043-240300-127-e07 UM0043 Homo sapiens cDNA
3365	15973	28450	4.17	5.0E-58	AA988183.1	EST_HUMAN	cr98607.s1 NCL CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1603908 3'
4345	16932	28373	0.78	5.0E-58	AI638745.1	EST_HUMAN	ts89607.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2239468 3' similar to SW:PRO2_AACA
5105	17677		1.12	5.0E-58	AW849834.1	EST_HUMAN	P19984 PROFILIN II ;
5811	18435		2.08	5.0E-58	11496282	NT	IL3-CT0214-080300-081-F06 CT0214 Homo sapiens cDNA
6325	18931	31707	5.73	5.0E-58	H23072.2	EST_HUMAN	Homo sapiens placenta-specific 1 (PLAC1), mRNA
6528	19128	31922	0.87	5.0E-58	AI163265.2	NT	ym51h07.r1 Soares Infant brain 1NIB Homo sapiens cDNA clone IMAGE:52071 5'
6597	19194	31999	1.24	5.0E-58	11421330	NT	Homo sapiens chromosome 21 segment HS21C085
7161	19693	32539	0.72	5.0E-58	4885400	NT	Homo sapiens apical protein, Xenopus laevis-like (APXL), mRNA
							Homo sapiens holocytochrome c synthase (cytochrome c heme-lyase) (HCCS) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7910	20452	33359	9.67	5.0E-58	8922693	NT	Homo sapiens hypothetical protein FLJ10826 (FLJ10826), mRNA
8294	20835	33757	0.74	5.0E-58	AB046837.1	NT	Homo sapiens mRNA for KIAA1617 protein, partial cds
9263	21789	34739	0.72	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNA568PL) mRNA
9263	21789	34740	0.72	5.0E-58	5231227	NT	Homo sapiens ribonuclease 6 precursor (RNA568PL) mRNA
9771	22269	35253	0.74	5.0E-58	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Prp18 (PRP18), mRNA
10030	22525	35521	1.39	5.0E-58	AL103218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10300	22794	35784	0.59	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
10300	22794	35785	0.59	5.0E-58	AB014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
11859	24987		6.17	5.0E-58	11526293	NT	Homo sapiens cat eye syndrome chromosome region, candidate 1 (CECR1), mRNA
12331	25016		1.81	5.0E-58	11428423	NT	Homo sapiens acyl-Coenzyme A carboxylase alpha (ACACA), mRNA
12577	24673		1.34	5.0E-58	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
12653	24725	30853	1.37	5.0E-58	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12653	24725	30854	1.37	5.0E-58	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
396	13042	25532		4.0E-58	4502302	NT	Homo sapiens ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin sensitivity conferring protein) (ATP5O) mRNA
828	13446	25953	1.76	4.0E-58	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
1517	14109	26845	1.86	4.0E-58	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2611	15173	27741	1.13	4.0E-58	AF265555.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
2660	15219	27790	1.75	4.0E-58	U36251.1	NT	Homo sapiens ubiquitin-conjugating BIR-domain enzyme APOLLON mRNA, complete cds
3367	15975	28452	1.62	4.0E-58	D16470.1	NT	Human mRNA, Xq terminal portion
3803	16403	28867	1.26	4.0E-58	5031660	NT	Homo sapiens EGF-like repeats and discoidin-like domains 3 (EDIL3), mRNA
11221	23724	36779	0.92	4.0E-58	11424059	NT	Homo sapiens E1B-55kDa-associated protein 5 (E1B-AP5), mRNA
337	13006		1.77	3.0E-58	R17879.1	EST_HUMAN	Yg10e02.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
1433	14026	26554	2.23	3.0E-58	4758981	NT	Homo sapiens peptide YY (PYY) mRNA
3059	15675		0.73	3.0E-58	R17879.1	EST_HUMAN	Yg10e02.1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:31693 5'
3212	15824	28300	3.1	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
3212	15824	28301	3.1	3.0E-58	BF569848.1	EST_HUMAN	602185789F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4309943 5'
6407	19010	31792	0.72	3.0E-58	BE089508.1	EST_HUMAN	QV0-B10702-170400-194-409 B10702 Homo sapiens cDNA
6572	19170	31867	0.98	3.0E-58	F07056.1	EST_HUMAN	HSC1T G081 normalized infant brain cDNA Homo sapiens cDNA clone c-1908
6751	19344	32151	1.25	3.0E-58	AV712977.1	EST_HUMAN	AV712877 DCA Homo sapiens cDNA clone DCAAZG04 5'
976	13588	26103	8.92	2.0E-58	AF069824.1	NT	Homo sapiens 5-aminolevulinic synthase 2 (ALAS2) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1333	13927		30.8	2.0E-58	BE208532.1	EST_HUMAN	ba08b07.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823733 5' similar to gb:X69391.60S RIBOSOMAL PROTEIN L6 (HUMAN); gb:X81987.M.musculus mRNA for TAX responsive element binding protein (MOUSE);
5539	18171	30586	0.75	2.0E-58	AW074831.1	EST_HUMAN	xa08a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567704 3'
5560	24746	30607	4.01	2.0E-58	BE907186.1	EST_HUMAN	601499981F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
5560	24745	30637	4.01	2.0E-58	BE907186.1	EST_HUMAN	601499981F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901911 5'
6207	18817	31588	1.26	2.0E-58	BF513488.1	EST_HUMAN	UJ-H-BW1-ams-g-11-0-UJ.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071060 3'
6270	18878	31646	2.1	2.0E-58	AI124874.1	EST_HUMAN	am57e02.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539674 3' similar to WP:ZK328.1 CE05065 UBIQUITIN CONJUGATING ENZYME; RECOVERIN SUBFAMILY OF EF-HAND CALCIUM BINDING PROTEIN;
6302	18909	31691	0.89	2.0E-58	R92567.1	EST_HUMAN	yq08h06.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:196379 5'
7006	19504	32323	1	2.0E-58	AI291407.1	EST_HUMAN	qm84c01.x1 NCL_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1895424 3'
7210	19741	32594	2.91	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
7210	19741	32595	2.91	2.0E-58	AF134838.1	NT	Homo sapiens endocytic receptor Endo180 (ENDO180) mRNA, complete cds
10620	23152	36184	19.73	2.0E-58	BF307745.1	EST_HUMAN	601890812F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131891 5'
10844	23365	36381	2.67	2.0E-58	AW872641.1	EST_HUMAN	hm25f08.x1 NCL_CGAP_Thy4 Homo sapiens cDNA clone IMAGE:3013671 3'
751	13371	25865	4.83	1.0E-58	M65134.1	NT	Human complement component C5 mRNA, 3'end
1106	13710	26219	5.91	1.0E-58	6274549	NT	Homo sapiens NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9 (22kD, B22) (NDUFB9), mRNA
1372	13966	26492	1.24	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences; MAGD Homo sapiens cDNA
1372	13966	26493	1.24	1.0E-58	AW957182.1	EST_HUMAN	EST369252 MAGE resequences; MAGD Homo sapiens cDNA
1440	14033	26581	2.04	1.0E-58	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1704	14297	26834	0.9	1.0E-58	BE486132.1	EST_HUMAN	hy10f08.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3198935 3'
2828	15380	27950	1.17	1.0E-58	4759169	NT	Homo sapiens steroid regulatory element binding transcription factor 2 (SREBF2) mRNA
3590	16194	28679	0.62	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3590	16194	28680	0.62	1.0E-58	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
3783	16383	28848	0.57	1.0E-58	4507828	NT	Homo sapiens transition protein 1 (during histone to protamine replacement) (TNP1) mRNA
5106	17678	30117	6.84	1.0E-58	AI141063.1	EST_HUMAN	oz43h01.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1678129 3'
6007	18627	31382	1.2	1.0E-58	BE061880.1	EST_HUMAN	RC1-BT0254-280100-016-e01 BT0254 Homo sapiens cDNA
6946	19523	32345	0.73	1.0E-58	11422031	NT	Homo sapiens hypothetical protein (LOC51280), mRNA
8803	21342	34268	0.7	1.0E-58	4505314	NT	Homo sapiens myomesin (M-protein) 2 (165kD) (MYOM2), mRNA
8912	21450	34371	0.83	1.0E-58	AV751001.1	EST_HUMAN	AV751001 NPC Homo sapiens cDNA clone NPCACH09 5'
9010	21547	34475	0.65	1.0E-58	AA412397.1	EST_HUMAN	289705.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'
9010	21547	34476	0.65	1.0E-58	AA412397.1	EST_HUMAN	289705.r1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:730497 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10089	22584	35577	0.55	1.0E-58	11432984	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2), mRNA
11610	24053		5.43	1.0E-58	X63392.1	NT	H. sapiens immunoglobulin kappa light chain variable region L14
2273	14847	27423	16.05	8.0E-59	4507378	NT	Homo sapiens TATA box binding protein (TBP) mRNA
8121	20662	33572	2.08	8.0E-59	AI761983.1	EST_HUMAN	wh50406.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384171 3'
190	15409		2.18	6.0E-59	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3662088 5'
8188	20729	33641	0.58	6.0E-59	AI750970.1	EST_HUMAN	cn06h02.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06h02 random
1790	14380	26924	1.32	5.0E-59	AW157281.1	EST_HUMAN	au63h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
1790	14380	26925	1.32	5.0E-59	AW157281.1	EST_HUMAN	TR-075786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
3161	15775	28243	7.81	5.0E-59	AI807484.1	EST_HUMAN	au63h05.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783865 3' similar to
4762	17343	26791	4.42	5.0E-59	X63497.1	NT	TR-075786 O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1.;
5896	18509	31235	0.81	5.0E-59	6005698	NT	Wf49c11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2358836 3'
7064	18083	30440	8.32	5.0E-59	AW162304.1	EST_HUMAN	H. sapiens DNA for ZNF80-linked ERV9 long terminal repeat
8741	21280	34203	1.35	5.0E-59	11421778	NT	Homo sapiens ataxin 2 related protein (A2LP), mRNA
9621	22121	35085	1.85	5.0E-59	AV762869.1	EST_HUMAN	au66c07.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781228 3' similar to contains element TAR1 repetitive element ;
10786	23310	36317	3.47	5.0E-59	11434908	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
826	13443	25951	2.85	4.0E-59	D80006.1	NT	AV762869 MDS Homo sapiens cDNA clone MDSEIC12 5'
5728	18354	31058	1.22	4.0E-59	11034810	NT	Homo sapiens hypothetical protein (LOC57143), mRNA
12004	24917		5.54	4.0E-59	AF057720.1	NT	Human mRNA for KIAA0184 gene, partial cds
10	12689		4.75	3.0E-59	AW965524.1	EST_HUMAN	Homo sapiens catenin (cadherin-associated protein), delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2), mRNA
245	12804	25385	3.86	3.0E-59	7662247	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, promoter region and exon 1
1748	14338	26884	8.2	3.0E-59	4505860	NT	EST377582 MAGE (resequences, MAGI Homo sapiens cDNA
1748	14338	26885	8.2	3.0E-59	4505860	NT	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
2174	14751	27320	7.15	3.0E-59	AB029035.1	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2174	14751	27321	7.15	3.0E-59	AB029035.1	NT	Homo sapiens plasminogen activator, tissue (PLATa) mRNA
2788	15477	27920	1.29	3.0E-59	AF232298.1	NT	Homo sapiens mRNA for KIAA1112 protein, partial cds
3074	15689	28161	0.77	3.0E-59	T18865.1	EST_HUMAN	Homo sapiens NF1-2 pseudogene, exon 17
3074	15689	28162	0.77	3.0E-59	T18865.1	EST_HUMAN	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
3163	15777	28247	4.67	3.0E-59	4502014	NT	h020171 Testis 1 Homo sapiens cDNA clone h02017 5' end
							Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3163	15777	28248	4.67	3.0E-59	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3897	16496	28956	1.12	3.0E-59	4508044	NT	Homo sapiens zona pellucida glycoprotein 2 (sperm receptor) (ZP2) mRNA
4798	17374	29826	0.98	3.0E-59	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4967	17541	29984	1.33	3.0E-59	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
6389	18973	31751	2.1	3.0E-59	8924074	NT	Homo sapiens hypothetical protein PRO1741 (PRO1741), mRNA
7395	19920	32785	1.87	3.0E-59	5454137	NT	Homo sapiens nuclear receptor co-repressor 1 (NCOR1), mRNA
7872	20414	33321	1.26	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
7872	20414	33322	1.26	3.0E-59	X12556.1	NT	Human mRNA for dbl proto-oncogene
9957	22452	35433	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
9957	22452	35434	1.04	3.0E-59	X70251.1	NT	H. sapiens CKII-alpha gene
11980	24291		1.26	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLAT1), mRNA
12130	24386		9.09	3.0E-59	11417866	NT	Homo sapiens gamma-glutamyltransferase-like activity 1 (GGTLAT1), mRNA
6044	18663	31402	0.98	2.0E-59	BF509383.1	EST_HUMAN	UI-H-B14-ay-b-02-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
6044	18663	31403	0.98	2.0E-59	BF509383.1	EST_HUMAN	UI-H-B14-ay-b-02-0-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086522 3'
9555	22055		5.27	2.0E-59	AA309774.1	EST_HUMAN	EST180633 Jurkat T-cells V Homo sapiens cDNA 5' end
10419	22913		1.34	2.0E-59	BF365554.1	EST_HUMAN	RCO-NT0036-100700-032-a07 NT0036 Homo sapiens cDNA
10710	23238	36252	2.49	2.0E-59	AW410698.1	EST_HUMAN	h07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981654 5'
10710	23238	36253	2.49	2.0E-59	AW410698.1	EST_HUMAN	h07h04.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981654 5'
11879	24228	31046	5.76	2.0E-59	AI631809.1	EST_HUMAN	w36c12.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300182 3' similar to TR:Q86542
12437	24943	30821	2.86	2.0E-59	L11845.1	NT	Q86542 RTVL-H PROTEIN; contains LTR7 b1 LTR7 repetitive element;
174	12837		18.31	1.0E-59	BE268411.1	EST_HUMAN	Homo sapiens alpha-tubulin mRNA, complete cds
2516	15080	27652	1.02	1.0E-59	AI139341.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2516	15080	27653	1.02	1.0E-59	AI139341.1	EST_HUMAN	601176757F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531927 5'
2849	15208		1.45	1.0E-59	AA748468.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1710254 3'
7563	20080	32856	1.98	1.0E-59	AJ130894.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1710254 3'
7703	20212	33101	0.93	1.0E-59	BE256814.1	EST_HUMAN	qc21c08.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537
7703	20212	33101	0.93	1.0E-59	BE256814.1	EST_HUMAN	Q13537 MER37 TRANSPOSABLE ELEMENT, COMPLETE CONSENSUS SEQUENCE.;
9307	21907	34855	1.2	1.0E-59	11419630	NT	0a56h11.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309029 3' similar to TR:Q13537
9522	22022	34979	0.82	1.0E-59	11428849	NT	Homo sapiens zinc finger protein 275 (ZNF275), mRNA
9522	22022	34980	0.82	1.0E-59	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
10734	22080	32956	9.52	1.0E-59	AJ130894.1	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
795	13413	25917	1.28	8.0E-60	AW977845.1	EST_HUMAN	Homo sapiens mRNA for transcription factor
							EST389849 IMAGE resequences, MAGO Homo sapiens cDNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1520	14112	26848	3.21	8.0E-60	4750159	NT	Homo sapiens small nuclear ribonucleoprotein D3 polypeptide (18kD) (SNRPD3) mRNA
2216	14791	27384	1.95	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
2216	14791	27365	1.95	8.0E-60	5174656	NT	Homo sapiens differentiation-related gene 1 (nickel-specific induction protein) (RTP) mRNA
6135	18749	31506	1.01	8.0E-60	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6628	19224	32029	1.85	8.0E-60	S83182.1	NT	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]
7684	20195	33083	0.76	8.0E-60	11420841	NT	Homo sapiens phosphate cytidylyltransferase 1, choline, beta isoform (PCYT1B), mRNA
7906	20448	33355	2.60	8.0E-60	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8869	21408	34332	4.03	8.0E-60	11428949	NT	Homo sapiens S-antigen, retina and pineal gland (arresin) (SAG), mRNA
9392	21815	34764	0.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9392	21815	34765	0.98	8.0E-60	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10465	22859	35969	0.68	8.0E-60	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
10712	23240	36256	5.93	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
10712	23240	36255	5.93	8.0E-60	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
784	13403	25907	12.12	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
785	13403	25907	52.6	7.0E-60	AF055066.1	NT	Homo sapiens MHC class 1 region
848	13464	25972	1.28	7.0E-60	4504634	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
2173	14750	27319	1.95	7.0E-60	AF077183.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
4258	16844	29293	2.74	7.0E-60	4505488	NT	Homo sapiens ornithine decarboxylase 1 (ODC1) mRNA
9328	21842	34794	3.6	7.0E-60	H58041.1	EST_HUMAN	yr1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
11243	23773	36830	1.87	7.0E-60	H58041.1	EST_HUMAN	yr1204.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:205087 5' similar to contains LTR5 repetitive element;
8376	20916		7.56	8.0E-60	H52456.1	EST_HUMAN	yq78h09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:201953 5' similar to contains OFR repetitive element;
87	12763	25245	1.13	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
87	12763	25246	1.13	5.0E-60	AI807917.1	EST_HUMAN	wf52c07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2359212 3'
3000	15616		1.47	4.0E-60	AA299037.1	EST_HUMAN	EST11498 Uterus Homo sapiens cDNA 5' end similar to similar to retrovirus-related pol
7390	19915	32779	0.7	4.0E-60	BF196068.1	EST_HUMAN	h86105.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
9054	21591		0.82	4.0E-60	AL163278.2	NT	Q61085 GTP-RHO BINDING PROTEIN 1;
1899	14484	27044	5.26	3.0E-60	BE562611.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C078
1899	14484	27045	5.26	3.0E-60	BE562611.1	EST_HUMAN	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'
1910	14495		2.4	3.0E-60	6031190	NT	601336446F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3690395 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4556	17139	26587	1.88	3.0E-60	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
5822	18446	31168	2.04	3.0E-60	AW836196.1	EST_HUMAN	RC3-LT0023-200-012-g01 LT0023 Homo sapiens cDNA
7034	18054	30477	1	3.0E-60	A1792814.1	EST_HUMAN	cl60h11.y6 NCI CGAP_K143 Homo sapiens cDNA clone IMAGE:1534053 5' similar to SW:UDP_MOUSE
8341	20882	33802	5.3	3.0E-60	5174644	NT	P52624 URIDINE PHOSPHORYLASE
8341	20882	33803	5.3	3.0E-60	5174644	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8519	21058	33981	0.51	3.0E-60	A104235.1	EST_HUMAN	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
8677	21216	34136	4.75	3.0E-60	5174644	NT	ox56d09.x1 Soares NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1660337 3' similar to
12520	24980		1.71	3.0E-60	AA485286.1	EST_HUMAN	SW:FORM_MOUSE Q05860 FORMIN
33	12712	25171	2.84	2.0E-60	AY008285.1	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
1470	14062	26597	2.86	2.0E-60	Z11694.1	NT	ab07h04.r1 Strabagene lung (#937210) Homo sapiens cDNA clone IMAGE:840151 5' similar to contains
1759	14349	26893	1.24	2.0E-60	M24603.1	NT	LTR10.11 LTR10 repetitive element
3638	16241	28717	0.72	2.0E-60	4757867	NT	Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
3987	16585	29056	0.78	2.0E-60	AF231919.1	NT	H. sapiens 41kDa protein kinase related to rat ERK2
4203	16792		0.65	2.0E-60	BF513458.1	EST_HUMAN	Human bcr protein mRNA, 5' end
6443	18045	31833	0.94	2.0E-60	A1701952.1	EST_HUMAN	Homo sapiens v-raf murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
6618	19215	32020	1.65	2.0E-60	AF004877.1	NT	Homo sapiens chromosome 21 unknown mRNA
6818	19407	32224	0.89	2.0E-60	AF15476.1	NT	U1-H-BW1-ams-05-0-U1.st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3070952 3'
6934	18042	30486	2.08	2.0E-60	4503044	NT	nm011f12.y5 NCI CGAP_Co8 Homo sapiens cDNA clone IMAGE:1076495 5' similar to contains THR.11 THR
6934	18042	30487	2.08	2.0E-60	4503044	NT	repetitive element
7164	19696	32542	8.14	2.0E-60	AA311159.1	EST_HUMAN	Homo sapiens pro-alpha 2(I) collagen (COL1A2) gene, complete cds
7164	19696	32543	8.14	2.0E-60	AA311159.1	EST_HUMAN	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
7628	20140		1.05	2.0E-60	BF512808.1	EST_HUMAN	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
7947	20489	33399	1.05	2.0E-60	X85597.1	EST_HUMAN	Homo sapiens corticotropin releasing hormone receptor 2 (CRHR2) mRNA
8601	21340	34267	3.38	2.0E-60	L36033.1	NT	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha
9888	22385	35362	2.67	2.0E-60		NT	EST181949 Jurkat T-cells V Homo sapiens cDNA 5' end similar to prothymosin, alpha
9888	22385	35363	2.67	2.0E-60		NT	U1-H-BW1-ams-02-0-U1.st NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071210 3'
12168	24407		3.98	2.0E-60		NT	HS15B5T human adult testis Homo sapiens cDNA clone CAM_EST15
						NT	Human pre-B cell stimulating factor homologue (SDF1b) mRNA, complete cds
						NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
						NT	(SEMA6A), mRNA
						NT	Homo sapiens sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
						NT	(SEMA6A), mRNA
						NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12309	24908		1.71	2.0E-60	AF088757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12311	24503		1.88	2.0E-60	11418068	NT	Homo sapiens similar to HSPC022 protein (H. sapiens) (LOC53504), mRNA
12329	24515		1.95	2.0E-60	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
548	13179	26657	0.92	1.0E-60	BE178586.1	EST_HUMAN	PM3-H10605-270200-001-e06 HT0605 Homo sapiens cDNA
3970	16568	29037	0.95	1.0E-60	AU143389.1	EST_HUMAN	AU143389 Y79AA1 Homo sapiens cDNA clone Y79AA1001854 5'
5091	17664	30104	1.32	1.0E-60	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
7889	20431	33340	0.73	1.0E-60	BE064410.1	EST_HUMAN	RC4-BT0311-141199-011-006 BT0311 Homo sapiens cDNA
							nc04e12.11 NCL_CGAP_P11 Homo sapiens cDNA clone IMAGE:1007182 similar to contains L1.11 L1
8690	21229		2.93	1.0E-60	AA244041.1	EST_HUMAN	repetitive element
8717	21266	34176	1.51	1.0E-60	AV754081.1	EST_HUMAN	AV754081 TP Homo sapiens cDNA clone TPGAED05 5'
1136	13741	26250	2.37	9.0E-61	AU119344.1	EST_HUMAN	AU119344 HEMBA1 Homo sapiens cDNA clone HEMBA1005583 5'
2694	15251	27821	1.11	8.0E-61	AW006478.1	EST_HUMAN	W05b10.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2694	15251	27822	1.11	8.0E-61	AW006478.1	EST_HUMAN	W05b10.x1 NCL_CGAP_C03 Homo sapiens cDNA clone IMAGE:2506555 3'
2978	15594		2.53	8.0E-61	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV9)
7836	20378	33284	0.79	8.0E-61	AA593968.1	EST_HUMAN	nn59g06.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088218 3'
133	12799	25286	0.99	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
133	12799	25287	0.99	7.0E-61	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
287	12943	25428	3.39	6.0E-61	BE403310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
844	13460	25969	2.13	6.0E-61	BE403310.1	EST_HUMAN	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
1366	13960	26485	13.81	6.0E-61	AF119860.1	NT	Homo sapiens PRO2014 mRNA, complete cds
1672	14264	26788	0.91	6.0E-61	BE257400.1	EST_HUMAN	601109238F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350145 5'
1689	14281	26816	2.23	6.0E-61	AA596033.1	EST_HUMAN	nn66h09.s1 NCL_CGAP_Lar1 Homo sapiens cDNA clone IMAGE:1088897 3'
							Homo sapiens solute carrier (SLC25A18) mRNA, complete cds; nuclear gene for mitochondrial product
2172	14749	27318	0.93	6.0E-61	AY008285.1	NT	AU130689 NT2RP3 Homo sapiens cDNA clone NT2RP3001263 5'
3347	15957	28433	11.6	6.0E-61	AU130689.1	EST_HUMAN	Ig-beta/B29=CD79b (alternatively spliced) [human, B cells, mRNA, partial, 375 nt]
6182	18792	31561	3.06	6.0E-61	S79249.1	NT	Human autosomal dominant polycystic kidney disease protein 1 (PKD1) gene
7380	19806	32771	1.71	6.0E-61	U24498.1	NT	Homo sapiens general transcription factor 2-i (GTF2i) mRNA, complete cds
7814	20127	33004	1.95	6.0E-61	AF035737.1	NT	601300938F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635480 5'
12065	13460	25969	1.38	6.0E-61	BE403310.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
236	12896	25379	2.06	5.0E-61	8922990	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
236	12896	25380	2.06	5.0E-61	8922990	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
382	13029	25517	0.61	5.0E-61	4507500	NT	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA
1718	14310	26849	2.36	5.0E-61	4506008	NT	Homo sapiens chromosome 21 segment HS21C079
3071	15686	28158	1.9	5.0E-61	AL163279.2	NT	Homo sapiens chromosome 21 segment HS21C079

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4053	16650		1.91	5.0E-61	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
5144	13029	25517	0.89	5.0E-61	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11856	24215		4.95	4.0E-61	AV731140.1	EST_HUMAN	AV731140 HTF Homo sapiens cDNA clone HTFAR801 5'
4292	16878	29325	0.98	3.0E-61	BE366279.1	EST_HUMAN	601309785F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3631220 5'
8390	20900	33821	0.63	3.0E-61	AF150190.1	EST_HUMAN	AF150190 Human mRNA from cd34+ stem cells Homo sapiens cDNA clone CBDAGB04
8629	21168	34083	0.51	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
8629	21168	34084	0.51	3.0E-61	AA301233.1	EST_HUMAN	EST14323 Testis tumor Homo sapiens cDNA 5' end
524	13158	26538	1.29	2.0E-61	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
1254	13851	26368	1.98	2.0E-61	BE188410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1254	13851	26369	1.98	2.0E-61	BE188410.1	EST_HUMAN	QV3-HT0513-060400-147-401 HT0513 Homo sapiens cDNA
1705	14298	26835	1.22	2.0E-61	N53039.1	EST_HUMAN	y63d11.s1 Soares fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:246453 3' similar to
2687	15225		1.54	2.0E-61	N39397.1	EST_HUMAN	gbL25444 60S RIBOSOMAL PROTEIN L35A (HUMAN).
							y03f11.1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:270189 5'
6557	19155	31951	0.85	2.0E-61	11428168	NT	Homo sapiens ATPase, H+ transporting, lysosomal (vacuolar proton pump) non-catalytic accessory protein 1A (110/116kD) (ATP8A1A), mRNA
8945	21483	34406	1.01	2.0E-61	AV694317.1	EST_HUMAN	AV694317 GKC Homo sapiens cDNA clone GKCELG06 5'
9481	21890		1.55	2.0E-61	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
9836	22334	35316	1.59	2.0E-61	AW500256.1	EST_HUMAN	UI-HF-BNO-akd-4-12-0-UI.s1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076774 5'
10149	22844	35636	1.99	2.0E-61	11421778	NT	Homo sapiens polymerase (RNA) III (DNA directed) (39kD) (RPC39), mRNA
10764	23288		9.83	2.0E-61	11419729	NT	Homo sapiens ribosomal protein L44 (RPL44), mRNA
490	13094		0.91	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
805	13422	25928	1.25	1.0E-61	5453829	NT	Homo sapiens origin recognition complex, subunit 2 (yeast homolog)-like (ORC2L) mRNA
1443	14036	26585	0.98	1.0E-61	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1898	14483	27043	3.87	1.0E-61	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
							xn11b09.y1 NCJ CGAP L15 Homo sapiens cDNA clone IMAGE:2693369 5' similar to contains element
2238	14813	27395	1.55	1.0E-61	AW827281.1	EST_HUMAN	MSR1 repetitive element ;
3422	16030	28511	0.88	1.0E-61	7692319	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
4534	17118	29584	1.48	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4534	17118	29585	1.48	1.0E-61	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
4982	17556	29998	10.61	1.0E-61	AW288181.1	EST_HUMAN	UI-H-BW0-ajl-b-08-0-UI.s1 NCJ CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
4982	17556	29999	10.61	1.0E-61	AW288181.1	EST_HUMAN	UI-H-BW0-ajl-b-08-0-UI.s1 NCJ CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732871 3'
5888	18490	31216	0.89	1.0E-61	7692303	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
6043	18692	31401	1.17	1.0E-61	11416891	NT	Homo sapiens survival of motor neuron 1, telomeric (SMN1), mRNA
6981	19479	32300	8.17	1.0E-61	M30135.1	NT	Human P40 T-cell and mast cell growth factor (HP40) gene, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7148	18681	32522	0.73	1.0E-61	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP128), mRNA
7242	19771	32627	1.54	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
7242	19771	32628	1.54	1.0E-61	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8075	20617	33531	6.26	1.0E-61	11034840	NT	Homo sapiens growth hormone releasing hormone (GHRH), mRNA
8255	20796	33713	3.19	1.0E-61	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
9206	21723		2.29	1.0E-61	AW699726.1	EST_HUMAN	MR0-BN0070-040400-010-0101 BN0070 Homo sapiens cDNA
9279	21805	34756	1.1	1.0E-61	11418280	NT	Homo sapiens cadherin 18 (CDH18), mRNA
9942	22437	35414	5.76	1.0E-61	11428892	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
10514	23052	36063	2.82	1.0E-61	11425578	NT	Homo sapiens actinin, alpha 4 (ACTN4), mRNA
11751	24966		1.58	1.0E-61	AB071399.1	NT	Homo sapiens gene for AF-8, complete cds
11793	24955	30629	3.23	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11793	24955	30630	3.23	1.0E-61	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12173	24412	30945	1.61	1.0E-61	M20809.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr1) variable region (subgroup V kappa I)
12494	24622	30891	17.77	1.0E-61	11418127	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
10259	22754	35742	1.82	9.0E-62	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
4849	17231	28698	1.03	8.0E-62	AA830420.1	EST_HUMAN	cc68h11.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354725 3' similar to SW:POL_MLVRK P31795 POL POLYPROTEIN
12652	24724		1.59	8.0E-62	AA788881.1	EST_HUMAN	nz75g01.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1301328 3'
1146	13749	26258	1.31	7.0E-62	AV714334.1	EST_HUMAN	AV714334 DCB Homo sapiens cDNA clone DCBAMA08 5'
3554	18158	28641	0.7	7.0E-62	P17480	SWISSPROT	NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1) (UBF-1) (AUTOANTIGEN NOR-90)
6075	18692	31438	0.96	7.0E-62	11427965	NT	Homo sapiens hypothetical protein (FLJ20261), mRNA
11229	23760	36816	5.72	7.0E-62	AI208681.1	EST_HUMAN	qg56a04.x1 Soares, testis_NHT Homo sapiens cDNA clone IMAGE:1839150 3' similar to TR:O15103 O15103 HYPOTHETICAL 27.3 KD PROTEIN
3029	15045		1.6	6.0E-62	U09410.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
3431	16039		4.97	6.0E-62	11418255	NT	Homo sapiens CGI-56 protein (CGI-56), mRNA
7621	20134	33011	3.43	6.0E-62	AI762801.1	EST_HUMAN	wf04402.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
7821	20134	33012	3.43	6.0E-62	AI762801.1	EST_HUMAN	wf04402.x1 NCL_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2389251 3'
8030	20572		0.75	6.0E-62	AW501124.1	EST_HUMAN	UI-HF-BPop-ait-d-09-Q-U1.1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072833 5'
8200	20741	33654	1.35	6.0E-62	11431139	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA
9276	21802	34752	3.92	6.0E-62	AW814393.1	EST_HUMAN	MR3-ST0203-130100-025-g09 ST0203 Homo sapiens cDNA
441	13074	25569	1.99	5.0E-62	AI950528.1	EST_HUMAN	wf51e07.x1 NCL_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN Q08379 GOLGIN-95, contains element MER22 repetitive element

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2451	15018	27589	3	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2451	15018	27590	3	5.0E-62	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
2626	15188	27755	0.87	5.0E-62	U98487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
2626	15188	27756	0.87	5.0E-62	U98487.1	NT	Human xanthine dehydrogenase/oxidase mRNA, complete cds
3466	16073	28546	2.52	5.0E-62	4506758	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
4421	17006	29449	2.23	5.0E-62	AA431093.1	EST_HUMAN	zr78a09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782344 3' similar to SW:NRDC_RAT
4657	17239	33941	0.95	5.0E-62	AW605887.1	EST_HUMAN	P47245 NARDILYSIN
8485	21024	33941	0.64	5.0E-62	4506758	NT	RC5-NN1089-100500-021-H03 NN1089 Homo sapiens cDNA
9436	21962	34911	5.85	5.0E-62	AW410887.1	EST_HUMAN	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
11144	23652	36693	2.54	5.0E-62	11425574	NT	fh07g09.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2981616 5'
11144	23652	36694	2.54	5.0E-62	11425574	NT	Homo sapiens muscle specific gene (M9), mRNA
873	13488	26003	4.05	4.0E-62	AW161479.1	EST_HUMAN	Homo sapiens muscle specific gene (M9), mRNA
873	13488	26004	4.05	4.0E-62	AW161479.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
874	13488	26003	3.94	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
874	13488	26004	3.94	4.0E-62	AW161479.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1511	14103		1.01	4.0E-62	AA311281.1	EST_HUMAN	au71d03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2781701 5' similar to gb:M37104
2498	15062	27636	1.7	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
2498	15062	27637	1.7	4.0E-62	A1827900.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
3446	16054		7.95	4.0E-62	4557887	NT	EST182043 Jurkat T-cells V Homo sapiens cDNA 5' end
8081	18698	31445	1.79	4.0E-62	4506978	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
8439	19041	31829	2.58	4.0E-62	11420654	NT	gb:X57138.maf1 HISTONE H2B.2 (HUMAN);
7223	19754	32609	1.86	4.0E-62	11421047	NT	wf12b08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2350359 3' similar to
7630	20142	33021	2.5	4.0E-62	7657057	NT	gb:X57138.maf1 HISTONE H2B.2 (HUMAN);
7630	20142	33022	2.5	4.0E-62	7657057	NT	gb:X57138.maf1 HISTONE H2B.2 (HUMAN);
8112	20853	33562	0.95	4.0E-62	11429873	NT	Homo sapiens keratin 18 (KRT18) mRNA
							Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2) mRNA
							Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
							Homo sapiens phosphoribosyl pyrophosphate synthetase 2 (PRPS2), mRNA
							Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens eukaryotic translation initiation factor 2B, subunit 2 (beta, 39kD) (EIF2B2), mRNA
							Homo sapiens 26S proteasome-associated peptidyl homologue (POH1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8780	21319	34243	5.44	4.0E-62	AB030089.1	NT	Homo sapiens mRNA for KIAA1263 protein, partial cds
10890	23411	36429	2.16	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18D3
10890	23411	36430	2.16	4.0E-62	Z78766.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA18D3
11149	23654	36896	2.05	4.0E-62	AW023559.1	EST_HUMAN	df56g04.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487751 5'
12003	24912	30887	1.89	4.0E-62	11418192	NT	Homo sapiens non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1), mRNA
12420	24608	30887	1.78	4.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12475	24600	30884	15	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12475	24600	30885	15	4.0E-62	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12528	24642	30898	2.68	4.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
78	12755	25236	0.85	3.0E-62	4557764	NT	Homo sapiens neurofibromin 2 (bilateral acoustic neuroma) (NF2), mRNA
3082	15697	28169	0.93	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3082	15697	28170	0.93	3.0E-62	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3761	16362	28830	5.68	3.0E-62	X52858.1	NT	Human cyclophilin-related processed pseudogene
8477	21016	33932	3.96	3.0E-62	AI632733.1	EST_HUMAN	wa33f04.xt NC1 CGAP Kid11 Homo sapiens cDNA clone IMAGE:2299903 3' similar to contains THR.12
1274	13870	26390	2.31	2.0E-62	AL163284.2	NT	THR repetitive element.
8709	21248	34170	4.31	2.0E-62	BF329911.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C084
8709	21248	34171	4.31	2.0E-62	BF329911.1	EST_HUMAN	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
10076	22571		3.84	2.0E-62	AF224699.1	NT	RCO-BN0284-300500-031-e05 BN0284 Homo sapiens cDNA
11537	23985		19.58	2.0E-62	BF330676.1	EST_HUMAN	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3
1082	13687	26199	1.74	1.0E-62	AF248540.1	NT	(UBE2D3) genes, complete cds
1592	14185	26717	9.15	1.0E-62	L78810.1	NT	QV4-BT0257-081189-017-e03 BT0257 Homo sapiens cDNA
1834	14422	26972	1.05	1.0E-62	AA625207.1	EST_HUMAN	Homo sapiens intersecin 2 (SH3D1B) mRNA, complete cds
2839	15556	28031	1.22	1.0E-62	AL039044.1	EST_HUMAN	Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4625	17208	28658	1.46	1.0E-62		NT	Homo sapiens Nhl-IMPu_S1 Homo sapiens cDNA clone IMAGE:1047404 5' similar to WP:K01H12.1
5305	17867	30290	0.74	1.0E-62	AA148822.1	EST_HUMAN	CE03453.
7188	19720	32567	1.01	1.0E-62	AA490060.1	EST_HUMAN	DKFP566F104_r1 568 (synonym: hfkd2) Homo sapiens cDNA clone DKFP566F104 5'
7199	19730	32581	3	1.0E-62	AA722878.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
7199	19730	32582	3	1.0E-62	AA722878.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20212 (FLJ20212), mRNA
8692	21231	34151	0.71	1.0E-62	AA280050.1	EST_HUMAN	206608.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:491511 5' similar to
8988	21526	34455	1.64	1.0E-62		NT	SW:CS61 BOVIN P10897 CYTOCHROME B561.

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8988	21528	34458	1.64	1.0E-62	7682289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9030	21567	34493	2.39	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9030	21567	34498	2.39	1.0E-62	X15533.1	NT	H. sapiens lysosomal acid phosphatase gene (EC 3.1.3.2) Exon 9
9476	21875	34822	2.95	1.0E-62	AA465170.1	EST_HUMAN	aa33308.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815055 3'
11245	23775	36832	2.49	1.0E-62	Z78698.1	NT	H. sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA14D8
12289	24490		6.66	1.0E-62	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
12508	24630	30894	2.04	1.0E-62	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
360	13009	25492	1.88	9.0E-63	AW816405.1	EST_HUMAN	QV4-ST0234-181199-037-f05 ST0234 Homo sapiens cDNA
2383	14952		2.15	9.0E-63	C18159.1	EST_HUMAN	C18159 Human placenta cDNA (TFujijwara) Homo sapiens cDNA clone GEN-558C10 5'
4114	16708	29162	9.09	9.0E-63	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4114	16708	29163	9.09	9.0E-63	AB002348.2	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA
5453	18022	37142	3.93	9.0E-63	11418185	NT	Homo sapiens mRNA for PKB kinase
5657	18284	30762	1.55	9.0E-63	Y15066.1	NT	Homo sapiens nucleoporin 89kD (NUP88), mRNA
7234	19764	32620	3.66	9.0E-63	11426985	NT	Homo sapiens Ras association (RalGDS/AF-6) domain family 2 (RASSF2), mRNA
8268	20809	33729	1.12	9.0E-63	11421160	NT	
2382	14951	27524	1.5	8.0E-63	4557734	NT	Homo sapiens monoamine oxidase A (MAOA), nuclear gene encoding mitochondrial protein, mRNA
2412	14980	27555	2.47	8.0E-63	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
3508	16113	28590	4.62	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
3508	16113	28591	4.62	8.0E-63	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
4352	16939	28381	3.64	8.0E-63	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
964	13575		2.31	7.0E-63	AB72137.1	EST_HUMAN	wm55g11.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2439908 3'
5542	18174		34.88	6.0E-63	AA420803.1	EST_HUMAN	nc63f02.11 NCI_CGAP_P11 Homo sapiens cDNA clone IMAGE:745947 similar to gb.Y00361 60S
8807	21346	34270	0.5	5.0E-63	11528464	NT	RIBOSOMAL PROTEIN (HUMAN);
3363	15971	28449	0.81	4.0E-63	AL163278.2	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
3881	16479	28940	0.98	4.0E-63	AB014607.1	NT	Homo sapiens chromosome 21 segment HS21C078
3881	16479	28941	0.98	4.0E-63	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
6573	19171	31968	5.46	4.0E-63	AW750372.1	EST_HUMAN	Homo sapiens mRNA for KIAA0707 protein, partial cds
6573	19171	31969	5.46	4.0E-63	AW750372.1	EST_HUMAN	CM3-BT0595-180100-072-a09 BT0595 Homo sapiens cDNA
11012	23526	36561	2.3	4.0E-63	AW134709.1	EST_HUMAN	CM3-BT0595-180100-072-a09 BT0595 Homo sapiens cDNA
11012	23526	36562	2.3	4.0E-63	AW134709.1	EST_HUMAN	UIH-B11-abq-e-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
1979	14562	27121	1.75	3.0E-63	AB018280.1	NT	UIH-B11-abq-e-02-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2712482 3'
2807	15359	27926	1.56	3.0E-63	J00310.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
							Human Met-tRNA-I gene 1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2848	13877	26399	11.17	3.0E-63	6005963	NT	Homo sapiens zinc finger protein 144 (MEL-18) (ZNF144), mRNA
6600	19197	32002	29.68	3.0E-63	11545810	NT	Homo sapiens hepatocellular carcinoma antigen gene 520 (LOC83928), mRNA
9622	22122	35086	0.77	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
9622	22122	35087	0.77	3.0E-63	BE876158.1	EST_HUMAN	601485656F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888253 5'
205	12866	25351	3.47	2.0E-63	U07804.1	NT	Human DNA topoisomerase I mRNA, partial cds
212	12873	25359	1.4	2.0E-63	4885228	NT	Homo sapiens eyes absent (Drosophila) homolog 2 (EYA2), mRNA
523	13155		5.21	2.0E-63	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (72.8kD) (GLCLC) mRNA
859	13475	25988	6.8	2.0E-63	7657042	NT	Homo sapiens Down syndrome candidate region 1 (DSCR1), mRNA
1612	14205	28739	3.37	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1612	14205	28740	3.37	2.0E-63	AB030388.1	NT	Homo sapiens RHCE mRNA for Rh blood CE group antigen polypeptide, complete cds
1803	14393	26838	1.06	2.0E-63	BE410739.1	EST_HUMAN	601301627F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636103 5'
2128	14706	27277	1.33	2.0E-63	AI863961.1	EST_HUMAN	wj54802.x1 NCJ_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2408603 3' similar to gb:M57609 GLI3 PROTEIN (HUMAN);
3192	15804	28277	1	2.0E-63	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
3324	15934	28411	1.7	2.0E-63	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
3976	16574	29044	2.09	2.0E-63	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
4990	17584	30009	1.18	2.0E-63	AF111187.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene
5487	24742	30420	1.95	2.0E-63	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
6045	18684	31404	2.51	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6045	18684	31405	2.51	2.0E-63	BF373541.1	EST_HUMAN	QV1-FT0170-040700-265-c05 FT0170 Homo sapiens cDNA
6333	18939	31715	1.04	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
6333	18939	31716	1.04	2.0E-63	11421940	NT	Homo sapiens protein kinase, cAMP-dependent, regulatory, type II, beta (PRKAR2B), mRNA
							Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2N1T, TCRBV6S1A1T, TCRBV6S1A1T, TCRBV6S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV6S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S>
6803	18394	32210	1.62	2.0E-63	U66059.1	NT	Homo sapiens MIST mRNA, partial cds
6844	19434	32249	0.87	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
6844	19434	32250	0.87	2.0E-63	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7135	19474	32295	1.43	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA
7135	19474	32296	1.43	2.0E-63	9910365	NT	Homo sapiens Carbonic anhydrase-related protein 10 (LOC56934), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7755	20263	33158	0.89	2.0E-63	AB046844.1	NT	Homo sapiens mRNA for KIAA1624 protein, partial cds
8470	21010	33927	2.91	2.0E-63	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
8984	21522	34449	1.12	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
8984	21522	34450	1.12	2.0E-63	11420949	NT	Homo sapiens kinesin family member 3B (KIF3B), mRNA
8982	22350	35331	0.9	2.0E-63	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
10825	23157	36170	22.7	2.0E-63	N78945.1	EST_HUMAN	zb18b05.a1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:302385 3' similar to gb:X17206.40S RIBOSOMAL PROTEIN S4 (HUMAN);
10852	23184	36198	2.83	2.0E-63	AF098810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
10852	23184	36199	2.83	2.0E-63	AF098810.1	NT	Homo sapiens neuroxin III-alpha gene, partial cds
11886	24851	30702	6.92	2.0E-63	11418185	NT	Homo sapiens acinase 2, mitochondrial (ACO2), mRNA
12623	24701	30864	1.4	2.0E-63	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
4434	17020	29460	3.52	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
4434	17020	29461	3.52	1.0E-63	F08485.1	EST_HUMAN	HSCZVD111 normalized infant brain cDNA Homo sapiens cDNA clone c-zvd11
5555	18187	30602	1.32	1.0E-63	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
5943	18563	31293	1.38	1.0E-63	AW582268.1	EST_HUMAN	QVO-S10215-060100-083-b09 ST0215 Homo sapiens cDNA
8408	20948		2.21	1.0E-63	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
12581	24970		17.03	1.0E-63	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
6122	18737	31489	1.08	9.0E-64	AW401433.1	EST_HUMAN	UI-HF-BKO-seq-b-09-0-UI11 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3053153 5'
7808	20351	33259	4.35	9.0E-64	A1478186.1	EST_HUMAN	tr50b07.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2161525 3'
1084	13689		13.09	8.0E-64	BE280798.1	EST_HUMAN	601155232F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139038 5'
6289	18897	31668	3.17	8.0E-64	BE885755.1	EST_HUMAN	601508968F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3910336 5'
11694	24109		1.48	8.0E-64	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
11752	24148		3.56	8.0E-64	T60651.1	EST_HUMAN	y598b02.r1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:79179 5'
3582	16186		0.84	7.0E-64	BE394321.1	EST_HUMAN	601311455F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3633204 5'
4838	17416	29868	2.85	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
4838	17416	29869	2.85	7.0E-64	4507490	NT	Homo sapiens thimet oligopeptidase 1 (THOP1) mRNA
7766	20274	33172	0.68	7.0E-64	4506796	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
8946	22441	35418	4.54	7.0E-64	Y07848.1	NT	Homo sapiens EWS, gar22, rrp22 and bsm22 genes
1760	14350	28894	2.4	8.0E-64	A1851982.1	EST_HUMAN	wb51e07.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
1760	14350	28895	2.4	8.0E-64	A1851982.1	EST_HUMAN	wb51e07.x1 NCI CGAP_G06 Homo sapiens cDNA clone IMAGE:2309220 3' similar to gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
3156	15770	28236	4.46	6.0E-64	AW026445.1	EST_HUMAN	wt13e03.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'
3156	15770	28237	4.46	6.0E-64	AW026445.1	EST_HUMAN	wt13e03.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2529436 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5805	18430	31149	3.71	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5805	18430	31150	3.71	6.0E-64	Y18933.1	NT	Homo sapiens MCP-1 gene and enhancer region
5823	18447	31169	5.6	6.0E-64	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7286	19814	32670	2.45	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
7286	19814	32671	2.45	6.0E-64	11525879	NT	Homo sapiens mesenchyme homeo box 1 (MEOX1), mRNA
9250	21776	34721	9.24	6.0E-64	11420555	NT	Homo sapiens acetyl-CoA synthetase (LOC55902), mRNA
9425	21934	34983	2	6.0E-64	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
9634	22134	36195	7.87	6.0E-64	S76475.1	NT	tKIC [human, brain, mRNA, 2715 nt]
10849	23181	36195	7.87	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10849	23181	36195	7.87	6.0E-64	11420197	NT	Homo sapiens stromal antigen 3 (STAG3), mRNA
10896	15770	28236	1.64	6.0E-64	AW026445.1	EST_HUMAN	Homo sapiens cDNA clone IMAGE:2529436 3'
10896	15770	28237	1.64	6.0E-64	AW026445.1	EST_HUMAN	ww13e03.x1 NCI_CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2529436 3'
11903	24242	31008	2.45	6.0E-64	11526193	NT	Homo sapiens interleukin 10 receptor, beta (IL10RB), mRNA
853	13469	25979	3.09	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
853	13469	25980	3.09	5.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1383	13977	26504	0.95	5.0E-64	AB020710.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1467	14059	26593	2.55	5.0E-64	L40633.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1467	14059	26594	2.55	5.0E-64	L40633.1	NT	Homo sapiens phosphoglucomutase-related protein (PGMRP) gene, complete cds
1748	14339	26866	1.52	5.0E-64	U89358.1	NT	Human I(3)mbt protein homolog mRNA, complete cds
2853	14120	26657	3.5	5.0E-64		NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
2853	14120	26658	3.5	5.0E-64		NT	Homo sapiens KIAA0618 gene product (KIAA0618), mRNA
4032	16630	29099	7.79	5.0E-64	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
4181	16771	29220	0.68	5.0E-64	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
10692	23222	36235	3.91	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10692	23222	36236	3.91	4.0E-64	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
2239	14814	27386	3.14	3.0E-64	C18895.1	EST_HUMAN	C18895 Human placenta cDNA (TF-1/14) Homo sapiens cDNA clone GEN:569E02 5'
3293	16904	28384	0.76	3.0E-64	BE794381.1	EST_HUMAN	601389865F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943577 5'
3491	18096	28570	2.57	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
3491	18096	28571	2.57	3.0E-64	AV711714.1	EST_HUMAN	AV711714 DCA Homo sapiens cDNA clone DCAAMC01 5'
6232	18841	31613	1.53	3.0E-64	Z26273.1	NT	H sapiens isoform 1 gene for L-type calcium channel, exon 28
6619	19216	32021	3.11	3.0E-64	BF370000.1	EST_HUMAN	RC8-FN0019-280600-011-G11 FN0019 Homo sapiens cDNA
8402	20942	33864	1.83	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds
8402	20942	33865	1.83	3.0E-64	AF248953.1	NT	Homo sapiens golgi matrix protein GM130 (GOLGA2) mRNA, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8432	20972	33885	4.49	3.0E-64	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:108069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
8432	20972	33886	4.49	3.0E-64	BE208521.1	EST_HUMAN	bb72h12.y1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3047975 5' similar to gb:108069 DNAJ PROTEIN HOMOLOG 2 (HUMAN);
9348	21862	34810	1.23	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9348	21862	34811	1.23	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
9433	21959	34907	0.72	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
9433	21959	34908	0.72	3.0E-64	AW977384.1	EST_HUMAN	EST389493 MAGe resequences, MAGO Homo sapiens cDNA
11118	23627	36669	1.83	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11118	23627	36670	1.83	3.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11539	22987	37058	4.89	3.0E-64	AA609940.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C027
1127	13730	26241	1.26	2.0E-64	AL163227.2	EST_HUMAN	af09d08.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1031151 3'
1441	14034	26562	8.3	2.0E-64	475770.1	NT	Homo sapiens aIF4E-like cap-binding protein (4EHP) mRNA Homo sapiens cDNA clone IMAGE:2492281 3' similar to contains element w087b01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2492281 3' similar to contains element L1 repetitive element 1;
2566	15130		1.88	2.0E-64	AI927030.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
2570	15133	27702	1.25	2.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2570	15133	27703	1.25	2.0E-64	AL163246.2	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)(GOT2), nuclear gene encoding mitochondrial protein, mRNA
3174	15787	28259	1.17	2.0E-64	4504088	NT	EST370215 MAGe resequences, MAGe Homo sapiens cDNA
3855	18453	28918	0.63	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGe Homo sapiens cDNA
3855	18453	28917	0.63	2.0E-64	AW958145.1	EST_HUMAN	EST370215 MAGe resequences, MAGe Homo sapiens cDNA
6157	18770	31534	2.28	2.0E-64	AU124387.1	EST_HUMAN	AU124387 NT2RM2 Homo sapiens cDNA clone NT2RM2002113 5'
6389	18992	31772	1.52	2.0E-64	AF113708.1	NT	Homo sapiens angiotensinogen 4 (ANG4) mRNA, partial cds
6811	19208	32018	4.45	2.0E-64	BF68537.1	EST_HUMAN	602123474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280395 5'
6708	18301	32105	1.36	2.0E-64	AI076387.1	EST_HUMAN	602123474F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4280395 5'
6802	18383	32209	53.03	2.0E-64	M77185.1	NT	oz28b03.x1 Soares total fetus Nb2HFB_9w Homo sapiens cDNA clone IMAGE:1676717 3'
8603	21142	34055	1.98	2.0E-64	11434008	NT	H. sapiens dopamine receptor D5 pseudogene 1, partial cds
8603	21142	34056	1.98	2.0E-64	11434008	NT	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9157	21692	34636	1.14	2.0E-64	AU132570.1	EST_HUMAN	Homo sapiens lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA
9889	22386	35384	0.48	2.0E-64	T06397.1	EST_HUMAN	AU132570 NT2RP4 Homo sapiens cDNA clone NT2RP4000109 5'
9889	22386	35365	0.48	2.0E-64	T06397.1	EST_HUMAN	EST04286 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBD588
10643	23175	36187	2.38	2.0E-64	BF528114.1	EST_HUMAN	EST04286 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBD588
10929	23447	36468	5.36	2.0E-64	AI922811.1	EST_HUMAN	602042892F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180556 5'
10929	23447	36469	5.36	2.0E-64	AI922811.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'
10929	23447	36469	5.36	2.0E-64	AI922811.1	EST_HUMAN	wn81b08.x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2452211 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11112	23622	36663	1.78	2.0E-64	AW884773.1	EST_HUMAN	PM2-SN0018-220300-002-e12 SN0018 Homo sapiens cDNA
11826	24194	31034	1.5	2.0E-64	8597387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
12285	24487		2.44	2.0E-64	H55162.1	EST_HUMAN	CHR220101 Chromosome 22 exon Homo sapiens cDNA clone C22_132 5'
279	12936	25421	1.64	1.0E-64	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
1815	14405	26949	9.93	1.0E-64	A1929419.1	EST_HUMAN	gb:L21698 cds1 PROTHYMOSIN ALPHA (HUMAN); contains element MSR1 repetitive element ;
3045	15661	28142	0.82	1.0E-64	4507334	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
3561	18165	28648	5.94	1.0E-64	AF196779.1	NT	Homo sapiens transcription factor (GHM) enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds, and L-type calcium channel α
3844	18247	28722	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3844	18247	28723	1.14	1.0E-64	AF228527.1	NT	Homo sapiens TRIAD3 mRNA, partial cds
3968	18566	29035	0.87	1.0E-64	8922829	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026), mRNA
9976	22471	35454	0.84	1.0E-64	AA042975.1	EST_HUMAN	ZK5308.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486567 3'
11798	24178		1.37	1.0E-64	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2315	14887	27462	1.02	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2315	14887	27463	1.02	9.0E-65	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
11410	23861		35.61	9.0E-65	BF330676.1	EST_HUMAN	QV4-BT0257-081169-017-e03 BT0257 Homo sapiens cDNA
11383	23895	36897	14.63	8.0E-65	A1929244.1	EST_HUMAN	au58107.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2519005 3' similar to
10059	22534	35550	2.06	7.0E-65	BE081653.1	EST_HUMAN	SW:RL21_HUMAN P48778 60S RIBOSOMAL PROTEIN L21. ;
1094	13699	26209	1.68	6.0E-65	AV721898.1	EST_HUMAN	QV2-BT0635-240400-162-c02 BT0635 Homo sapiens cDNA
1966	14550		5.21	6.0E-65	AA550929.1	EST_HUMAN	AV721898 HTB Homo sapiens cDNA clone HTEBZC08 5'
8681	21220	34140	2.24	6.0E-65	AW083252.1	EST_HUMAN	n86410.s1 NCL CGAP_P111 Homo sapiens cDNA clone IMAGE:999379 similar to gb:K03002 60S
8941	21479	34400	4.18	6.0E-65	AA427878.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
8941	21479	34401	4.18	6.0E-65	AA427878.1	EST_HUMAN	xc07609.x1 NCL CGAP_Co21 Homo sapiens cDNA clone IMAGE:2583545 3' similar to TR:Q63306 Q63306
9004	21541	34471	1.04	6.0E-65	A085314.1	EST_HUMAN	LONG INTERSPERSED REPEATITIVE DNA CONTAINING 7 ORFS. ; contains L1.52 L1 repetitive element ;
9004	21541	34472	1.04	6.0E-65	A085314.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
10752	23276	36289	12.35	6.0E-65	BE587816.1	EST_HUMAN	zw53b06.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:773747 3'
11135	23643	36683	1.73	6.0E-65	AW206752.1	EST_HUMAN	qf18r05.x1 NCL CGAP_Bin25 Homo sapiens cDNA clone IMAGE:1750425 3'
11369	23821	36883	4.4	6.0E-65	AL163210.2	NT	qf18r05.x1 NCL CGAP_Bin25 Homo sapiens cDNA clone IMAGE:1750425 3'
							601340-485F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:1750425 3'
							UIH-B1'-efg-d-10-0-U1.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:368267 5'
							Homo sapiens chromosome 21 segment HS21C010

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
659	13282	25762	0.75	5.0E-65	AF064604.1	NT	Homo sapiens KE03 protein mRNA, partial cds
1397	13991	26518	1.8	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
1397	13991	26519	1.8	5.0E-65	7661951	NT	Homo sapiens KIAA0156 gene product (KIAA0156), mRNA
2200	14776	27349	0.87	5.0E-65	AB033768.1	NT	Homo sapiens HPAD-colony10 mRNA for peptidylarginine deaminase type I, complete cds
3294	15905	28385	2.39	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
3294	15905	28386	2.39	5.0E-65	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
10364	22858	35850	0.99	5.0E-65	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
207	12668	25354	2.15	4.0E-65	AL120419.1	EST_HUMAN	DKFZp761G108_r1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761G108 5'
775	13364	25894	1.3	4.0E-65	AI268468.1	EST_HUMAN	qim46e01.x1 Soares_placenta_8tc9weeks_2NbhHP8tc9w Homo sapiens cDNA clone IMAGE:1891800 3'
775	13394	25895	1.3	4.0E-65	AI268468.1	EST_HUMAN	qim46e01.x1 Soares_placenta_8tc9weeks_2NbhHP8tc9w Homo sapiens cDNA clone IMAGE:1891800 3'
1117	13720	26232	1.52	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
1593	14126	26662	17.23	4.0E-65	4506638	NT	Homo sapiens ribosomal protein L34 (RPL34) mRNA
2374	14944	27516	1.14	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
2374	14944	27517	1.14	4.0E-65	BE221469.1	EST_HUMAN	hu25e04.x1 NCI_CGAP_Mel15 Homo sapiens cDNA clone IMAGE:3171102 3'
6303	18910	31682	4.44	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
6303	18910	31683	4.44	4.0E-65	AB033093.1	NT	Homo sapiens mRNA for KIAA1287 protein, partial cds
7171	19703	32550	0.85	4.0E-65	M19879.1	NT	Human clabindin 27 gene, exons 10 and 11, and L1 and Alu repeats
7271	19769	32656	2.39	4.0E-65	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7783	20328	33230	0.81	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
7783	20328	33231	0.81	4.0E-65	5453765	NT	Homo sapiens nel (chicken)-like 2 (NELL2), mRNA
8072	21609	34539	0.8	4.0E-65	11429127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10473	22987		2.55	4.0E-65	AJ277546.2	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
10833	23354	36369	1.93	4.0E-65	AV738794.1	EST_HUMAN	AV738794 CB Homo sapiens cDNA clone CBC08E05 5'
10977	23492	36522	3.39	4.0E-65	AF119846.1	NT	Homo sapiens PRO1474 mRNA, complete cds
12124	13720	26232	1.41	4.0E-65	4826735	NT	Homo sapiens fragile X mental retardation, autosomal homolog 1 (FXR1), mRNA
101	12778	25261	2.51	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
102	12778	25261	2.35	3.0E-65	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1275	15393		11.57	3.0E-65	X78932.1	NT	H sapiens HZF9 mRNA for zinc finger protein
1605	14197	26729	0.98	3.0E-65	4504628	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1881	14449	27007	1	3.0E-65	AI00692.1	EST_HUMAN	ov23f03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3019	15635	28111	0.8	3.0E-65	D87078.2	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
3315	15925	28403	0.98	3.0E-65	4504950	NT	Homo sapiens laminin, beta 1 (LAMB1), mRNA
3784	16384	28849	1.19	3.0E-65	A1000692.1	EST_HUMAN	α2303.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638173 3' similar to contains element MSR1 repetitive element;
4754	17335	29779	1.36	3.0E-65	6912385	NT	Homo sapiens rab6 GTPase activating protein (GAP and centrosome-associated) (GAPCENA), mRNA
9681	22476	35458	1.44	3.0E-65	BE787368.1	EST_HUMAN	601479686F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882405 5'
11267	23005	36013	13.23	3.0E-65	AA430006.1	EST_HUMAN	zw65a06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781042 5'
3451	16058	28534	5.71	2.0E-65	BF680294.1	EST_HUMAN	602155062F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4285968 5'
6657	19253		5.63	2.0E-65	BE263373.1	EST_HUMAN	601190883F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3534741 5'
7186	19718	32565	25.57	2.0E-65	BF576922.1	EST_HUMAN	602134359F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289295 5'
8779	21318	34241	1.21	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
8779	21318	34242	1.21	2.0E-65	AK024463.1	NT	Homo sapiens mRNA for FLJ00056 protein, partial cds
11750	24147		6.58	2.0E-65	AA307904.1	EST_HUMAN	EST176755 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end similar to endogenous retrovirus
12241	24832		2.26	2.0E-65	BF246086.1	EST_HUMAN	601854033F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4073769 5'
94	12770		0.76	1.0E-65	BF125644.1	EST_HUMAN	601763488F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4026501 5'
564	13195	25674	1.4	1.0E-65	7657495	NT	Homo sapiens putative Rab5 GDP/GTP exchange factor homologue (RABEX5), mRNA
2084	14665	27236	0.95	1.0E-65	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
3419	16027	28508	0.94	1.0E-65	BE466881.1	EST_HUMAN	Homo sapiens mRNA for KIAA1513 protein, partial cds
4070	16666	29127	1.85	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4070	16666	29128	1.85	1.0E-65	4504082	NT	Homo sapiens glycican 4 (GPC4) mRNA
4285	16871	29317	2.39	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
4285	16871	29318	2.39	1.0E-65	AW029340.1	EST_HUMAN	wx09c09.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2543152 3'
5668	18295	30775	0.74	1.0E-65	AI243738.1	EST_HUMAN	qh88h07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854109 3' similar to TR:Q07823 Q07823 MAC30 PROTEIN
8196	20737	33648	4.11	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8196	20737	33649	4.11	1.0E-65	AW820481.1	EST_HUMAN	QV2-ST0298-140200-042-f12 ST0298 Homo sapiens cDNA
8222	20763	33678	0.56	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8222	20763	33680	0.56	1.0E-65	BE732118.1	EST_HUMAN	601566124F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3841012 5'
8261	20802	33719	2.05	1.0E-65	AU141295	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1003356 5'
8261	20802	33720	2.05	1.0E-65	AU141295	EST_HUMAN	AU141295 THYRO1 Homo sapiens cDNA clone THYRO1003356 5'
8774	21313	34235	2.42	1.0E-65	BF688707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
8950	21488	34410	2.86	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8950	21488	34411	2.86	1.0E-65	AU128040.1	EST_HUMAN	AU128040 NT2RP2 Homo sapiens cDNA clone NT2RP2004714 5'
8961	21499		2.54	1.0E-65	11431994	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
9098	21821	34770	5.09	1.0E-65	A1191716.1	EST_HUMAN	FINGER PROTEIN 8 (HUMAN); contains MER19.11 MER19 repetitive element ;
9800	22298	35283	1.39	1.0E-65	AU153793.1	EST_HUMAN	AU153793 NT2RP3 Homo sapiens cDNA clone NT2RP3004016 3'
10203	22698	35692	0.65	1.0E-65	AA069559.1	EST_HUMAN	z175a04.r1 Soares_pineal_gland_N3HPG Homo sapiens cDNA clone IMAGE:382734 5'
10463	22957	35968	1.12	1.0E-65	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10528	23088	36078	3.58	1.0E-65	M26167.1	NT	Human platelet factor 4 variant 1 (PF4var1) gene, complete cds
10556	23188	36204	22.3	1.0E-65	4506660	NT	Homo sapiens ribosomal protein L7a (RPL7A) mRNA
11010	23524	36558	2.79	1.0E-65	BF698707.1	EST_HUMAN	602126239F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4283313 5'
11088	23800	36638	2.25	1.0E-65	A1621017.1	EST_HUMAN	ts7a06.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2237170 3' similar to gb.L15533_rna1
11799	24179		2.28	1.0E-65	11418041	NT	PANCREATITIS ASSOCIATED PROTEIN 1 PRECURSOR (HUMAN);
11896	24238	31005	5.17	1.0E-65	11418322	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
75	12753	25232	4.57	9.0E-66	AL160311.1	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
75	12753	25233	4.57	9.0E-66	AL160311.1	NT	Novel human gene mapping to chromosome 22
1398	13992	26520	1.54	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1398	13992	26521	1.54	9.0E-66	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1531	14123		4.45	9.0E-66	M87289.1	NT	Human transposon-like element, partial
4802	17380	29830	0.57	9.0E-66	AL137163.1	NT	Novel human gene mapping to chromosome X
4801	17379	29829	0.66	8.0E-66	AA424304.1	EST_HUMAN	z190c05.r1 Soares_NhrMPu_S1 Homo sapiens cDNA clone IMAGE:767048 5'
11225	23756		1.78	7.0E-66	BE084410.1	EST_HUMAN	RC4-BT0311-141199-011-H06/BT0311 Homo sapiens cDNA
4455	17041	29483	1.11	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
4455	17041	29484	1.11	6.0E-66	A1924653.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
4455	17041	29485	1.11	6.0E-66	A1924653.1	EST_HUMAN	CE18595 ;
6373	20913		0.48	6.0E-66	BE178563.1	EST_HUMAN	wn57h07.x1 NCI_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2449597 3' similar to WP.F15G9.4A
11038	23552	36587	7.01	6.0E-66	X69181.1	NT	PM2-HT0604-030300-001-b08 HT0604 Homo sapiens cDNA
1411	14004	26532	1.25	5.0E-66	BE064410.1	EST_HUMAN	H. sapiens mRNA for ribosomal protein L31
5278	17840	30266	0.57	5.0E-66	BE898644.1	EST_HUMAN	RC4-BT0311-141199-011-H06/BT0311 Homo sapiens cDNA
5278	17840	30267	0.57	5.0E-66	BE898644.1	EST_HUMAN	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
9218	21735	34677	14.1	5.0E-66	11420557	NT	601681592F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951791 5'
							Homo sapiens thyroid hormone receptor binding protein (AIB3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
823	13440	25947	1.13	4.0E-66	6679816	NT	Mus musculus fragile X mental retardation syndrome 1 homolog (Fmr1), mRNA
1771	14361	26906	0.87	4.0E-66	AW897798.1	EST_HUMAN	RC1-NN0063-100500-022-a02 NN0063 Homo sapiens cDNA
2319	14891	27468	1.64	4.0E-66	X89211.1	NT	H. sapiens DNA for endogenous retroviral like element
2513	15077		2.35	4.0E-66	AJ223384.1	NT	Homo sapiens germ-line DNA upstream of Jkappa locus
4898	17473		6.76	4.0E-66	9835487	NT	Human endogenous retrovirus, complete genome
5739	18365	31072	3.33	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
5918	18540	31268	0.9	4.0E-66	AW939119.1	EST_HUMAN	QV1-DT0069-110200-087-g10 DT0069 Homo sapiens cDNA
6940	18048	30470	4.82	4.0E-66	AW965473.1	EST_HUMAN	EST377546 IMAGE resequences, MAGI Homo sapiens cDNA
7185	19717	32564	7.41	4.0E-66	U78168.1	NT	Homo sapiens cAMP-regulated guanine nucleotide exchange factor 1 (cAMP-GEFI) mRNA, complete cds
7625	18365	31072	1.05	4.0E-66	11428643	NT	Homo sapiens methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase (MTHFD2), mRNA
8022	20564	33466	6.44	4.0E-66	11421638	NT	Homo sapiens hypothetical protein FLJ20116 (FLJ20116), mRNA
8078	20618	33532	0.96	4.0E-66	X57147.1	NT	Human endogenous retrovirus PHE.1 (ERV9)
1473	14065	26601	11.5	3.0E-66	4502088	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
1473	14065	26602	11.5	3.0E-66	4502088	NT	Homo sapiens solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5 (SLC25A5), nuclear gene encoding mitochondrial protein, mRNA
2026	14608	27173	1	3.0E-66	N55323.1	EST_HUMAN	Y27g12.1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2 [2] PIR:B56612
2026	14608	27174	1	3.0E-66	N55323.1	EST_HUMAN	Y27g12.1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2 [2] PIR:B56612
2026	14608	27175	1	3.0E-66	N55323.1	EST_HUMAN	Y27g12.1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:284326 5' similar to SW:H2B1_TIGCA P35088 HISTONE H2B.1/H2B.2 [2] PIR:B56612
2732	15287	27854	3.43	3.0E-66	11141880	NT	Homo sapiens TGF-beta1-induced transcription factor 2 (TGIF2), mRNA
3151	15765	28232	6.89	3.0E-66	7662223	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
5658	18285	30763	0.9	3.0E-66	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5946	18566	31296	2.07	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
5948	18566	31297	2.07	3.0E-66	11417946	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
9444	21970	34918	0.59	3.0E-66	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
9835	22135	35100	0.89	3.0E-66	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
9985	22480	35464	0.8	3.0E-66	7019480	NT	Homo sapiens protocadherin beta 1 (PCDH-beta1), mRNA
10415	22909	35908	0.92	3.0E-66	AF155659.1	NT	Homo sapiens molybdenum cofactor biosynthesis protein E (MCBPE) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11384	23836	36898	9.34	3.0E-66	5453949	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), alpha isoform (PPP2R5A) mRNA
55	12735	25203	1.34	2.0E-66	7657334	NT	Homo sapiens Misshepen/NIK-related kinase (MINK), mRNA
55	12735	25204	1.34	2.0E-66	7657334	NT	Homo sapiens Misshepen/NIK-related kinase (MINK), mRNA
447	12676	25132	1.21	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
447	12676	25133	1.21	2.0E-66	4505524	NT	Homo sapiens origin recognition complex, subunit 5 (yeast homolog)-like (ORC5L) mRNA, and translated products
1886	14452	27011	1.73	2.0E-66	AL163301.2	NT	Homo sapiens chromosome 21 segment HS21C101
3002	15618	28096	1.55	2.0E-66	X65859.1	NT	H. sapiens pseudogene for the low affinity IL-8 receptor
3572	16176	28658	0.97	2.0E-66	8923280	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3828	16428	28889	0.72	2.0E-66	AL117233.1	NT	Novel human gene mapping to chromosome 1
4139	16731	29184	0.57	2.0E-66	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
4760	17341	29788	16.35	2.0E-66	AJ133267.2	NT	Homo sapiens HLA-B gene for human leukocyte antigen B
5982	18602	31336	0.8	2.0E-66	AW968854.1	EST_HUMAN	Homo sapiens HLA-B gene for human leukocyte antigen B
5982	18602	31337	0.8	2.0E-66	AW968854.1	EST_HUMAN	Homo sapiens HLA-B gene for human leukocyte antigen B
8781	21320	34244	2.24	2.0E-66	IN45480.1	EST_HUMAN	EST380930 IMAGE resequences, MAGJ Homo sapiens cDNA
12132	25057		1.8	2.0E-66	11418318	NT	EST380930 IMAGE resequences, MAGJ Homo sapiens cDNA
2919	15536	28010	1.65	1.0E-66	AV717817.1	EST_HUMAN	Y59502.1 Soares multiple sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:277826 5'
2919	15536	28011	1.65	1.0E-66	AV717817.1	EST_HUMAN	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
4474	15536	28010	3.57	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'
4474	15536	28011	3.57	1.0E-66	AV717817.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'
5583	18214	30663	5.49	1.0E-66	BF673088.1	EST_HUMAN	AV717817 DCB Homo sapiens cDNA clone DCBADCO7 5'
5952	18574	31307	0.68	1.0E-66	BE765232.1	EST_HUMAN	602152896F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4284151 5'
5952	18574	31308	0.68	1.0E-66	BE765232.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
7018	19516	32338	0.95	1.0E-66	BF326823.1	EST_HUMAN	IL2-NT0101-280700-116-E04 NT0101 Homo sapiens cDNA
8395	20935	33857	1.8	1.0E-66	AA668858.1	EST_HUMAN	RC5-BN0183-010900-034-G08 BN0183 Homo sapiens cDNA
8347	21861	34809	0.74	1.0E-66	AA018828.1	EST_HUMAN	aa60604 st NC1 CGAP GC81 Homo sapiens cDNA clone IMAGE:827282 3'
10273	22768	35756	0.75	1.0E-66	AV748749.1	EST_HUMAN	ze57e12.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363118 5'
10273	22768	35757	0.75	1.0E-66	AV748749.1	EST_HUMAN	AV748748 NPC Homo sapiens cDNA clone NPCBVA05 5'
10509	23003	36011	0.51	1.0E-66	BE044585.1	EST_HUMAN	AV748748 NPC Homo sapiens cDNA clone NPCBVA05 5'
10821	23342	36357	1.98	1.0E-66	AF111167.2	NT	h047h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040563 3'
							Homo sapiens Jun dimerization protein gene, partial cds; cfos gene, complete cds, and unknown gene

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11901	24240		3	9.0E-67	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
403	13078	25570	3.59	7.0E-67	AW162232.1	EST_HUMAN	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
1425	14018	26547	1.75	7.0E-67	AA383416.1	EST_HUMAN	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
1601	14193	26724	1.25	7.0E-67	W85947.1	EST_HUMAN	EST98812 Testis 1 Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid
1601	14193	26725	1.25	7.0E-67	W85947.1	EST_HUMAN	ZK353
2836	13078	25570	3.15	7.0E-67	AW162232.1	EST_HUMAN	zh56b05.r1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
6231	18840	31612	0.98	7.0E-67	10190895	NT	zh56b05.r1 Soares fetal_liver_spleen_INFLS_S1 Homo sapiens cDNA clone IMAGE:416049 5'
6416	19018	31802	1.79	7.0E-67	11425572	NT	au75d02.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782083 3' similar to gb:M37104
6416	19018	31803	1.79	7.0E-67	11425572	NT	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR (HUMAN);
6823	19413	32230	1.03	7.0E-67	4885084	NT	Homo sapiens zinc finger protein 304 (ZNF304), mRNA
7627	20139	33018	0.99	7.0E-67	11419212	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
7627	20139	33019	0.99	7.0E-67	11419212	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8012	20554	33457	0.49	7.0E-67	4826895	NT	Homo sapiens phosphodiesterase 1/nucleotide pyrophosphatase 3 (PDNIP3) mRNA
8265	20806	33724	0.8	7.0E-67	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8862	21401	34326	0.76	7.0E-67	10835044	NT	Homo sapiens retinaldehyde dehydrogenase 2 (RALDH2), mRNA
11525	23973	37043	2.92	7.0E-67	U82486.1	NT	Human cytochrome oxidase subunit VIa (COX6A1P) pseudogene, complete cds
11675	24094	37147	2.95	7.0E-67	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11675	24094	37148	2.95	7.0E-67	11430480	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12159	24399	30979	1.44	7.0E-67	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
585	13215	25692	1.84	6.0E-67	X88968.1	NT	H. sapiens mRNA for acetyl-CoA carboxylase
828	13445	25952	1.64	6.0E-67	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
1316	13910	26430	1.2	6.0E-67	Y14320.1	NT	Homo sapiens PMP69 gene, exons 3,4,5,6 & 7
3485	16090	28562	1.47	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
3485	16090	28563	1.47	6.0E-67	4507332	NT	Homo sapiens Synapsin III (SYN3) mRNA, and translated products
4205	16794	29240	0.74	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4205	16794	29241	0.74	6.0E-67	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
4815	17393	29845	3.86	6.0E-67	7657020	NT	Homo sapiens DKFZ434P211 protein (DKFZ434P211), mRNA
4815	17393	29846	3.86	6.0E-67	7657020	NT	Homo sapiens DKFZ434P211 protein (DKFZ434P211), mRNA
3258	15870	28350	2.65	5.0E-67	AF009680.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
10883	23384		1.9	5.0E-67	BE10038.1	EST_HUMAN	PM3-BN0176-100400-001-g04 BN0176 Homo sapiens cDNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1373	13967	28494	1.16	4.0E-67	R0819.1	EST_HUMAN	yn02d11.1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:167253 5'
7984	20506	33413	0.68	4.0E-67	AF33032.1	EST_HUMAN	q126c05.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1493286 3' similar to SW:Z33A_HUMAN
8322	20863		1.3	4.0E-67	BF357321.1	EST_HUMAN	Q06730 ZINC FINGER PROTEIN 33A ;
10942	23458		1.92	4.0E-67	AA714294.1	EST_HUMAN	RC0-HT0834-150900-028-c03 HT0834 Homo sapiens cDNA
2839	13284	25765	5.7	3.0E-67	AA333768.1	EST_HUMAN	hw08a01.s1 NCI_CGAP_SS1 Homo sapiens cDNA clone IMAGE:1238472 3' similar to TR:O10385 O10385
4804	17382	28832	3.38	3.0E-67	AW869159.1	EST_HUMAN	PRO-POL-DUTPASE POLYPROTEIN ;
4831	17409		0.93	3.0E-67	AL163279.2	NT	EST37903 Embryo, 9 week Homo sapiens cDNA 5' end
8122	20663	33573	1.17	3.0E-67	BF196068.1	EST_HUMAN	MR3-SN0066-040500-008-f01 SN0066 Homo sapiens cDNA
11139	23847		22.61	3.0E-67	AA927874.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C079
201	12882	25346	1.74	2.0E-67	BE348354.1	EST_HUMAN	hr81f05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3134913 3' similar to SW:RHOP_MOUSE
878	13492	26010	4.99	2.0E-67	AW816405.1	EST_HUMAN	Q81085 GTP-RHO BINDING PROTEIN 1 ;
1144	13747		1.84	2.0E-67	AF187480.1	NT	om18b07.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1541365 3'
1928	14512	27069	1.5	2.0E-67	BE303037.1	EST_HUMAN	hw16g09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3183138 3' similar to WP:F23H11.9
1928	14512	27070	1.5	2.0E-67	BE303037.1	EST_HUMAN	CE09617 ;
2428	14995	27570	2.84	2.0E-67	AF309581.1	NT	QV4-ST0234-181199-037-05 ST0234 Homo sapiens cDNA
2475	15042	27610	0.95	2.0E-67	4758795	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exons 2a, 2, 3, and 4
3514	16119	28599	4.48	2.0E-67	AA825755.1	EST_HUMAN	Homo sapiens developmentally regulated GTP-binding protein 1 (DRG1), mRNA
4074	16670	29131	2.76	2.0E-67	AL163300.2	NT	zu01g01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:746392 3'
6222	18831	31605	0.83	2.0E-67	AL049784.1	NT	Homo sapiens chromosome 21 segment HS21C100
6273	18881	31649	5.18	2.0E-67	BF240758.1	EST_HUMAN	Novel human gene mapping to chromosome 13
6438	19040	31827	2.25	2.0E-67	AB051763.1	NT	601875351F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4091893 5'
6438	19040	31828	2.25	2.0E-67	AB051763.1	NT	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8493	21032	33952	0.96	2.0E-67	AA334609.1	EST_HUMAN	Homo sapiens mRNA for NADPH-cytochrome P-450 reductase, complete cds
8493	21032	33953	0.96	2.0E-67	AA334609.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8927	21465	34381	1.09	2.0E-67	AW602635.1	EST_HUMAN	EST38850 Embryo, 9 week Homo sapiens cDNA 5' end similar to similar to cerebellin
8927	21465	34382	1.09	2.0E-67	AW602635.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9498	21943	34890	1.24	2.0E-67	AV731333.1	EST_HUMAN	RC4-BT0566-170100-011-c07 BT0566 Homo sapiens cDNA
9625	22125	35089	1.19	2.0E-67	AW263024.1	EST_HUMAN	AV731333 HTF Homo sapiens cDNA clone HTFARD03 5'
							UI-H-B12-ahn-e-10-0-U1.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2727283 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10781	23305	36313	1.57	2.0E-67	BF685788.1	EST_HUMAN	602140470F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4301705 5'
10934	25127		3.62	2.0E-67	11436448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
11107	23617	36859	1.85	2.0E-67	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
11330	23028	36037	2.01	2.0E-67	BF377169.1	EST_HUMAN	PM2-TN0103-040900-001-c02 TN0103 Homo sapiens cDNA
12034	24911	30714	2.53	2.0E-67	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12347	24528	30925	2.26	2.0E-67	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
274	12831	25418	3.31	1.0E-67	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
737	13357	25851	1.2	1.0E-67	AA702794.1	EST_HUMAN	z80b04.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:448015 3'
2220	14795	27368	1.73	8.0E-68	BE870732.1	EST_HUMAN	601448568F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3852254 5'
3937	16535	29001	5.37	8.0E-68	AA209459.1	EST_HUMAN	z82h10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
3937	16535	29002	5.37	8.0E-68	AA209459.1	EST_HUMAN	z82h10.r1 Stratagene hNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648163 5' similar to SW:SAV_SULAC Q07590 SAV PROTEIN ;
8045	20587	33493	0.53	7.0E-68	A1810505.1	EST_HUMAN	wb89a03.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2312860 3'
10348	22840	35638	2.53	6.0E-68	11422088	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
12349	24530		3.32	6.0E-68	BE612554.1	NT	601462067F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855761 5'
835	15389	25660	0.67	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
835	15389	25961	0.67	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
852	13468	25977	4.54	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
852	13468	25978	4.54	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
2808	15360	27927	72.53	5.0E-68	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
3181	15794	28266	3.22	5.0E-68	AB037852.1	NT	Homo sapiens mRNA for KIAA1431 protein, partial cds
4260	16846		0.63	5.0E-68	4826887	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
4590	17173	29618	1.21	5.0E-68	AL157645.1	EST_HUMAN	DKFZp547D207.r1 547 (synonym: hbr1) Homo sapiens cDNA clone DKFZp547D207 5'
5111	17683		8.62	4.0E-68	P04406	SWISSPROT	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER
6118	18734	31487	0.76	4.0E-68	AF157063.1	NT	Homo sapiens sedlin (SED1) gene, exon 4
6870	19604	32437	6.01	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
6870	19604	32438	6.01	4.0E-68	11055991	NT	Homo sapiens serine carboxypeptidase 1 precursor protein (HSCP1), mRNA
7674	20185	33073	0.92	4.0E-68	7681683	NT	Homo sapiens DKFZP586L0724 protein (DKFZP586L0724), mRNA
8970	21508	34429	5.04	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
8970	21508	34430	5.04	4.0E-68	D63479.2	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
9106	21642	34582	2.9	4.0E-68	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
10882	23403	38420	5.14	4.0E-68	4506292	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10882	23403	36421	5.14	4.0E-68	4506282	NT	Homo sapiens protein tyrosine phosphatase type IVA, member 1 (PTP4A1) mRNA
12225	24446	30953	2.91	4.0E-68	11417966	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
3722	16323	28780	2.56	3.0E-68	AF236082.1	NT	Mus musculus G-protein coupled receptor GPR73 (Gpr73) mRNA, complete cds
9378	20317		6.15	3.0E-68	AI342323.1	EST_HUMAN	q38h02.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1950291 3' similar to contains THR 12 THR repetitive element ;
10396	22890	35884	1.77	3.0E-68	F28784.1	EST_HUMAN	HSPD18178 HM3 Homo sapiens cDNA clone s3000023D09
12571	24829		2.05	3.0E-68	AW939485.1	EST_HUMAN	QV1-DT0072-010200-056-H06 DT0072 Homo sapiens cDNA
2887	18011		27.71	2.0E-68	D00522.1	NT	Cricetulus longicaudatus mRNA for EF-1 alpha, complete cds
4097	16892	29149	0.78	2.0E-68	BE875766.1	EST_HUMAN	715f02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:3294747 3' similar to TR:O80828 O80828
4789	17369	29821	1.56	2.0E-68	AB009681.1	NT	HYPOTHETICAL 88.8 KD PROTEIN ;
6957	19534		8.88	2.0E-68	R45008.1	EST_HUMAN	Homo sapiens gene for activin receptor type IIB, complete cds
7123	19463	32280	4.61	2.0E-68	BF035316.1	EST_HUMAN	y33g04.s1 Soares infant brain IN1B Homo sapiens cDNA clone IMAGE:34896 3'
8879	21417	34341	0.84	2.0E-68	Q05859	SWISSPROT	601456514F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3852034 5'
10494	22988	35996	0.46	2.0E-68	N78483.1	EST_HUMAN	FORMIN 4 (LIMB DEFORMITY PROTEIN)
11792	25077		2.11	2.0E-68	BE897376.1	EST_HUMAN	y278d07.r1 Soares_multiple_sclerosis_2NbrHSP Homo sapiens cDNA clone IMAGE:289165 5'
12639	24714		1.84	2.0E-68	AW016803.1	EST_HUMAN	601437367F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922192 5'
83	12758	25242	0.78	1.0E-68	4505222	NT	UI-H-B10-aam-b-05-0-U1.s1 NCI CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709824 3'
318	12872	25461	12.22	1.0E-68	AW816405.1	EST_HUMAN	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
2294	14868	27443	0.89	1.0E-68	AB011149.1	NT	QV4-ST0234-181199-037-105 ST0234 Homo sapiens cDNA
2294	14868	27444	0.89	1.0E-68	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2785	15336	27909	1.12	1.0E-68	AW451832.1	EST_HUMAN	Homo sapiens mRNA for KIAA0577 protein, complete cds
5178	17745	30174	0.66	1.0E-68	AA897343.1	EST_HUMAN	UI-H-B13-alk-f01-Q-J1.s1 NCI CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2737272 3'
5233	17797	30215	0.88	1.0E-68	BE296032.1	EST_HUMAN	al47g12.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460518 3'
5525	18157	30572	1.51	1.0E-68	7662349	NT	601177002F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532344 5'
10085	22580	35573	0.49	1.0E-68	11419429	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
10732	23258	36274	2.83	1.0E-68	11418869	NT	Homo sapiens similar to ecdonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
10732	23258	36275	2.83	1.0E-68	11418869	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
10783	23307	36314	3.41	1.0E-68	L76416.1	NT	Homo sapiens phosphodiesterase 7B (PDE7B), mRNA
11072	23594	36625	1.72	1.0E-68	11433277	NT	Homo sapiens MIF2 suppressor (HSMIT3) mRNA, complete cds
11179	23685	36731	2.23	1.0E-68	U50319.1	NT	Homo sapiens myosin IC (MYO1C), mRNA
11179	23685	36732	2.23	1.0E-68	U50319.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5
11517	23685	37036	2.1	1.0E-68	11418431	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 4-5

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11517	23985	37037	2.1	1.0E-68	11418431	NT	Homo sapiens CGI-76 protein (LOC51632), mRNA
12330	12759	25242	2.37	1.0E-68	4505222	NT	Homo sapiens meningioma (disrupted in balanced translocation) 1 (MN1), mRNA
12618	24697		1.62	1.0E-68	11418213	NT	Homo sapiens ADP-ribosylation factor GTPase activating protein 1 (ARFGAP1), mRNA
23	12702	25158	13.45	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
23	12702	25159	13.45	9.0E-69	5031976	NT	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
1085	13670	26180	1.44	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
1085	13670	26181	1.44	9.0E-69	5031980	NT	Homo sapiens 26S proteasome-associated pad1 homolog (POH1) mRNA
4208	16797	29245	0.69	9.0E-69	4757867	NT	Homo sapiens v-rat murine sarcoma viral oncogene homolog B1 (BRAF) mRNA
5384	17943	30356	0.9	9.0E-69	AF057177.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
10769	23293		11.7	9.0E-69	AU117241.1	EST_HUMAN	AU117241 HEMBA1 Homo sapiens cDNA clone HEMBA1000988 5'
3433	16041		1.56	8.0E-69	AJ237744.1	NT	Homo sapiens RIBIIR gene (partial), exon 12
6493	19094	31878	5.18	7.0E-69	9968912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
7804	20347	33264	22.34	6.0E-69	A192764.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1743601 3' similar to
7804	20347	33265	22.34	6.0E-69	A192764.1	EST_HUMAN	gbL11566 60S RIBOSOMAL PROTEIN L18 (HUMAN);
8904	21442	34365	0.98	5.0E-69	AAB26039.1	EST_HUMAN	q62h01.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1372300 3'
546	13177		1.07	4.0E-69	A1873630.1	EST_HUMAN	cd60a03.x1 NCI CGAP_GCBT Homo sapiens cDNA clone IMAGE:2437125 3'
5934	24751	31283	1.56	4.0E-69	BE561063.1	EST_HUMAN	wm26h11.x1 NCI CGAP_UK Homo sapiens cDNA clone IMAGE:3677641 5'
6009	18629	31364	4.7	4.0E-69	A1764973.1	EST_HUMAN	601344705F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2384819 3' similar to TR.O55137
6739	19333	32139	2.45	4.0E-69	4557732	NT	O55137 ACYL-COA THIOESTERASE ;
6739	19333	32140	2.45	4.0E-69	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8845	21384	34309	0.59	4.0E-69	AU119634.1	EST_HUMAN	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
12653	24733		2.96	4.0E-69	A187952.1	EST_HUMAN	AU119634 HEMBA1 Homo sapiens cDNA clone HEMBA1006283 5'
409	13084	25577	4.92	3.0E-69	BE258012.1	EST_HUMAN	qet3f05.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738881 3'
640	13263	25739	2.24	3.0E-69	AF221712.1	NT	60111037F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3351352 5'
							Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
1602	14194		1.13	3.0E-69	T80514.1	EST_HUMAN	yd08a02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:24880 5' similar to SP.A48836
2415	14983		1.34	3.0E-69	5728910	NT	A48836 SPEGF III-EGF REPEAT-CONTAINING FIBROBLAST-LIKE PROTEIN - SEA URCHIN ;
4688	17270		0.77	3.0E-69	T96234.1	EST_HUMAN	Homo sapiens lymphatic vessel endothelial hyaluronan receptor 1 (LYVE-1) mRNA
5407	17270		0.61	3.0E-69	T96234.1	EST_HUMAN	ye48h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121015 5'
5452	18021	37141	1.37	3.0E-69	11418185	NT	ye48h04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121015 5'
							Homo sapiens aconitase 2, mitochondrial (ACO2), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6894	19628		0.89	3.0E-69	AJ27557.1	NT	Homo sapiens dNT-2 gene for mitochondrial 5(3')-deoxyribonucleotidase (dNT-2 gene), exons 1-5
7407	19932	32796	0.87	3.0E-69	AF095703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
7449	19973	32840	1.42	3.0E-69	U52351.1	NT	Homo sapiens arm-repeat protein NPRAP/neurojungin (CTNND2) mRNA, partial cds
7554	20073	32949	7.75	3.0E-69	AF288075.1	NT	Homo sapiens TRAF6-binding protein T6BP mRNA, complete cds
8313	20854	33780	0.87	3.0E-69	AW138646.1	EST_HUMAN	UIH-B11-actw-g-01-O-UI.s1 NC1 CGAP Sub3 Homo sapiens cDNA clone IMAGE:2715840 3'
8703	21242		1.8	3.0E-69	AA376309.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' and similar to similar to ribosomal protein S18
8907	21445	34367	0.5	3.0E-69	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
9334	21848	34797	1.77	3.0E-69	X13223.1	NT	H. sapiens mRNA for N-acetylglucosaminide-(beta 1-4)-galactosyltransferase
							Human mRNA for calcium-binding protein in macrophages (MRP-14) macrophage migration inhibitory factor (MIF)-related protein
9452	21978	34930	8.92	3.0E-69	X06233.1	NT	
9743	22241	35222	0.55	3.0E-69	5730036	NT	Homo sapiens SEC10 (S. cerevisiae)-like 1 (SEC10L1), mRNA
10520	23058	36068	3.93	3.0E-69	11432120	NT	Homo sapiens ribosomal protein S15a (RPS15A), mRNA
10721	23249		12.34	3.0E-69	AA376399.1	EST_HUMAN	EST88807 HSC172 cells II Homo sapiens cDNA 5' end similar to similar to ribosomal protein S18
11813	24185		3.86	3.0E-69	11419157	NT	Homo sapiens HGO6.2 protein (HGO6.2), mRNA
134	13062	25556	1.07	2.0E-69	AF160292.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
134	13062	25557	1.07	2.0E-69	AF160292.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
429	13062	25556	5.07	2.0E-69	AF160292.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
429	13062	25557	5.07	2.0E-69	AF160292.1	NT	Homo sapiens KIAA0553 protein gene, complete cds; and alpha1b protein gene, partial cds
1929	14513	27071	1.46	2.0E-69	BE257857.1	EST_HUMAN	601109444F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350074 5'
2869	15487		2.88	2.0E-69	AA431157.1	EST_HUMAN	zw71g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781682 5'
8489	21028	33946	0.82	2.0E-69	AA114270.1	EST_HUMAN	zrn29g01.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:527088 5'
1740	14330	28874	1.89	1.0E-69	AF053788.1	NT	Rattus norvegicus brain specific cortactin-binding protein GBP90 mRNA, partial cds
5173	17740		0.58	1.0E-69	BE409094.1	EST_HUMAN	601301284F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635781 5'
6201	18811	31580	0.76	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3658532 5'
6201	18811	31581	0.76	1.0E-69	BE902501.1	EST_HUMAN	601675788F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3658532 5'
6717	19311	32114	4.38	1.0E-69	AW393669.1	EST_HUMAN	QV0-TT0010-031199-045-c07 TT0010 Homo sapiens cDNA
6908	19642	32478	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6908	19642	32479	1.4	1.0E-69	7662263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
6924	19583	32412	3.33	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
6924	19583	32413	3.33	1.0E-69	AB032973.1	NT	Homo sapiens mRNA for KIAA1147 protein, partial cds
							TCBAP1E2878 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project-TCBA Homo sapiens cDNA clone TCBAP 2678
10077	22572	35566	5.1	1.0E-69	BE245070.1	EST_HUMAN	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10077	22572	35567	5.1	1.0E-68	BE245070.1	EST_HUMAN	TCBAP1E2678 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP2678
10169	22684	35659	1.41	1.0E-68	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
10313	22807	35788	0.47	1.0E-68	BF528429.1	EST_HUMAN	602043782F1 NCI CGAP Bm67 Homo sapiens cDNA clone IMAGE:4181325 5'
10751	23275		14.22	1.0E-68	4504918	NT	Homo sapiens keratin 8 (KRT8) mRNA
11745	24144	36768	1.61	1.0E-68	BF125887.1	EST_HUMAN	601762902F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025785 5'
12169	24408		4.69	1.0E-68	A1806994.1	EST_HUMAN	wf64608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2380390 3' similar to contains Alu repetitive element; contains element MIR repetitive element
2370	15464	27513	1.52	8.0E-70	AA230303.1	EST_HUMAN	nc13d12.11 NCI CGAP P11 Homo sapiens cDNA clone IMAGE:1008023
4463	17049	28493	1.81	8.0E-70	L77686.1	NT	Homo sapiens DGS-1 mRNA, 3' end
1849	14437	26893	1.65	7.0E-70	A1497807.1	EST_HUMAN	tm89101.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1849	14437	26894	1.65	7.0E-70	A1497807.1	EST_HUMAN	tm89101.x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2165305 3'
1874	14558	27115	1.64	7.0E-70	AA282955.1	EST_HUMAN	215H04.11 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:713239 5'
2109	14687		3.14	7.0E-70	5031668	NT	Homo sapiens tumor suppressor deleted in oral cancer-related 1 (DOC-1R) mRNA
4309	16895	29339	4.83	7.0E-70	4757723	NT	Homo sapiens adenylate cyclase 3 (ADCY3) mRNA
5674	18301	30762	5.56	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
5674	18301	30763	5.56	7.0E-70	AB032369.1	NT	Homo sapiens MIST mRNA, partial cds
7004	19502	32321	3.22	7.0E-70	AJ000052.1	NT	Homo sapiens gene encoding splicing factor SF1, exons 2-8
7745	20253	33147	0.67	7.0E-70	AB037715.1	NT	Homo sapiens titin immunoglobulin domain protein (myotilin) (TTID), mRNA
8370	20910	33829	2.67	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8370	20910	33830	2.67	7.0E-70	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
8856	21195	34114	3.59	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
8856	21195	34115	3.59	7.0E-70	M74099.1	NT	Human displacement protein (CCAAT) mRNA
9084	21620	34555	3.99	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9084	21620	34556	3.99	7.0E-70	X59841.1	NT	Human PBX3 mRNA
9356	20285	33184	3.84	7.0E-70	AF153715.1	NT	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
9382	20320	33223	2.01	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9382	20320	33224	2.01	7.0E-70	11525964	NT	Homo sapiens karyopherin beta 2b, transportin (TRN2), mRNA
9575	22075	35038	1.33	7.0E-70	4557624	NT	Homo sapiens glutamate-cysteine ligase (gamma-glutamylcysteine synthetase), catalytic (GLCLC) mRNA
10199	22694	35686	0.61	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
10199	22694	35687	0.61	7.0E-70	AB036429.1	NT	Homo sapiens NDST4 mRNA for N-deacetylaseN-sulfotransferase 4, complete cds
10953	23468	36492	1.59	7.0E-70	11429685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA
10953	23468	36493	1.59	7.0E-70	11429685	NT	Homo sapiens spastic paraplegia 4 (autosomal dominant; spastin) (SPG4), mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11468	23918	36986	2.2	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, <i>S. cerevisiae</i>) homolog A (HIRA), mRNA
11468	23918	36987	2.2	7.0E-70	11526319	NT	Homo sapiens HIR (histone cell cycle regulation defective, <i>S. cerevisiae</i>) homolog A (HIRA), mRNA
904	13518	26036	2	6.0E-70	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
2182	14758	27328	1.02	6.0E-70	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
2551	15115	27685	1.42	6.0E-70	8923899	NT	Homo sapiens CMP-N-acetylneuraminic acid synthase (LOC55907), mRNA
2588	15470	27715	1.68	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
2588	15470	27716	1.68	5.0E-70	7662307	NT	Homo sapiens KIAA0792 gene product (KIAA0792), mRNA
11756	24151		3.79	5.0E-70	BE766034.1	EST_HUMAN	MR3-HT0487-150200-115-a08 HT0487 Homo sapiens cDNA
6851	18440	32255	153.56	4.0E-70	T06037.1	EST_HUMAN	EST03926 Fetal brain, <i>Stratagene</i> (cat#38206) Homo sapiens cDNA clone HFBDN25
6887	18622	32456	0.79	4.0E-70	AW793226.1	EST_HUMAN	GM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
6887	18622	32457	0.79	4.0E-70	AW793226.1	EST_HUMAN	GM4-UM0003-010300-105-g08 UM0003 Homo sapiens cDNA
1633	14225	28757	1.19	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
1633	14225	28757	1.19	3.0E-70	BE071796.1	EST_HUMAN	RCO-BT0522-071289-011-a12 BT0522 Homo sapiens cDNA
8100	18716	31487	0.9	3.0E-70	A1831975.1	EST_HUMAN	W800403.x1 NCI_CGAP CLL1 Homo sapiens cDNA clone IMAGE:2388005 3'
6511	19111	31897	2.36	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4302808 5'
6511	19111	31898	2.36	3.0E-70	BF685233.1	EST_HUMAN	602141561F1 NIH_MGC 48 Homo sapiens cDNA clone IMAGE:4302808 5'
41	12720	25181	0.89	2.0E-70	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
718	13339	25826	11.56	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
718	13339	25827	11.56	2.0E-70	N42161.1	EST_HUMAN	Y07a10.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:270522 5' similar to SW:D3HI_RAT P28286 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR ;
734	13354	25850	3.41	2.0E-70	A1246899.1	EST_HUMAN	q55h01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004913 3'
1059	13694	26175	1.89	2.0E-70	8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
1226	13825	26340	1.29	2.0E-70	7681883	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1226	13825	26341	1.29	2.0E-70	7681883	NT	Homo sapiens KIAA0193 gene product (KIAA0193), mRNA
1778	14368	26912	1.48	2.0E-70	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
2359	14930		4.22	2.0E-70	AA054010.1	EST_HUMAN	z48g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:380214 5' similar to SW:GAG_HTL1A
3688	16289	28758	2.21	2.0E-70	H37888.1	EST_HUMAN	P03345 GAG POLYPROTEIN ;
3891	16490	28950	0.8	2.0E-70	AL133207.2	NT	yp58p04.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:191599 5'
4123	16716	29172	5.05	2.0E-70	M69181.1	NT	Novel human gene mapping to chromosome X Human nonmuscle myosin heavy chain-B (MYH10) mRNA, partial cds

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5706	18332	30836	8.49	2.0E-70	X72662.1	NT	H.sapiens gene for schwannomin (CS9)
5706	18332	30837	8.49	2.0E-70	X72662.1	NT	H.sapiens gene for schwannomin (CS9)
6351	18956	31735	1.22	2.0E-70	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
6745	19338	32144	1.97	2.0E-70	DT2625.1	NT	Human mRNA for NF1 protein isoform (neurofibromin isoform), complete cds
6773	19365	32176	9.77	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
6773	19365	32177	9.77	2.0E-70	AF123074.1	NT	Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
7070	18089	30446	1.64	2.0E-70		NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
7434	19958	32823	0.84	2.0E-70	AF286207.1	NT	Homo sapiens cystenyl-RNA synthetase mRNA, complete cds, alternatively spliced
7859	20401	33307	6.42	2.0E-70	M21741.1	NT	Human guanine nucleotide-binding protein alpha-subunit gene (G-s-alpha), exons 4 and 5
8164	20705	33621	0.75	2.0E-70		NT	Homo sapiens amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III) (AGL), mRNA
8594	21133		0.8	2.0E-70	H47859.1	EST_HUMAN	ye79g02.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:183882 5'
9096	21632	34571	0.97	2.0E-70		NT	Homo sapiens dynactin p62 subunit (LOC51164), mRNA
10044	22539	35536	1.3	2.0E-70	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10490	22984	35992	0.6	2.0E-70	AB033042.1	NT	Homo sapiens mRNA for KIAA1216 protein, partial cds
10950	23465	36487	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
10950	23465	36488	3.48	2.0E-70	8923420	NT	Homo sapiens hypothetical protein FLJ20450 (FLJ20450), mRNA
11497	23946	37016	7.73	2.0E-70	4503520	NT	Homo sapiens eukaryotic translation initiation factor 3, subunit 6 (48kD) (EIF3S6) mRNA
12157	24397	30976	2.52	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12157	24397	30977	2.52	2.0E-70	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
3440	16048		2.73	1.0E-70		NT	Homo sapiens transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM3) mRNA
9204	21721		0.64	1.0E-70	W85795.1	EST_HUMAN	zh55g05.r1 Soares_fetal_liver_spleen_1NFLS S1 Homo sapiens cDNA clone IMAGE:416024 5'
9714	22212		0.81	1.0E-70	AA442292.1	EST_HUMAN	zv54c03.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757444 5'
10814	23335	36348	15.93	1.0E-70	AV739538.1	EST_HUMAN	AV739538 CB Homo sapiens cDNA clone CB1GB810 5'
						EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6099	18715	31465	9.2	9.0E-71	A1143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE.;
						EST_HUMAN	qe04f01.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1738009 3' similar to TR:O14045
6099	18715	31468	9.2	9.0E-71	A1143870.1	EST_HUMAN	O14045 PHOSPHOTRANSFERASE.;
7098	19689	32508	1.82	9.0E-71	A1654903.1	EST_HUMAN	wb52c05.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;
14300	10660	32508	5.11	9.0E-71	A1654903.1	EST_HUMAN	wb52c05.x1 NC1 CGAP_G08 Homo sapiens cDNA clone IMAGE:2309288 3' similar to TR:P97213 P97213 CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4 GENES.;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9000	21537		3.85	8.0E-71	AA171451.1	EST_HUMAN	zp21d11.r1 Stratagene neuroepithelium (#837231) Homo sapiens cDNA clone IMAGE:610101 5' similar to TR:G1143061 G1143061 STRAIN XA34 POL :
7410	19935	32800	7.39	7.0E-71	AA442230.1	EST_HUMAN	z60h06.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:758075 5'
8612	21151	34065	1.34	7.0E-71	AA705457.1	EST_HUMAN	z91a06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462226 3'
11211	23714	36769	5.33	7.0E-71	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
2251	14925	27401	7.82	5.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
4197	16787	29236	1.17	5.0E-71	AW818405.1	EST_HUMAN	QV4-ST0234-181198-037-05 ST0234 Homo sapiens cDNA
6041	18660	31399	1.72	5.0E-71	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6768	19361	32170	1.8	5.0E-71	11641408	NT	Homo sapiens keratin, hair, acidic, 7 (KRT47), mRNA
7000	19498	32318	0.8	5.0E-71	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7200	19731	32583	0.87	5.0E-71	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7520	20040	32909	2.64	5.0E-71	M38108.1	NT	Human neurofibromatosis protein type 1 mRNA, 3' end of cds
7693	20202	33089	0.72	5.0E-71	11528445	NT	Homo sapiens MAGUK protein p55T, Protein Associated with Lins 2 (LOC51878), mRNA
7716	20224	33113	20.65	5.0E-71	AF072810.1	NT	Homo sapiens transcription factor WSTF mRNA, complete cds
8460	21000	33916	0.89	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
8480	21000	33917	0.89	5.0E-71	5453777	NT	Homo sapiens nuclear factor related to kappa B binding protein (NFKB) mRNA
9825	22323		2.26	5.0E-71	X13467.1	NT	Human PreA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 2)
10513	23051	36092	1.57	6.0E-71	5728900	NT	Homo sapiens (GF-I) mRNA-binding protein 3 (KOC1), mRNA
10859	23380	36399	4.63	5.0E-71	11436314	NT	Homo sapiens pro-platelet basic protein (includes platelet basic protein, beta-thromboglobulin, connective tissue-activating peptide III, neutrophil-activating peptide-2) (PPBP), mRNA
11071	23583	36624	2.24	5.0E-71	11438069	NT	Homo sapiens similar to hypothetical protein FLJ20163 (H. sapiens) (LOC633325), mRNA
11706	24119	37152	1.76	5.0E-71	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
108	12784	25267	1.08	4.0E-71	4507592	NT	Homo sapiens tumor necrosis factor (ligand) superfamily, member 10 (TNFSF10) mRNA
372	13021	25507	116.83	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
372	13021	25507	116.83	4.0E-71	AF157626.1	NT	Equus caballus glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds
2911	15528	27996	3.25	4.0E-71	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4519	17103	29549	5.18	4.0E-71	AF056322.1	NT	Homo sapiens SP100-HMG nuclear autoantigen (SP100) mRNA, complete cds
5123	17695	30132	6.54	4.0E-71	7657602	NT	Homo sapiens putative heme-binding protein (SOUL), mRNA
7977	20519		1.23	3.0E-71	AU135734.1	EST_HUMAN	AU135734 PLACE1 Homo sapiens cDNA clone IMAGE:1043683 similar to contains PTR5.3 PTR5
							repetitive element:
10572	23107	36121	4.09	3.0E-71	AA557683.1	EST_HUMAN	
1273	13869	26389	6.26	2.0E-71	AL183206.2	NT	Homo sapiens chromosome 21 segment HS21C006
5523	18155	30570	6.94	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds
5523	18155	30571	6.94	2.0E-71	D87462.1	NT	Human mRNA for KIAA0272 gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10478	22972	35979	2.97	2.0E-71	AF085703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10478	22972	35980	2.97	2.0E-71	AF085703.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds
10574	23109	36122	3.75	2.0E-71	BE018477.1	EST_HUMAN	b681a06.yt NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048754 5' similar to SW.R23B_HUMAN P54727 UV EXCISION REPAIR PROTEIN PROTEIN RAD23 HOMOLOG B ;
11454	23904	36971	1.96	2.0E-71	R55626.1	EST_HUMAN	y177c11.r1 Soares breast 2NBH8st Homo sapiens cDNA clone IMAGE:154772 5'
11825	24193		10.18	2.0E-71	T05489.1	EST_HUMAN	y643e09.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:120520 5'
666	13290	25771	1.4	1.0E-71	A077927.1	EST_HUMAN	oy15e03.s1 Soares senescent fibroblasts NBHSF Homo sapiens cDNA clone IMAGE:1665916 3' similar to contains LOR1.b2 LOR1 repetitive element ;
977	13589	26104	2.23	1.0E-71	7706281	NT	Homo sapiens neuronal cell death-related protein (LOC51816), mRNA
1139	13742	26251	4.37	1.0E-71	AF205880.1	NT	Homo sapiens disabled-2 gene, exons 2 through 15 and complete cds
1385	13979	26506	10.24	1.0E-71	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pikK230) mRNA, complete cds
2129	14707	27278	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2129	14707	27278	1.38	1.0E-71	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
2717	15274	27840	3.73	1.0E-71	7657153	NT	Homo sapiens hairy/enhancer-of-split related with YRPW motif-like (HEYL), mRNA
3549	16163	28635	1.24	1.0E-71	AF119685.1	NT	Homo sapiens inorganic pyrophosphatase mRNA, complete cds
3656	16259	28730	6.17	1.0E-71	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3656	16259	28730	6.17	1.0E-71	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3656	16259	28731	6.17	1.0E-71	AF248219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
3710	16311	28778	0.95	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3710	16311	28779	0.95	1.0E-71	BE122850.1	EST_HUMAN	02_15 Human Epidermal Keratinocyte Subtraction Library- Upregulated Transcripts Homo sapiens cDNA clone 02_15 5' similar to Homo sapiens chromosome 19
3804	16404	28868	2.11	1.0E-71	AF218904.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 19
4569	17152	29598	2.19	1.0E-71	D28476.1	NT	Human mRNA for KIAA0045 gene, complete cds
4695	17277	29723	0.91	1.0E-71	H23170.1	EST_HUMAN	ym56h10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:52528 5'
6840	19430	32246	1.54	1.0E-71	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2), mRNA
7144	19877	32517	1.33	1.0E-71	AB011131.1	NT	Homo sapiens mRNA for KIAA0559 protein, partial cds
7352	19878	32743	11.94	1.0E-71	U80753.1	NT	Homo sapiens CAGL79 mRNA, partial cds
8089	20630	33543	0.87	1.0E-71	AF105267.1	NT	Homo sapiens glycican-6 (GPC6) mRNA, complete cds
8110	20851	33559	2.11	1.0E-71	11425430	NT	Homo sapiens myomesin (M-protein) 2 (165KD) (MYOM2), mRNA
8383	20923	33842	3.93	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA
8383	20923	33843	3.93	1.0E-71	8922811	NT	Homo sapiens hypothetical protein FLJ10998 (FLJ10998), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9155	21690	34634	0.97	1.0E-71	S72369.1	NT	GSNK2A1=casein kinase II (CKII) subunit alpha [human, Genomic, 18862 nt]
9920	22416	35391	7.06	1.0E-71	AY007943.1	NT	Homo sapiens cytochrome c oxidase subunit VIIa-related protein gene, complete cds
9880	22475		4.9	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10431	22825	35931	1.97	1.0E-71	11433142	NT	Homo sapiens activated leucocyte cell adhesion molecule (ALCAM), mRNA
10663	23195		6.4	1.0E-71	AV761217.1	EST_HUMAN	AV761217 MDS Homo sapiens cDNA clone MDSEIA03 5'
10762	23286	36298	2.09	1.0E-71	11418903	NT	Homo sapiens coagulation factor XIII, A1 polypeptide (F13A1), mRNA
11025	23539	36574	1.82	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
11025	23539	36575	1.82	1.0E-71	11417191	NT	Homo sapiens leucyl/cystinyl aminopeptidase (LNPEP), mRNA
12208	24432		15.2	1.0E-71	AB011399.1	NT	Homo sapiens gene for AF-8, complete cds
432	13065	25559	1.33	9.0E-72	A1857635.1	EST_HUMAN	wk95g03.xt NC1 CGAP Lu19 Homo sapiens cDNA clone IMAGE:2423188 3' similar to TR:O86705 O86705
432	13065	25560	1.33	9.0E-72	A1857635.1	EST_HUMAN	HYPOTHETICAL 38.6 KD PROTEIN, :contains Alu repetitive element;
6259	18668	31638	0.87	8.0E-72	BF035752.1	EST_HUMAN	wk95g03.xt NC1 CGAP Lu19 Homo sapiens cDNA clone IMAGE:3882451 5'
10990	23504	36533	2.04	8.0E-72	11424480	NT	HYPOTHETICAL 38.6 KD PROTEIN, :contains Alu repetitive element;
10990	23504	36534	2.04	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
10990	23504	36535	2.04	8.0E-72	11424480	NT	Homo sapiens nuclear RNA helicase, DECD variant of DEAD box family (DDXL), mRNA
4190	16779	29225	1.48	7.0E-72		NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4190	16779	29226	1.48	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
4190	16779	29227	1.48	7.0E-72	4501866	NT	Homo sapiens aconitase 2, mitochondrial (ACO2), nuclear gene encoding mitochondrial protein, mRNA
7178	19710	32558	3.23	7.0E-72	S41694.1	NT	{pseudogene} PTMAP2=prothymosin alpha [human, Genomic, 1192 nt, segment 2 of 3]
12339	24521		1.9	7.0E-72	F28256.1	EST_HUMAN	HSPD13670 HM3 Homo sapiens cDNA clone s4000051G02
8324	20865		4.31	6.0E-72	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
67	12746	25223	1.56	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-a11 CS0010 Homo sapiens cDNA
67	12746	25224	1.56	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-a11 CS0010 Homo sapiens cDNA
68	12746	25223	10.23	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-a11 CS0010 Homo sapiens cDNA
68	12746	25224	10.23	5.0E-72	BF333707.1	EST_HUMAN	QV0-CS0010-150900-398-a11 CS0010 Homo sapiens cDNA
1178	13780		2.72	5.0E-72	L11645.1	NT	Homo sapiens alpha-tubulin mRNA, complete cds
7030	19564	32391	1.36	5.0E-72	AU128584.1	EST_HUMAN	AU128584 NT2RP2 Homo sapiens cDNA clone NT2RP2003751 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8711	21250	34173	3.16	5.0E-72	AW161274.1	EST_HUMAN	au80c03.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782584 5' similar to
9871	22368	35346	0.62	5.0E-72	AV724632.1	EST_HUMAN	TR:Q99785 Q99785 HYPOTHETICAL 32.4 KD PROTEIN, contains element MSR1 repetitive element ;
11122	23630	36672	3.44	5.0E-72	BF331571.1	EST_HUMAN	AV724632 HTB Homo sapiens cDNA clone HTBAKB01 5'
11122	23630	36673	3.44	5.0E-72	BF331571.1	EST_HUMAN	MR4-BT0598-010600-005-005 BT0598 Homo sapiens cDNA
11500	23949	37018	1.62	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823606 5'
11500	23949	37019	1.62	5.0E-72	BE208545.1	EST_HUMAN	ba08g08.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823606 5'
11895	25047		2.89	5.0E-72	BE926645.1	EST_HUMAN	QV1-BT0632-280800-342-a10 BT0632 Homo sapiens cDNA
4948	17523		1.21	4.0E-72	11034844	NT	Homo sapiens hypothetical protein DJ1057820.2 (DJ1057820.2), mRNA
5422	17979	30387	1.05	4.0E-72	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
5656	18283	30761	0.72	4.0E-72	AF170025.1	NT	Homo sapiens zinc finger protein ZFP-95 (ZFP95) mRNA, alternatively spliced, complete cds
6674	19270	32075	0.81	4.0E-72	T67947.1	EST_HUMAN	yd83a01.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115752 5' similar to
7439	19863	32829	3.01	4.0E-72		EST_HUMAN	SP:A44282 A44282 RETROVIRUS-RELATED POLYPROTEIN - HUMAN ;
9699	22198	35171	1.64	4.0E-72	5729887	NT	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
					8923669	NT	Homo sapiens hypothetical protein FLJ20758 (FLJ20758), mRNA
10318	22812	35807	0.98	4.0E-72	AJ248796.1	EST_HUMAN	qh87c02.x1 Soares fetal liver spleen 1NFLS_S1 Homo sapiens cDNA clone IMAGE:1849730 3' similar to
11402	23853	36918	7.8	4.0E-72	H79421.1	EST_HUMAN	TR:Q14498 Q14498 SPLICING FACTOR, [1]: contains Alu repetitive element; contains element L1 repetitive element ;
11528	23976	37046	2.48	4.0E-72	T61910.1	EST_HUMAN	yu28a03.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:235084 5'
12263	24473	30933	4.5	4.0E-72	AJ277546.2	NT	yd29d09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:109649 3'
22	12701	25157	3.55	3.0E-72	5031976	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
936	13549		1.46	3.0E-72	AA723823.1	EST_HUMAN	Homo sapiens pre-B-cell colony-enhancing factor (PBEF) mRNA
						EST_HUMAN	ah63a06.s1 Soares_testis_NHT Homo sapiens cDNA clone 1310290 3'
1196	13797	26307	7.76	3.0E-72	U16306.1	NT	Homo sapiens WEE1 gene for protein kinase and partial ZNF143 gene for zinc finger transcription factor
1196	13797	26308	7.76	3.0E-72	U16306.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1235	13834	26348	1.33	3.0E-72	U80226.1	NT	Human chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide mRNA, complete cds
1235	13834	26349	1.33	3.0E-72	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1567	14159	26690	0.98	3.0E-72	BE242161.1	EST_HUMAN	Human gamma-aminobutyric acid transaminase mRNA, partial cds
3110	15725	28196	13.29	3.0E-72	AJ229043.1	NT	TCAAP/IE1252 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP1252
						EST_HUMAN	Homo sapiens 959 kb contig between AML1 and CBIR1 on chromosome 21q22, segment 3/3

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3317	15927	28404	2.84	3.0E-72	8923548	NT	Homo sapiens hypothetical protein FLJ20585 (FLJ20585), mRNA
3895	16494	28955	2.71	3.0E-72	S77589.1	NT	TCR V delta 2-C alpha =T-cell receptor delta and C alpha fusion gene (alternatively spliced, splice junction)
4509	17093	29540	0.94	3.0E-72	AF143892.1	NT	[human, precursor B-cell line REH, mRNA Partial, 211 nt]
4509	17093	29541	0.94	3.0E-72	AF143892.1	NT	Homo sapiens thioredoxin-like protein (TXNL) gene, exon 3
4643	17225	29679	2.89	3.0E-72	11416198	NT	Homo sapiens thioredoxin-like protein (TXNL) gene, exon 3
5711	18337		1.07	3.0E-72	4759093	NT	Homo sapiens hypothetical protein (FLJ11127), mRNA
6134	18748	31504	1.98	3.0E-72	AF073367.1	NT	Homo sapiens semaphorin W (SEMAW) mRNA
6134	18748	31505	1.98	3.0E-72	AF073367.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6314	18921	31697	4.49	3.0E-72	AB028004.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 5
6314	18921	31698	4.49	3.0E-72	AB028004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
6726	19320	32125	3.59	3.0E-72	4826987	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7585	20100	32675	1.92	3.0E-72	U80017.1	NT	Homo sapiens ribosomal protein L3-like (RPL3L) mRNA
8118	20857	33568	1.52	3.0E-72	5031892	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nalp) and survival motor neuron protein (smn) genes, complete cds
10328	22622	35818	1.87	3.0E-72	X98289.1	NT	Homo sapiens nuclear receptor subfamily 1, group H, member 3 (NR1H3), mRNA
12174	24413	30946	2.03	3.0E-72	AB011399.1	NT	Homo sapiens S100A12 gene for Calgranulin C, exon 2 and joined cds
6113	18729	31482	1.41	2.0E-72	11426871	NT	Homo sapiens gene for AF-8, complete cds
9025	21562	34490	0.76	2.0E-72	BF308560.1	EST_HUMAN	Homo sapiens solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2 (SLC13A2), mRNA
9025	21562	34491	0.76	2.0E-72	BF308560.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
10619	23151	36163	2.52	2.0E-72	AA789277.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
12260	24470	30630	4.78	2.0E-72	AF182714.1	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
2120	14698	27267	1.03	1.0E-72	AA846225.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
5940	18560	31289	4.04	1.0E-72	7657676	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
6676	19272	32076	1.18	1.0E-72	11321578	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
6676	19272	32077	1.18	1.0E-72	11321578	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
6744	24768	32143	1.3	1.0E-72	AV751818.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
7633	20145	33026	3.81	1.0E-72	BE175434.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
7633	20145	33027	3.81	1.0E-72	BE175434.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9510	22010	34968	7.2	1.0E-72	AF222742.1	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
9510	22010	34969	7.2	1.0E-72	AF222742.1	NT	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'
1508	14100	26637	1.26	9.0E-73	AW374968.1	EST_HUMAN	601890419F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131461 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6190	18800	31570	0.98	9.0E-73	11525983	NT	Homo sapiens membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3) (MPP3), mRNA
10829	23350		27.89	9.0E-73	11424099	NT	Homo sapiens ribosomal protein L13a (RPL13A), mRNA
1076	13680	26190	1.62	8.0E-73	AW071755.1	EST_HUMAN	ws55c06.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2501098 3' similar to TR:Q69050
3332	15942	28417	0.61	8.0E-73	11435180	NT	Q59050 HYPOTHETICAL PROTEIN MJ1656. ;
5768	18394	31108	0.76	8.0E-73	4505798	NT	Homo sapiens gephyrin (GPH), mRNA
6897	19283	32096	4.21	8.0E-73	11426469	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
8039	20581	33488	2.58	8.0E-73	AF113129.1	NT	Homo sapiens lysosyme homolog (LOC57151), mRNA
							Homo sapiens vacuolar ATPase isoform VA68 mRNA, complete cds
9275	21801	34751	5.4	8.0E-73	BE019900.1	EST_HUMAN	bb62a06.y1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3030034 5' similar to gb:X04098_cds1 ACTIN, CYTOPLASMIC 2 (HUMAN); gb:M21495 Mouse cytoskeletal gamma-actin mRNA, complete cds (MOUSE);
9655	22184	35123	1.83	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
9655	22154	35124	1.83	8.0E-73	11526037	NT	Homo sapiens interleukin 12 receptor, beta 1 (IL12RB1), mRNA
12324	24511	30919	7.07	8.0E-73	11418189	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
1173	13775	26285	1.37	7.0E-73	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
3340	15950	28426	1.27	7.0E-73	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
							Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SK12W), RD, complement factor B (Bf), and complement component C2 (C2) genes.>
4298	16894	28329	2.59	7.0E-73	AF019413.1	NT	Homo sapiens chromosome 21 segment HS21C082
5079	17652		1.64	7.0E-73	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C018
169	12832		2.14	6.0E-73	AL163218.2	NT	Homo sapiens chromosome 21 segment HS21C018
7224	19755	32810	3.52	6.0E-73	BE168574.1	EST_HUMAN	QV0-HT0494-020300-137-d03 HT0494 Homo sapiens cDNA
5460	18095	30413	1.78	4.0E-73	11422159	NT	Homo sapiens HELG protein (FAM4A1), mRNA
1902	14487	27048	1.78	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
1902	14487	27049	1.78	3.0E-73	11435913	NT	Homo sapiens heme-binding protein (HEBP), mRNA
6799	18390	32205	1.03	3.0E-73	AA136403.1	EST_HUMAN	zn95604.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:565950 3' similar to
8693	21232	34152	0.63	3.0E-73	AV729428.1	EST_HUMAN	gb:Z23064_cds1 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HUMAN);
8693	21232	34153	0.63	3.0E-73	AV729428.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAA4071 5'
11478	23928		1.58	3.0E-73	A1004040.1	EST_HUMAN	AV729428 HTC Homo sapiens cDNA clone HTCAA4071 5'
12578	24675		1.34	3.0E-73	AL163246.2	NT	ou11002.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1625955 3'
12583	24877		1.87	3.0E-73	AW898081.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C046
884	13498	26016	2.4	2.0E-73	AF139897.1	NT	RC3-NN0068-270400-011-c04 NN0068 Homo sapiens cDNA
							Homo sapiens BASS1 (BASS1) mRNA, partial cds

Table 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1989	14571		2.46	2.0E-73	AW89081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
3215	15827	28305	2.05	2.0E-73	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8) mRNA
3604	18208	28688	0.68	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
3604	18208	28687	0.68	2.0E-73	7689539	NT	Homo sapiens Parkinson disease (autosomal recessive, juvenile) 2, parkin (PARK2), transcript variant 3, mRNA
6607	19204	32011	6.35	2.0E-73	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
6801	19392	32207	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6801	19392	32208	1.52	2.0E-73	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
9451	21977	34828	0.68	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
9451	21977	34829	0.68	2.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
10320	22814	35810	1.46	2.0E-73	4504168	NT	Homo sapiens glutathione synthetase (GSS) mRNA
10391	22885	35880	1.18	2.0E-73	11496980	NT	Homo sapiens supervillin (SVL), transcript variant 1, mRNA
10391	22885	35881	1.18	2.0E-73	11496980	NT	Homo sapiens supervillin (SVL), transcript variant 1, mRNA
10933	23451	36472	3.48	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10933	23451	36473	3.48	2.0E-73	4557612	NT	Homo sapiens galactosylceramidase (Krabbe disease) (GALC), mRNA
10962	23477	36502	1.85	2.0E-73	AB028982.1	NT	Homo sapiens mRNA for KIAA1059 protein, partial cds
12098	14571		2.75	2.0E-73	AW89081.1	EST_HUMAN	RC3-NN0066-270400-011-c04 NN0066 Homo sapiens cDNA
12665	24735	30825	1.41	2.0E-73	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
1818	14408	26953	1.74	1.0E-73	AU121585.1	EST_HUMAN	AU121585 MAMMA1 Homo sapiens cDNA clone MAMMA1000490 5'
2525	15089	27661	0.97	1.0E-73	AF198349.1	NT	Gallus gallus Dach2 protein (Dach2) mRNA, complete cds
8500	19100	31885	1.05	1.0E-73	BE151283.1	EST_HUMAN	OM1-HT0282-11109-042-h10 HT0282 Homo sapiens cDNA
							qq61b07.r1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:1839637 5' similar to contains element
9419	21928	34874	1.41	1.0E-73	A1147427.1	EST_HUMAN	MER22 repetitive element
11325	23023	38032	3.93	1.0E-73	BE385477.1	EST_HUMAN	601276071F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3817105 5'
770	13389	28888	2.42	8.0E-74	4557420	NT	Homo sapiens CD39-like 4 (CD39L4) mRNA
6073	18690	31435	1.87	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
6073	18690	31436	1.87	8.0E-74	S83194.1	NT	Ca2+/calmodulin-dependent protein kinase IV kinase isoform [rats, brain, mRNA, 3429 nt]
1982	14574	27133	3.26	7.0E-74	AJ001689.1	NT	Homo sapiens NKGD2 gene, exon 10
3371	19879	28456	1.18	7.0E-74	AL163248.2	NT	Homo sapiens chromosome 21 segment HS21C046
9167	21744	34887	2.49	7.0E-74	BE967432.1	EST_HUMAN	601849284F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932987 5'
12323	24510	30918	6.87	7.0E-74	BE268305.1	EST_HUMAN	601191027F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3535855 5'
							Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds
1161	13764	28275	4.55	6.0E-74	AF109607.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1688	14261	26794	0.9	6.0E-74	AW263177.1	EST_HUMAN	xn78g07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2700636 3'
2355	14926	27499	10.83	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2355	14926	27500	10.83	6.0E-74	BE388260.1	EST_HUMAN	601283521F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605453 5'
2889	15506	27977	1.22	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-eah-h-03-q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
2889	15508	27978	1.22	6.0E-74	AW014039.1	EST_HUMAN	UI-H-B10-eah-h-03-q-U1.s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709365 3'
3775	16375	28840	1.64	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
3775	16375	28841	1.64	6.0E-74	BE048846.1	EST_HUMAN	hr54e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3132332 3'
5177	17744	30172	0.85	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5177	17744	30173	0.85	6.0E-74	4758135	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase) (DDX11) mRNA
5568	18199	30647	3.28	6.0E-74	11056013	NT	Homo sapiens actin filament associated protein (AFAP), mRNA
938	13551	26067	1.37	5.0E-74	AW020886.1	EST_HUMAN	df17c09.y1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2483704 5'
2726	15281		4.42	5.0E-74	AW362756.1	EST_HUMAN	PMO-CT0289-271099-001-h07 CT0289 Homo sapiens cDNA
5603	18232	30682	1.98	5.0E-74	11425417	NT	Homo sapiens phosphatidylinositol glycan, class L (PIGL), mRNA
5961	18583	31317	11.6	5.0E-74	X89670.1	NT	H. sapiens mRNA for TPCR16 protein
6004	18624	31359	8.09	5.0E-74	4507866	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6057	18684	31428	2.33	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6057	18684	31427	2.33	5.0E-74	11431471	NT	Homo sapiens interleukin 4 receptor (IL4R), mRNA
6976	19552	32377	3.35	5.0E-74	7682263	NT	Homo sapiens KIAA0716 gene product (KIAA0716), mRNA
7880	20522	33428	3.2	5.0E-74	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
10614	23147	36158	1.96	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
10614	23147	36159	1.96	5.0E-74	Y09420.1	NT	H. sapiens mRNA for HIP-1
301	12956	25446	2.86	4.0E-74	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
885	13499	26017	9.19	4.0E-74	AB028942.1	NT	Homo sapiens mRNA for KIAA1016 protein, partial cds
2005	14587	27146	2.26	4.0E-74	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2005	14587	27147	2.26	4.0E-74	AB026998.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
2117	14695	27263	2.03	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2117	14695	27264	2.03	4.0E-74	4506192	NT	Homo sapiens proteasome (prosome, macropain) subunit, beta type, 1 (PSMB1) mRNA
2178	14755	27325	1.21	4.0E-74	AB032994.1	NT	Homo sapiens mRNA for KIAA1168 protein, partial cds
2471	15038	27606	0.89	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3127	15741	28210	4.58	4.0E-74	AJ006976.1	NT	Homo sapiens PLP gene
3580	16184	28566	1.14	4.0E-74	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
4136	16728	29181	1.01	4.0E-74	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4655	17237	29592	1.71	4.0E-74	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
4720	17301	29746	0.79	4.0E-74	Z17227.1	NT	Homo sapiens mRNA for transmembrane receptor protein
5168	17737	30184	0.61	4.0E-74	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
8486	21025		21.13	3.0E-74	AA300378.1	EST_HUMAN	EST13131 Thymus tumor III Homo sapiens cDNA 5' end similar to similar to ribosomal protein L37
8510	21049	33971	0.47	3.0E-74	9966912	NT	Homo sapiens actin-related protein 3-beta (ARP3BETA), mRNA
9284	21894	34841	2.47	3.0E-74	M7984.1	EST_HUMAN	EST01132 Subtracted Hippocampus, Striatum (cat. #938205) Homo sapiens cDNA clone HHCFF91
10241	22736	35728	2.42	3.0E-74	AA601493.1	EST_HUMAN	no17905.s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100984 3'
993	13605	26119	172.8	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
993	13605	26120	172.8	2.0E-74	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
1217	13817	26332	0.92	2.0E-74	AF020092.1	NT	Human endogenous retrovirus HERV-K-T47D
1287	13982	26407	1.84	2.0E-74	AI950528.1	EST_HUMAN	W651607.x1 NCI_CGAP_Lu28 Homo sapiens cDNA clone IMAGE:2547204 3' similar to SW:GG95_HUMAN
1639	14231	26764	4.17	2.0E-74	4885198	NT	Q08379 GOLGIN-95, contains element MER22 repetitive element ;
1639	14231	26765	4.17	2.0E-74	4885198	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
5149	17719	30149	2.97	2.0E-74	AL355092.1	NT	Homo sapiens epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog) (EGFR) mRNA
5149	17719	30150	2.97	2.0E-74	AL355092.1	NT	Novel human gene mapping to chromosome 22
5155	17725	30156	3.93	2.0E-74	J02963.1	NT	Novel human gene mapping to chromosome 22
5966	24752	31322	1.72	2.0E-74	BE711134.1	EST_HUMAN	Human platelet glycoprotein IIb mRNA, 3' end
6055	24755	31412	2.03	2.0E-74	11439587	NT	RO6-HT0678-220500-011-C03 HT0678 Homo sapiens cDNA
6055	24755	31413	2.03	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6120	24755	31412	2.72	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
6120	24755	31413	2.72	2.0E-74	11439587	NT	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
7160	19692	32539	1.3	2.0E-74	BF030788.1	EST_HUMAN	Homo sapiens PDZ-73 protein (PDZ-73NY-CO-38), mRNA
7881	20423	33331	1.56	2.0E-74	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
9304	21904	34853	7.76	2.0E-74	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
12033	24323		3.9	2.0E-74	AA198181.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C004
12605	24689	30882	1.99	2.0E-74	BF666568.1	EST_HUMAN	z98g06.s1 Striatum muscle 937209 Homo sapiens cDNA clone IMAGE:628018 3'
57	12737	25207	2.04	1.0E-74	7657334	NT	602121426F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4278659 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
359	13008	25491	4.11	1.0E-74	AW818405.1	EST_HUMAN	QV4-ST0234-181199-037-405 ST0234 Homo sapiens cDNA
525	13157	25639	0.92	1.0E-74	8922828	NT	Homo sapiens hypothetical protein FLJ11026 (FLJ11026). mRNA
532	13183	25844	10.17	1.0E-74	X02344.1	NT	Homo sapiens beta 2 gene
627	13264	25728	1.88	1.0E-74	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
1037	13647	26159	2.13	1.0E-74	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
2268	14842	27419	3.73	1.0E-74	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
3173	15786	28258	2.7	1.0E-74	4758697	NT	Homo sapiens mannosidase, alpha, class 2A, member 1 (MAN2A1), mRNA
3994	16592	29064	0.63	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
3994	16592	29065	0.63	1.0E-74	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4040	16638	29106	6.11	1.0E-74	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4137	16729	29182	0.78	1.0E-74	BE083080.1	EST_HUMAN	RC2-BT0642-270300-019-f06 BT0642 Homo sapiens cDNA
4354	16941	29383	0.75	1.0E-74	BE467769.1	EST_HUMAN	h273h08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3213663 3' similar to WP.B0511.12
5351	17911	30326	1.97	1.0E-74	D83327.1	NT	CE17351
6806	19397	32211	1.51	1.0E-74	M89914.1	NT	Homo sapiens DCRR1 mRNA, partial cds
7622	20135	33013	1.23	1.0E-74	11417977	NT	Human neurofilament (NF1) gene, complete cds
8000	20542	33444	0.74	1.0E-74	BE549105.1	EST_HUMAN	Homo sapiens KIAA0852 protein (KIAA0852), mRNA
8000	20542	33445	0.74	1.0E-74	BE549105.1	EST_HUMAN	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8740	21279	34202	7.81	1.0E-74	AF214562.1	NT	601070088F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456260 5'
8768	21307	34230	0.81	1.0E-74	BF351951.1	EST_HUMAN	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
10378	22870	35863	1.37	1.0E-74	11420549	NT	MRO-HT0559-230500-021-e03 HT0559 Homo sapiens cDNA
11659	24086	37144	1.95	1.0E-74	11417856	NT	Homo sapiens hypothetical protein FLJ10783 (FLJ10783). mRNA
11746	24145		3.39	1.0E-74	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12400	24560		1.59	1.0E-74	AF240768.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2670	15228		4.06	8.0E-75	AF176228.1	NT	Homo sapiens DNA cytosine-5 methyltransferase 3B (DNMT3B) mRNA, complete cds
12056	24339		2.18	8.0E-75	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
5376	17935		1.01	6.0E-75	AA769285.1	EST_HUMAN	a28c08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391628 3' similar to TR:Q15377 Q15377 Y-CHROMOSOME RNA RECOGNITION MOTIF PROTEIN
8839	21378	34301	2.15	5.0E-75	BE272325.1	EST_HUMAN	601128088F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2989865 5'
9045	21582	34511	0.82	5.0E-75	AA132611.1	EST_HUMAN	zo17e08.r1 Stratiogene colon (#937204) Homo sapiens cDNA clone IMAGE:587174 5'
9122	21658	34599	0.8	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9122	21658	34600	0.8	5.0E-75	BE561655.1	EST_HUMAN	601346909F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687458 5'
9295	21895	34842	1.39	5.0E-75	BF690254.1	EST_HUMAN	602186616T1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298738 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10133	22628	35616	2.5	5.0E-75	AI638623.1	EST_HUMAN	t31c12.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2242390 3' similar to TR:P97361 P97361
117	12788	25270	1.81	4.0E-75	BE081333.1	EST_HUMAN	HYPOTHE TICAL 20.1 KD PROTEIN
484	13117		1.21	4.0E-75	N36757.1	EST_HUMAN	QV1.BT0632-210200-079-e02 BT0632 Homo sapiens cDNA
1802	14392	28937	1.43	4.0E-75	AW897230.1	EST_HUMAN	y680t08.r1 Soares melanocyte 2NbfHM Homo sapiens cDNA
2874	15492	27862	5.4	4.0E-75	BE409484.1	EST_HUMAN	CMO-NN0057-150400-335-a11 NN0057 Homo sapiens cDNA
5720	18346	31048	0.71	4.0E-75	11417948	NT	601303866F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3638344 5'
5720	18346	31048	0.71	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6415	19018	31801	5.28	4.0E-75	5579457	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6856	19444	32260	1.84	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
6856	19444	32261	1.84	4.0E-75	11417948	NT	Homo sapiens NIPSNAP, C. elegans, homolog 1 (NIPSNAP1), mRNA
10565	23101	36115	8.22	4.0E-75	7669505	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1040	13650	28162	2.75	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1041	13650	28162	9.08	3.0E-75	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1876	14482	27019	2.54	3.0E-75	AB011153.1	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
2158	14735	27308	1.47	3.0E-75	4507334	NT	Homo sapiens synaptobrevin 1 (SYNJ1), mRNA
2467	15034	27601	3.11	3.0E-75	4759153	NT	Homo sapiens synaptosomal-associated protein, 28kD (SNAP29) mRNA
3056	15672	28148	0.65	3.0E-75	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3223	15835	28313	1.12	3.0E-75	AB011153.1	NT	Homo sapiens mRNA for KIAA0581 protein, partial cds
3393	16001	28480	0.83	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
3393	16001	28481	0.83	3.0E-75	M72393.1	NT	Human calcium-dependent phospholipid-binding protein (PLA2) mRNA, complete cds
4530	17114	29558	0.67	3.0E-75	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA
5387	17927		0.61	3.0E-75	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5458	18083	30409	1.01	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
5458	18093	30410	1.01	3.0E-75	11420956	NT	Homo sapiens adaptor-related protein complex 1, sigma 2 subunit (AP1S2), mRNA
6867	19601	32432	1.42	3.0E-75			Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
6867	19601	32433	1.42	3.0E-75	11528319	NT	Homo sapiens HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A (HIRA), mRNA
7189	19721	32568	4.6	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7189	19721	32569	4.6	3.0E-75	7662209	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7618	20131	33006	3.35	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
7618	20131	33007	3.35	3.0E-75	4885632	NT	Homo sapiens Oncogene TIM (TIM) mRNA
8915	21453	34374	1.23	3.0E-75	11420804	NT	Homo sapiens snail 1 (drosophila homolog), zinc finger protein (SNAI1), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9596	22096	35059	0.85	3.0E-75	11420222	NT	Homo sapiens Drosophila Ketch like protein (DKELCHL), mRNA
10435	22928	35936	3.75	3.0E-75	11436430	NT	Homo sapiens synuclein, alpha (non A4 component of amyloid precursor) (SNCA), mRNA
5853	18477		1.45	2.0E-75	AV734680.1	EST_HUMAN	AV734680 cda Homo sapiens cDNA clone cA8ED02 5'
8685	21224	34144	2.43	2.0E-75	AI311783.1	EST_HUMAN	q91e02.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1915898 3' similar to TR:Q69386 Q69388 POL/ENV GENE:
2341	14912	27485	4.05	1.0E-75	AW168135.1	EST_HUMAN	xg60d02.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2632707 3' similar to contains P.T.R.7.11
2973	15588	28072	3.23	1.0E-75	X52221.1	NT	PTR7 repetitive element ;
5356	17916	30331	0.57	1.0E-75	BE894192.1	EST_HUMAN	H. sapiens ERCC2 gene, exons 1 & 2 (partial)
8353	20893		13.67	1.0E-75	AA398270.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
9349	21863	34812	4.14	1.0E-75	BF313645.1	EST_HUMAN	z157h03.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:726485 3' similar to gb:M13932 40S RIBOSOMAL PROTEIN S17 (HUMAN);
9349	21863	34813	4.14	1.0E-75	BF313645.1	EST_HUMAN	601900294F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
10763	23287		6.58	1.0E-75	AA684377.1	EST_HUMAN	601900284F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129678 5'
10970	23485	36513	3.06	1.0E-75	AF223391.1	NT	ac77b08.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868599 3'
11945	17916	30331	2.58	1.0E-75	BE894192.1	EST_HUMAN	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
48	12728	25191	2.19	9.0E-76	AI652648.1	EST_HUMAN	601437130F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922303 5'
48	12728	25192	2.19	9.0E-76	AI652648.1	EST_HUMAN	wb30b10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ;
9815	22313	35294	62.44	9.0E-76	M12837.1	NT	wb30b10.x1 NCI_CGAP_GC8 Homo sapiens cDNA clone IMAGE:2307163 3' similar to TR:O75235 O75235 TRAP1 ;
154	12817	25305	9	8.0E-76	AF154830.1	NT	Human ferritin Heavy subunit mRNA, complete cds
974	13586	26100	10.38	8.0E-76	4504374	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
974	13586	26101	10.38	8.0E-76	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
2835	15551	28028	1.25	8.0E-76	7706724	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
6319	18926	31703	5.69	8.0E-76	11421442	NT	Homo sapiens mediator (Sur2), mRNA
7500	20022	32885	1.84	8.0E-76	11435215	NT	Homo sapiens LIM domain kinase 1 (LIMK1), mRNA
7567	20084	32860	0.94	8.0E-76	11419212	NT	Homo sapiens serine/threonine kinase 2 (STK2), mRNA
8237	20778	33698	0.81	8.0E-76	11416981	NT	Homo sapiens mitochondrial carrier family protein (LOC55972), mRNA
10280	22776	33764	1.25	8.0E-76	M13792.1	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
10546	23083	36097	7.29	8.0E-76	10442821	NT	Human adenosine deaminase (ADA) gene, complete cds
12305	24501		2.28	8.0E-76	11417862	NT	Homo sapiens baculoviral IAP repeat-containing 6 (BIRC6), mRNA
							Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
808	13425	25931	2.84	7.0E-76	5016092	NT	Homo sapiens dihydrolipoamide dehydrogenase (E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex) (DLD) mRNA
3333	15943	28418	3.23	7.0E-76	AF056490.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
3339	15949	28425	5.78	7.0E-76	4505052	NT	Homo sapiens lymphocyte antigen 75 (L75) mRNA, and translated products
3379	15988	28467	1.99	7.0E-76	4757915	NT	Homo sapiens core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related (CBFA2T1) mRNA
4461	17047	29490	6.32	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
4461	17047	29491	6.32	7.0E-76	4507184	NT	Homo sapiens sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase) (SPR) mRNA
1277	13872	36047	30.59	6.0E-76	BE396253.1	EST_HUMAN	601312019F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658757 5'
11340	23038	36047	2.97	6.0E-76	BE273201.1	EST_HUMAN	601142283F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3508029 5'
1988	14568	27128	8.39	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1988	14568	27128	8.39	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
1988	14568	27130	8.39	5.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
3242	15854	28338	0.88	4.0E-76	BE814098.1	EST_HUMAN	QV3-BN0047-270700-283-908 BN0047 Homo sapiens cDNA
5474	18108	30427	1.22	4.0E-76	BE783412.1	EST_HUMAN	601471725F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874470 5'
9937	22432	35407	5.79	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujiwara) Homo sapiens cDNA clone GEN-178G01 5'
9937	22432	35408	5.79	4.0E-76	D81625.1	EST_HUMAN	HUM178G01B Human fetal brain (Tfujiwara) Homo sapiens cDNA clone GEN-178G01 5'
657	13260	25759	1.63	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-0-UI.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
657	13260	25760	1.63	3.0E-76	BF516262.1	EST_HUMAN	UIH-BW1-anz-b-04-0-UI.st NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083862 3'
1843	14235	26769	7.45	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
1843	14235	26770	7.45	3.0E-76	4503476	NT	Homo sapiens eukaryotic translation elongation factor 1 beta 2 (EEF1B2) mRNA
3476	16082	28555	5.2	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
3476	16082	28556	5.2	3.0E-76	BF375689.1	EST_HUMAN	RC5-ST0300-180100-033-A03 ST0300 Homo sapiens cDNA
5447	18018	37140	2.41	3.0E-76	Z41314.1	EST_HUMAN	HSC2D0042 normalized infant brain cDNA Homo sapiens cDNA clone c-zqd04 3'
5908	18530	31255	1.06	3.0E-76	AA180811.1	EST_HUMAN	z073c07.r1 Stratagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592524 5' similar to
6506	19106	31891	7.49	3.0E-76	AF286598.1	NT	gbl32978 MIXED LINEAGE KINASE 1 (HUMAN);
8091	20632	33545	1.03	3.0E-76	N42671.1	EST_HUMAN	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
9632	22132	35097	2.91	3.0E-76	AW289353.1	EST_HUMAN	y20g10.11 Soares melanocyte 2Nblm Homo sapiens cDNA clone IMAGE:271842 5'
9656	22155	35125	1.11	3.0E-76	AA442309.1	EST_HUMAN	xs49h01.xt NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2773009 3'
9656	22155	35126	1.11	3.0E-76	AA442309.1	EST_HUMAN	zs64411.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757481 5'
11849	24864	30708	1.73	3.0E-76	AW987984.1	EST_HUMAN	zs64411.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:757461 5'
11760	25090	30501	4.85	3.0E-76	AW656455.1	EST_HUMAN	EST380059 IMAGE resequences, MAGJ Homo sapiens cDNA
							EST368525 IMAGE resequences, MAGD Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
303	12958	25448	1.1	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
364	13013	25495	2.12	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
364	13013	25496	2.12	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
486	13119		1.12	2.0E-76	4557662	NT	Homo sapiens immunoglobulin (CD79A) binding protein 1 (IGBP1) mRNA
616	13243	25717	1.45	2.0E-76	4503944	NT	Homo sapiens glucagon (GCG) mRNA
1068	13673	26186	1.57	2.0E-76	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
1593	14176	26708	0.99	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1583	14176	26709	0.96	2.0E-76	4504028	NT	Homo sapiens GM2 ganglioside activator protein (GM2A) mRNA
1972	14556	27113	1.04	2.0E-76	AA253954.1	EST_HUMAN	zs6011.1.t1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:701925 3'
2867	15485	27958	2.64	2.0E-76	P23268	SWISSPROT	OLFACTORY RECEPTOR-LIKE PROTEIN F5
3336	15946	28422	2.3	2.0E-76	AA445982.1	EST_HUMAN	zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
3336	15946	28423	2.3	2.0E-76	AA445982.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ; zw64e02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:780986 3' similar to SW:ITB5_HUMAN
3832	16431	28993	0.7	2.0E-76	AA400700.1	EST_HUMAN	P18084 INTEGRIN BETA-5 SUBUNIT PRECURSOR. ; CE00281 ;
4215	12958	25448	0.62	2.0E-76	D84295.1	NT	Human mRNA for possible protein TPRDII, complete cds
5082	17655	30096	7.33	2.0E-76	AW879618.1	EST_HUMAN	QV3-OT0028-220300-132-b11 OT0028 Homo sapiens cDNA
5512	18145		0.98	2.0E-76	AF127845.1	NT	Gonilla gorilla olfactory receptor (GGO18) gene, partial cds
5903	18428	31147	4.95	2.0E-76	AB029004.1	NT	Homo sapiens mRNA for KIAA1081 protein, partial cds
7442	19966	32893	0.72	2.0E-76	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
7658	20170	33057	1.84	2.0E-76	11427410	NT	Homo sapiens TPCR86 protein (HSTPCR86P), mRNA
10182	22877	35670	7.63	2.0E-76	11437211	NT	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63150), mRNA
10801	23324	36334	2.79	2.0E-76	7549807	NT	Homo sapiens HIRA interacting protein 4 (dnaJ-like) (HIRIP4), mRNA
4385	16972	29420	4.17	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
4385	16972	29421	4.17	1.0E-76	D63874.1	NT	Human mRNA for HMG-1, complete cds
5639	18258	30741	5.55	1.0E-76	BE786537.1	EST_HUMAN	601589986F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944302 5'
6391	18994		0.7	1.0E-76	AA333207.1	EST_HUMAN	EST37301 Embryo, 8 week (Homo sapiens cDNA 5' end
7003	19501	32320	4.41	9.0E-77	BE889525.1	EST_HUMAN	601512435F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913737 5'
11115	23625	36667	1.68	9.0E-77	4506022	NT	Homo sapiens protein phosphatase 2, regulatory subunit B (B56), gamma isoform (PPP2R5C) mRNA
12474	24599		1.9	9.0E-77	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
200	12860	25344	1.36	8.0E-77	R83144.1	EST_HUMAN	yp11h02.r1 Soares_breast3NBHst Homo sapiens cDNA clone IMAGE:187165 5' similar to SP-ANKB_HUMAN_Q01484 ANKYRIN, BRAIN VARIANT 1 ;

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4620	17203	29652	1.27	8.0E-77	BF205181.1	EST_HUMAN	60186626F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4109503 5'
5844	18273	30747	2.93	8.0E-77	4506230	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 (Mov34 homolog) (PSMD7) mRNA
11264	23792	36849	2.67	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
11264	23792	36850	2.67	8.0E-77	AA019770.1	EST_HUMAN	ze62e02.r1 Soares refina N2b4HR Homo sapiens cDNA clone IMAGE:363578 5'
12451	24585	30916	21.88	8.0E-77	R00245.1	EST_HUMAN	ye69f04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:123007 3' similar to contains MER10 repetitive element;
1973	14557	27114	2.58	7.0E-77	AA625755.1	EST_HUMAN	zu87g01.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:745392 3'
2455	15022	27593	1.98	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
2455	15022	27594	1.98	7.0E-77	4505944	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide E (25kD) (POLR2E) mRNA
284	12940	25426	3.52	6.0E-77	4504600	NT	Homo sapiens interferon (alpha, beta and omega) receptor 2 (IFNAR2) mRNA
1181	13783	26283	3.04	6.0E-77	AW957753.1	EST_HUMAN	EST369823 MAGE resequences, MAGE Homo sapiens cDNA
1590	14183	28716	2.97	6.0E-77	A204068.1	EST_HUMAN	qe7h12.x1 Soares fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1745063 3'
156	12819	25307	3.77	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
156	12819	25308	3.77	5.0E-77	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
1278	13874	26394	1.69	5.0E-77	AF041015.1	NT	7 Homo sapiens glucokinase (GCK) gene, exon 2
1404	13987	28526	1.53	5.0E-77	4557250	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
2792	15345	27914	0.98	5.0E-77	4503160	NT	Homo sapiens cullin 1 (CUL1) mRNA
3574	16178	28681	1.03	5.0E-77	8394518	NT	Homo sapiens ubiquitin specific protease 18 (USP18) mRNA
4813	17391	29842	1.08	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin 1-like domains 3 (EDIL3), mRNA
4813	17391	29843	1.08	5.0E-77	5031660	NT	Homo sapiens EGF-like repeats and discoidin 1-like domains 3 (EDIL3), mRNA
5071	17844	30086	2.22	5.0E-77	AL043863.1	EST_HUMAN	DKFZp434G1728_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G1728 5'
5419	17976	30384	1.77	5.0E-77	AA861184.1	EST_HUMAN	ak33a05.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1407728 3' similar to contains Alu repetitive element; contains element PTR7 PTR7 repetitive element
6879	19813	32447	0.71	5.0E-77	M13975.1	NT	Homo sapiens protein kinase C beta-II type (PRKCB1) mRNA, complete cds
7366	19892	32755	0.68	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
7592	19892	32755	0.75	5.0E-77	X98296.1	NT	H. sapiens mRNA for ubiquitin hydrolase
8309	20850	33773	1.07	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
8309	20850	33774	1.07	5.0E-77	11428849	NT	Homo sapiens 3-hydroxyisobutyryl-Coenzyme A hydrolase (HIBCH), mRNA
9489	21945	34893	3.52	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
9489	21945	34894	3.52	5.0E-77	11421928	NT	Homo sapiens sorting nexin 5 (SNX5), mRNA
10385	22879	35872	0.51	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
10385	22879	35873	0.51	5.0E-77	AB002297.1	NT	Human mRNA for KIAA0299 gene, partial cds
2015	14597	27160	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2015	14597	27161	1.12	3.0E-77	5730038	NT	Homo sapiens SET domain and mariner transposase fusion gene (SETMAR) mRNA
10189	22684	35675	0.82	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10189	22684	35676	0.82	3.0E-77	H65167.1	EST_HUMAN	yu64g01.r1 Weizmann Offactory Epithelium Homo sapiens cDNA clone IMAGE:238608 5' similar to SP:S17447 S17447 PROBABLE LIGAND-BINDING PROTEIN RY2G5 - ;
10493	22987	35994	0.51	3.0E-77	A017333.1	EST_HUMAN	ov31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
10493	22987	35995	0.51	3.0E-77	A017333.1	EST_HUMAN	ov31h07.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1638973 3'
10754	23278	36291	4.39	3.0E-77	BF359917.1	EST_HUMAN	PM8-MT0078-080800-005-g03 MT0078 Homo sapiens cDNA
1396	13990	26517	1.82	2.0E-77	AV784617.1	EST_HUMAN	AV784617 MDS Homo sapiens cDNA clone MDSBTF10 5'
1479	14072	26611	3.43	2.0E-77	AW697712.1	EST_HUMAN	RC3-BN0053-170200-011-h01 BN0053 Homo sapiens cDNA
2138	14716	27288	1.24	2.0E-77	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
2151	14728	27301	2.37	2.0E-77	7706315	NT	Homo sapiens CGI-79 protein (LOC51634), mRNA
2630	15471	27760	2.26	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2630	15471	27761	2.26	2.0E-77	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
4105	16699	29153	1.36	2.0E-77	BE044316.1	EST_HUMAN	hw43b05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:3040113 3' similar to SW:GAG2_HUMAN P10264 RETROVIRUS-RELATED GAG POLYPROTEIN ;
4504	17088	29536	0.85	2.0E-77	A1813519.1	EST_HUMAN	hw22g02.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4504	17088	29537	0.85	2.0E-77	A1813519.1	EST_HUMAN	hw22g02.x1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2260466 3' similar to TR:O65245
4701	17283		1.38	2.0E-77	4504068	NT	Homo sapiens glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) (GOT2), nuclear gene encoding mitochondrial protein, mRNA
4883	17458	28910	4.3	2.0E-77	AA653025.1	EST_HUMAN	ns88g12.s1 NCI_CGAP_P12 Homo sapiens cDNA clone IMAGE:1188938 similar to SW:RL29_HUMAN
6109	18725	31478	1.78	2.0E-77	BE289940.1	EST_HUMAN	P47914 60S RIBOSOMAL PROTEIN L29, [1], contains element MSR1 repetitive element ;
6320	18927	31704	1.68	2.0E-77	BE787143.1	EST_HUMAN	601119852F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029436 5'
7228	18757	32612	14.03	2.0E-77	A1833003.1	EST_HUMAN	601478802F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:3879505 5'
8466	21006	33924	0.9	2.0E-77	A1362707.1	EST_HUMAN	at74g09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2377720 3' similar to TR:Q13311
9447	21973	34924	4.58	2.0E-77	U50321.1	NT	Q13311 TAXI-BINDING PROTEIN TXBP151, [1] ;
9447	21973	34925	4.96	2.0E-77	U50321.1	NT	qy70c08.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2017360 3' similar to WP:F29D11.1
9906	22403	35377	0.55	2.0E-77	BF310349.1	EST_HUMAN	CE05765 LOW DENSITY LIPID RECEPTOR-RELATED PROTEIN ; Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7 Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 7 601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9806	22403	35378	0.55	2.0E-77	BF310349.1	EST_HUMAN	601895183F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124541 5'
47	12726	25187	1.39	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
47	12726	25188	1.39	1.0E-77	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
294	12950	25437	2.09	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
294	12950	25438	2.09	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
908	15428	26041	2.98	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
908	15428	26042	2.98	1.0E-77	4502168	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1963	14547	27104	1.41	1.0E-77	AW058119.1	EST_HUMAN	w83e05.x1 Scores, thymus, NHF Th Homo sapiens cDNA clone IMAGE:2536160 3'
2488	15053	27625	0.99	1.0E-77	AB028024.1	NT	Homo sapiens mRNA for KIAA1101 protein, complete cds
3081	15696	28188	2.82	1.0E-77	4503300	NT	Homo sapiens 2,4-dienoyl CoA reductase 1, mitochondrial (DEOR1), mRNA
4445	17031	29472	3.95	1.0E-77	7706299	NT	Homo sapiens CGI-60 protein (LOC51626), mRNA
4622	17205	29654	20.39	1.0E-77	AJ228041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
4755	17336	29780	3.41	1.0E-77	6552322	NT	Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant BRCA1-exon4, mRNA
5098	17180	29627	0.59	1.0E-77	4758053	NT	Homo sapiens cAMP responsive element binding protein 1 (CREB1) mRNA
5228	17792	30211	1.05	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5228	17792	30212	1.05	1.0E-77	7681849	NT	Homo sapiens KIAA0005 gene product (KIAA0005), mRNA
5387	17948		4.13	1.0E-77	AL183247.2	NT	Homo sapiens chromosome 21 segment HS21C047
6086	18702	31449	1.46	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6086	18702	31450	1.46	1.0E-77	AF086944.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, exons 27 and 28
6198	18808	31577	1.4	1.0E-77	M25844.1	NT	Human von Willebrand factor gene, exon 20
6575	19173	31972	1.45	1.0E-77	4885182	NT	Homo sapiens diaphanous (Drosophila, homolog) 1 (DIAPH1), mRNA
7114	19454	32270	15.68	1.0E-77	5881412	NT	Homo sapiens elastin (supravalvular aortic stenosis, Williams-Beuren syndrome) (ELN), mRNA
7661	20173	33060	0.92	1.0E-77	11420159	NT	Homo sapiens cullin 1 (GUL1), mRNA
7740	20248	33141	0.78	1.0E-77	X04571.1	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
9189	21706	34649	1.31	1.0E-77	X94354.1	NT	H. sapiens DNA for Cene cGMP-PDE gene
9189	21706	34650	1.31	1.0E-77	X94354.1	NT	H. sapiens DNA for Cene cGMP-PDE gene
10416	22910	35809	1.01	1.0E-77	AB028368.1	NT	Homo sapiens hu-GIAT-P mRNA for glucuronyltransferase, complete cds
10416	22910	35910	1.01	1.0E-77	AB028368.1	NT	Homo sapiens hu-GIAT-P mRNA for glucuronyltransferase, complete cds
10956	23471	35496	2.92	1.0E-77	11433426	NT	Homo sapiens meningioma expressed antigen 6 (colloid-coil proline-rich) (MGEA6), mRNA
10444	22938	35948	2.4	9.0E-78	AW753302.1	EST_HUMAN	RC3-CT0254-280969-011-b05 CT0254 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6574	19172	31970	4.74	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
6574	19172	31971	4.74	8.0E-78	AW947061.1	EST_HUMAN	RC2-ET0023-080500-012-e05 ET0023 Homo sapiens cDNA
88	12785	25248	1.48	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
89	12785	25249	1.48	6.0E-78	AU118789.1	EST_HUMAN	AU118789 HEMBA1 Homo sapiens cDNA clone HEMBA1004354 5'
3356	15984	28441	0.72	6.0E-78	BF344101.1	EST_HUMAN	602016926F1 NCI CGAP_Bim84 Homo sapiens cDNA clone IMAGE:4152511 5'
6677	19273		2.29	6.0E-78	11432710	NT	Homo sapiens GDNF family receptor alpha 1 (GFRA1), mRNA
234	12894	25377	4.78	5.0E-78	11422488	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
2597	15159	27727	4.1	5.0E-78	AW673424.1	EST_HUMAN	ba54h03.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900405 5' similar to WP:Y48B0A.6
3432	16040	28522	3.88	5.0E-78	M5586.1	NT	CE22121
5807	18236	30686	2.29	5.0E-78	AF038536.1	NT	Human collagenase type IV (GLG4) gene, exon 6
5764	18390	31102	24.58	5.0E-78	11416585	NT	Homo sapiens Best's macular dystrophy related protein mRNA, partial cds
7208	19739	32583	2.2	5.0E-78	AW953120.1	EST_HUMAN	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFB1), mRNA
9012	21549	34478	6.88	5.0E-78	U08889.1	NT	EST365190 MAGE resequences, MAGB Homo sapiens cDNA
9013	21550	34479	3.6	5.0E-78	BE960836.1	EST_HUMAN	Human lysosomal alpha-mannosidase (manB) gene, exon 7
1176	13778	26288	1.64	4.0E-78	AL043314.2	EST_HUMAN	601648061F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:3931887 5'
1565	14157	26688	1.99	4.0E-78	AL355841.1	NT	DKFZp434N0323_1 434 (synonym: hhes3) Homo sapiens cDNA clone DKFZp434N0323 5'
2357	14928	27502	2.97	4.0E-78	AF107405.1	NT	Novel human gene mapping to chromosome 22
4414	18989	29441	1.23	4.0E-78	7656876	NT	Homo sapiens pre-mRNA splicing factor (SFRS3) mRNA, complete cds
4887	17462	29915	1.91	4.0E-78	4505806	NT	Homo sapiens syncytin (LOC30816), mRNA
4887	17462	29916	1.91	4.0E-78	4505806	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
5941	18561	31290	0.97	4.0E-78	11420732	NT	Homo sapiens phosphatidylinositol 4-kinase, catalytic, alpha polypeptide (PIK4CA) mRNA
7502	20024	32888	0.77	4.0E-78	4508736	NT	Homo sapiens SFRS protein kinase 2 (SRPK2), mRNA
8787	21326	34250	1.51	4.0E-78	AF012872.1	NT	Homo sapiens ribosomal protein S6 kinase, 70kD, polypeptide 1 (RPS6KB1) mRNA
8787	21326	34251	1.51	4.0E-78	AF012872.1	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
9280	21880	34837	0.61	4.0E-78	11417251	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (pi4K230) mRNA, complete cds
10341	22835	35829	2.03	4.0E-78	11560151	NT	Homo sapiens X-ray repair complementing defective repair in Chinese hamster cells 4 (XRCC4), mRNA
10341	22835	35830	2.03	4.0E-78	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10841	23173	36185	1.67	4.0E-78	11426610	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
11297	23749	36808	2.09	4.0E-78	AF169148.1	NT	Homo sapiens regulatory factor X-associated ankyrin-containing protein (RFXANK), mRNA
11432	23892	36948	4.15	4.0E-78	X05844.1	NT	Homo sapiens s-CaBP1 (CABP1) mRNA, complete cds
12337	24520	30923	4.58	4.0E-78	AB011399.1	NT	Human transforming growth factor-beta precursor gene exons 4-5 (and joined mature peptide)
172	12835	25318	2.42	3.0E-78	AF095601.1	NT	Homo sapiens gene for AF-8, complete cds
						NT	Homo sapiens eRF1 gene, complete cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
172	12835	25319	2.42	3.0E-78	AF095901.1	NT	Homo sapiens eRF1 gene, complete cds
3827	16427		1.16	3.0E-78	AU140804.1	EST_HUMAN	AU140804 PLACE3 Homo sapiens cDNA clone PLACE3000373 5'
4180	16488	28947	0.76	3.0E-78	4507334	NT	Homo sapiens synaptobrian 1 (SYNJ1), mRNA
10186	22681		5.78	3.0E-78	BE144798.1	EST_HUMAN	CMO-HT0180-041089-065-c07 HT0180 Homo sapiens cDNA
10860	23381	36400	5.65	3.0E-78	BE156318.1	EST_HUMAN	QV0-HT0387-150200-114-g09 HT0387 Homo sapiens cDNA
3155	15769		2.54	2.0E-78	U04489.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 20
4086	16682		1.8	2.0E-78	AA311872.1	EST_HUMAN	EST182583 Jurkat T-cells VI Homo sapiens cDNA 5' and
7483	20006	32870	1.38	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BKO-aag-g-10-Q-UI-r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7483	20006	32871	1.38	2.0E-78	AW402306.1	EST_HUMAN	UI-HF-BKO-aag-g-10-Q-UI-r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054139 5'
7714	20223	33110	3.47	2.0E-78	BF689800.1	EST_HUMAN	502186529F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4298599 5'
7894	20526	33432	1.73	2.0E-78	AV714177.1	EST_HUMAN	AV714177 DCB Homo sapiens cDNA clone DCBAWF09 5'
8389	20929	33848	1.8	2.0E-78	A1557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
8389	20929	33849	1.8	2.0E-78	A1557509.1	EST_HUMAN	P12.1_16_B07.r tumor2 Homo sapiens cDNA 3'
10859	23474	36469	3.39	2.0E-78	A1197837.1	EST_HUMAN	Q150H05.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1859961 3' similar to WP.R90.1
11003	23517	36552	3.47	2.0E-78	N66951.1	EST_HUMAN	CE06325 PROTEIN KINASE ;
5508	18141	30553	2.63	1.0E-78	11417304	NT	2a48f12.e1 Soares fetal liver spleen 1NFSL Homo sapiens cDNA clone IMAGE:295823 3'
7035	18055	30476	1.91	1.0E-78	AV648699.1	EST_HUMAN	Homo sapiens GAP-like protein (LOC51306), mRNA
8100	20641		2.25	1.0E-78	U52373.1	NT	AV648699 GLC Homo sapiens cDNA clone GLCBMC01 3'
11832	24197	31037	2.17	1.0E-78	11430460	NT	Human serine/threonine kinase MNB (mtb) mRNA, complete cds
							Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
11926	24261	31014	1.41	1.0E-78	11435903	NT	Homo sapiens similar to lymphocyte activation-associated protein (H. sapiens) (LOC63140), mRNA
4808	17386	29836	4.05	9.0E-79	11525891	NT	Homo sapiens peptide YY (PYY), mRNA
4988	17582	30006	3.34	9.0E-79	BE000837.1	EST_HUMAN	RC2-BN0074-090300-014-c12 BN0074 Homo sapiens cDNA
5624	18253	30722	13.77	9.0E-79	AG028070.1	NT	Homo sapiens mRNA for activator of S phase Kinase, complete cds
6482	19083	31864	2.48	9.0E-79	5454145	NT	Homo sapiens ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UB4/5) (UBE2E3) mRNA
6731	19325	32129	1.43	9.0E-79	11430822	NT	Homo sapiens hypothetical protein FLJ11284 (FLJ11284), mRNA
7388	24781		0.98	9.0E-79	11424427	NT	Homo sapiens hypothetical protein FLJ20345 (FLJ20345), mRNA
7575	20091	32968	0.89	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7575	20091	32969	0.89	9.0E-79	11421735	NT	Homo sapiens cAMP response element-binding protein CRE-BPa (H_GS165L15.1), mRNA
7612	20125	33002	0.72	9.0E-79	D30688.1	NT	Human T-cell mRNA for glycyl RNA synthetase, complete cds
8287	20828	33748	0.56	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA
8287	20828	33749	0.56	9.0E-79	11417260	NT	Homo sapiens threonyl-tRNA synthetase (TARS), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8993	21531	34460	7.08	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
8993	21531	34461	7.08	9.0E-79	J02853.1	NT	Homo sapiens casein kinase II alpha subunit mRNA, complete cds
9302	21902	34851	0.61	9.0E-79	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10267	22762	35749	0.59	9.0E-79	11438643	NT	Homo sapiens hypothetical protein FLJ20535 (FLJ20535), mRNA
10316	22810	35803	2.32	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10316	22810	35804	2.32	9.0E-79	AF062346.1	NT	Homo sapiens zinc finger protein 216 splice variant 1 (ZNF216) mRNA, complete cds
10946	23462	36484	2.73	9.0E-79	AY008273.1	NT	Homo sapiens TRAF6-regulated IKK activator 1 beta Uev1A mRNA, complete cds
11398	23840	36904	3.26	9.0E-79	11423827	NT	Homo sapiens suppressor of white apicort homolog 2 (SWAP2), mRNA
12549	24654	30900	2.05	9.0E-79	11417877	NT	Homo sapiens suppressor of white apicort homolog 2 (SWAP2), mRNA
3805	16405	28869	1.17	8.0E-79	AL163210.2	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), mRNA
11747	18035	30495	1.3	8.0E-79	8567387	NT	Homo sapiens chromosome 21 segment HS21C010
3291	15902	28382	10.29	7.0E-79	BE618648.1	EST_HUMAN	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
11876	24095		2.07	6.0E-79	AA698829.1	EST_HUMAN	601472786T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875657 3'
11368	23820	36882	3.85	5.0E-79	AL163282.2	NT	zfp4e0.4.s1 Soares fetal liver spleen_1NPLS_S1 Homo sapiens cDNA clone IMAGE:4101245 5'
5159	17728	30157	2.24	4.0E-79	BF210889.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C082
335	12887	25474	2.48	3.0E-79	AF114488.1	NT	601874522F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4101245 5'
1014	13624	26139	4.44	3.0E-79	AF232708.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3133	15747	28218	1.91	3.0E-79	U09410.1	NT	Homo sapiens cell-line tsA201a chloride ion current inducer protein (Cin) gene, complete cds
5292	17854	30278	0.94	3.0E-79	AF114488.1	NT	Human zinc finger protein ZNF131 mRNA, partial cds
5292	17854	30278	0.94	3.0E-79	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
5564	18195	30641	8.78	3.0E-79	AF110322.1	NT	Homo sapiens MSTP016 (MST016) mRNA, complete cds
5698	18520	31245	1.72	3.0E-79	AB020699.1	NT	Homo sapiens mRNA for KIAA0892 protein, partial cds
5922	18544	31270	1.01	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5922	18544	31271	1.01	3.0E-79	BE789470.1	EST_HUMAN	601482143F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884554 5'
5942	18562	31291	3.6	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
5942	18562	31292	3.6	3.0E-79	11426770	NT	Homo sapiens netrin 1 (NTN1), mRNA
6843	19433	32248	0.76	3.0E-79	BE256893.1	EST_HUMAN	601112055F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352885 5'
7120	19460	32275	3.07	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0820 protein, partial cds
7120	19460	32276	3.07	3.0E-79	AB014520.1	NT	Homo sapiens mRNA for KIAA0820 protein, partial cds
8105	20846	33555	1.58	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
8324	21838	34789	0.71	3.0E-79	10836036	NT	Homo sapiens tetratricopeptide repeat domain 3 (TTC3), mRNA
10249	22744		0.62	3.0E-79	AV698115.1	EST_HUMAN	AV698115 GK Homo sapiens cDNA clone GKCAHE11 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10740	23265	36280	1.97	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
10740	23265	36281	1.97	3.0E-79	AF249273.1	NT	Homo sapiens Bcl-2-associated transcription factor short form mRNA, complete cds
309	12964		1.05	2.0E-79	H63129.1	EST_HUMAN	y48f03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:208541 3'
662	13286	25767	1.38	2.0E-79	BE379926.1	EST_HUMAN	601159415F2 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3511107 5'
963	13574	26090	0.94	2.0E-79	4757841	NT	Homo sapiens BCL2-like 2 (BCL2L2) mRNA
1020	13630	26145	0.91	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1020	13630	26146	0.91	2.0E-79	4885234	NT	Homo sapiens Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog (FGR) mRNA
1073	13678		1.06	2.0E-79	AI523747.1	EST_HUMAN	th18f07.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2118685 3'
1824	14413	26958	1.21	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4) mRNA
1824	14413	26959	1.21	2.0E-79	7657024	NT	Homo sapiens Dickkopf gene 4 (DKK-4) mRNA
1918	14503	27060	1.01	2.0E-79	7662255	NT	Homo sapiens KIAA0703 gene product (KIAA0703), mRNA
2193	14769	27341	10.76	2.0E-79	4585963	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2193	14769	27342	10.76	2.0E-79	4585963	NT	Homo sapiens phosphodiesterase 8A, cGMP-specific, rod, alpha (PDE8A), mRNA
2352	14923	27498	2.42	2.0E-79	AF244138.1	NT	Homo sapiens hepatocellular carcinoma-associated antigen 88 (HCA88) mRNA, complete cds
2741	15296	27863	0.99	2.0E-79	AB023154.1	NT	Homo sapiens mRNA for KIAA0937 protein, partial cds
3985	16583	29054	0.65	2.0E-79	AF170492.1	NT	Homo sapiens chloride channel CLCA4 (CLCA) mRNA, complete cds
4245	16833	29284	1.24	2.0E-79	AJ271408.1	NT	Homo sapiens mRNA for Fas-associated factor, FAF1 (Faf1 gene)
4800	17378	29828	0.82	2.0E-79	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C006
5851	18475		1.16	2.0E-79	AA312223.1	EST_HUMAN	EST182826 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein, cosmid B0303.15
5901	18523	31248	0.9	2.0E-79	11181769	NT	Homo sapiens X transporter protein 3 (XT3), mRNA
6390	18993	31773	1.1	2.0E-79	AB020637.1	NT	Homo sapiens mRNA for KIAA0830 protein, partial cds
7040	18060	30482	0.96	2.0E-79	AF263613.1	NT	Homo sapiens membrane-associated calcium-independent phospholipase A2 gamma mRNA, complete cds
7219	19750	32605	1.76	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
7219	19750	32606	1.76	2.0E-79	7382479	NT	Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA
8044	20566	33492	1.22	2.0E-79	4508442	NT	Homo sapiens retinoblastoma-like 1 (p107) (RBL1) mRNA
8454	20994	33912	2.52	2.0E-79	11427428	NT	Homo sapiens hypothetical protein FLJ11006 (FLJ11006), mRNA
8701	21240	34163	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8701	21240	34164	0.55	2.0E-79	8923248	NT	Homo sapiens hypothetical protein FLJ20275 (FLJ20275), mRNA
8934	21472	34391	0.99	2.0E-79	11432184	NT	Homo sapiens similar to ATPase, H ⁺ -transporting, lysosomal (vacuolar proton pump) membrane sector associated protein M8-9 (H. sapiens) (LOC83961), mRNA
10004	22469	35488	1.94	2.0E-79	S72669.1	NT	H4(D10S1170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]
10004	22469	35489	1.94	2.0E-79	S72669.1	NT	H4(D10S1170)=putative cytoskeletal protein [human, thyroid, mRNA, 3011 nt]

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10808	23427	36444	5.07	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
10808	23427	36445	5.07	2.0E-79	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-110 BT0310 Homo sapiens cDNA
11716	18033	30493	5.59	2.0E-79	7662357	NT	Homo sapiens KIAA0879 protein (KIAA0879), mRNA
11806	24181	31029	5.85	2.0E-79	AB020640.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
12038	24326	30894	2.81	2.0E-79	11418322	NT	Homo sapiens cadherin EGF LAG seven-pass G-type receptor 1 (CELSR1), mRNA
6701	24766		3.27	1.0E-79	BF363071.1	EST_HUMAN	MRO-NN0087-260600-017-b10 NN0087 Homo sapiens cDNA
8187	20728	33640	0.74	1.0E-79	BF394211.1	EST_HUMAN	601311157F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632809 5'
11487	20936	37006	2.11	1.0E-79	BF087405.1	EST_HUMAN	QV2-H10540-120900-388-a05 HT0540 Homo sapiens cDNA
11834	25021		1.84	1.0E-79	A1460115.1	EST_HUMAN	ar79a04.x1 Berstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151438 3'
3180	15793	28264	5.7	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
3180	15793	28265	5.7	9.0E-80	AA725848.1	EST_HUMAN	ai23e05.s1 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
9926	22422	35386	1.33	9.0E-80	BE798603.1	EST_HUMAN	601581652F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936061 5'
11156	23663	36708	11.44	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
11156	23663	36709	11.44	9.0E-80	11433924	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 8 (SLC7A8), mRNA
3682	16264		1.19	8.0E-80	U94387.1	NT	Homo sapiens Y chromosome spermatogenesis candidate protein (RBM) pseudogene mRNA, partial cds
7600	20113	32889	2.92	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
7600	20113	32890	2.92	8.0E-80	11422647	NT	Homo sapiens KIAA0724 gene product (KIAA0724), mRNA
9323	21837	34787	1.07	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9323	21837	34788	1.07	8.0E-80	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
933	13548	28063	1.84	8.0E-80	A1422197.1	EST_HUMAN	tf58d02.x1 NCI CGAP_Bm23 Homo sapiens cDNA clone IMAGE:2103459 3' similar to SW:NUEM_HUMAN
1685	14277	26810	2.29	8.0E-80	U64898.1	NT	Q16795 NADH:UBIQUINONE OXIDOREDUCTASE 39 KD SUBUNIT PRECURSOR ;
2337	14908	27479	2.88	8.0E-80	6631094	NT	Homo sapiens NRD convertase mRNA, complete cds
2337	14908	27480	2.88	8.0E-80	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4372	18959	29403	0.98	8.0E-80	AB032981.1	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
4372	18959	29404	0.98	8.0E-80	AB032981.1	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
5969	18990	31325	2.15	8.0E-80	11421462	NT	Homo sapiens mRNA for KIAA1155 protein, partial cds
6226	18835	31608	3.16	8.0E-80	AJ404468.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), mRNA
6376	18980	31759	4.09	8.0E-80	11438736	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
6418	18021		0.88	8.0E-80	7662393	NT	Homo sapiens tubby like protein 3 (TULP3), mRNA
							Homo sapiens KIAA0941 protein (KIAA0941), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6464	19065	31850	0.84	6.0E-80	M18533.1	NT	Homo sapiens dystrophin (DMD) mRNA, complete cds
8758	21297	34217	2.43	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8758	21297	34218	2.43	6.0E-80	11528464	NT	Homo sapiens G protein-coupled receptor 51 (GPR51), mRNA
8949	21487	34409	1.6	6.0E-80	AL183301.2	NT	Homo sapiens chromosome 21 segment HS21C101
9281	21807	34759	0.88	6.0E-80	AF161495.1	NT	Homo sapiens HSPC146 mRNA, complete cds
9775	22273	35258	1.49	6.0E-80	U20211.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exon 21
10820	23341	36356	2.68	6.0E-80	11427368	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 1 (BIG1), mRNA
11103	23613	36653	22.81	6.0E-80	AF226730.1	NT	Homo sapiens Cyf19 mRNA, complete cds
11593	24036	37105	1.93	6.0E-80	AF102265.1	NT	Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds
11817	24896		1.64	6.0E-80	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12019	24316		5.01	6.0E-80	AB028900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12543	25028		1.95	6.0E-80	AJ133127.1	NT	Homo sapiens mRNA for sodium-glucose cotransporter (SGLT2 gene)
614	13241	25716	2.83	5.0E-80	4508228	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 3 (PSMD3) mRNA
868	13483	25908	1.9	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
868	13483	25909	1.9	5.0E-80	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
1231	13830		1.16	5.0E-80	X91947.1	NT	Hi.sapiens nct1 gene (exon 12)
1503	14095		2.88	5.0E-80	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2399	14987	27540	1.08	5.0E-80	U89358.1	NT	Human I(3)mbt protein homolog mRNA, complete cds
2474	15041	27609	2.56	5.0E-80	AB037855.1	NT	Homo sapiens mRNA for KIAA1434 protein, partial cds
2820	15372	27941	2.67	5.0E-80	4504292	NT	Homo sapiens H3 histone family, member J (H3F.J) mRNA
4112	16706	28160	0.93	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
4112	16706	29161	0.93	5.0E-80	AB019038.1	NT	Homo sapiens HMT-1 mRNA for beta-1,4 mannosyltransferase, complete cds
5089	17662	30102	1.29	5.0E-80	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C068
8288	20839	33760	1.04	5.0E-80	9910293	NT	Mus musculus keratin complex 2, gene 6g (Krt2-6g), mRNA
9182	21759	34705	15.52	4.0E-80	F25915.1	EST_HUMAN	HSPD13155 HM3 Homo sapiens cDNA clone c4000045F03
233	12893		11.18	3.0E-80	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5034	17808		6.93	3.0E-80	BE817465.1	EST_HUMAN	QV4-BN0263-040800-241-g10 BN0263 Homo sapiens cDNA
5988	18608	31340	2.04	3.0E-80	A091875.1	EST_HUMAN	co23e12.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1587054 3' similar to
1833	14421	28971	6.34	2.0E-80	R35321.1	EST_HUMAN	TR:O35790 O35790 FIG-L.;
1900	14485	27046	1.4	2.0E-80	A144821.1	EST_HUMAN	yg65a08.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:38080 5'
2100	14679	27247	5.6	2.0E-80	AL043116.2	EST_HUMAN	RET487 subcloned retina cDNA library Homo sapiens cDNA clone RET487
6393	18996	31775	0.71	2.0E-80	A923972.1	EST_HUMAN	DKFZp434D1323_r1 434 (synonym: hsc3) Homo sapiens cDNA clone DKFZp434D1323 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6393	18986	31776	0.71	2.0E-80	AB23072.1	EST_HUMAN	wn49c10.x1 NCL_CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2448786 3'
6897	19631	32469	1.06	2.0E-80	AA582952.1	EST_HUMAN	nr80d01.s1 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1090177 3'
6993	19491	32312	1.69	2.0E-80	11421930	NT	Homo sapiens Golgi transport complex protein (80 kDa) (GTO80). mRNA
7298	19828	32685	1	2.0E-80	775215.1	EST_HUMAN	yc86f12.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:22851 5' similar to SP:K1CR_XENLA P08802 KERATIN, TYPE I CYTOSKELETAL ENDO B ;
9098	21822	34558	1.25	2.0E-80	AW964270.1	EST_HUMAN	EST376343 IMAGE resequences, MAGH Homo sapiens cDNA
9883	22182	35156	1.13	2.0E-80	AJ07379.1	NT	Homo sapiens GGT gene, exon 6
10748	23272	36287	7.28	2.0E-80	AA393932.1	EST_HUMAN	z70f12.r1 Soares testis, NHT Homo sapiens cDNA clone IMAGE:727727 5' similar to TR:G191315
362	13011		1.44	1.0E-80	AL163303.2	NT	G191315 ANDROGEN-DEPENDENT EXPRESSED PROTEIN. ;
832	13449	25956	1.39	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 segment HS21C103
1987	14579		3.73	1.0E-80	AF32858.1	EST_HUMAN	Homo sapiens chromosome 21 unknown mRNA
4945	17520	29962	0.71	1.0E-80	N96520.1	EST_HUMAN	nr01f12.x5 NCL_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1076495 3' similar to contains OFR.t1 OFR repetitive element ;
5530	18182		6.77	1.0E-80	BE386615.1	EST_HUMAN	za39g07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:284972 5' similar to contains Alu repetitive element;
6126	18741	31494	5.9	1.0E-80	L10347.1	NT	601274305F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615433 5'
6624	19221	32026	1.67	1.0E-80	5174540	NT	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds
7258	19786	32642	1.39	1.0E-80	AJ224172.1	NT	Homo sapiens malate dehydrogenase 2, NAD (mitochondrial) (MDH2), nuclear gene encoding mitochondrial protein, mRNA
7574	20080	32966	2.64	1.0E-80	A1948731.1	EST_HUMAN	Homo sapiens mRNA for lipophilin B
7574	20090	32967	2.64	1.0E-80	A1948731.1	EST_HUMAN	wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
8173	20714	33630	1.25	1.0E-80	11421211	NT	wq25c05.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2472286 3'
8634	21173	34091	0.96	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA). mRNA
8634	21173	34092	0.96	1.0E-80	11421211	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA). mRNA
9209	21726	34668	1.79	1.0E-80	AF245219.1	NT	Homo sapiens protein tyrosine phosphatase, receptor type, A (PTPRA). mRNA
9209	21726	34669	1.79	1.0E-80	AF245219.1	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10323	22817	35813	0.93	1.0E-80	D63478.2	NT	Homo sapiens probable mannose binding C-type lectin DC-SIGNR mRNA, complete cds
10531	23068	36080	2.64	1.0E-80	11641276	NT	Homo sapiens mRNA for KIAA0145 protein, partial cds
10531	23068	36081	2.64	1.0E-80	11641276	NT	Homo sapiens similar to rat myomegalin (LOC64182). mRNA
12091	24359	36967	2.04	1.0E-80	11417801	NT	Homo sapiens meningo (disrupted in balanced translocation) 1 (MN1). mRNA
10564	23100	36113	3.56	8.0E-81	A1251752.1	EST_HUMAN	qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854298 3'
10564	23100	36114	3.56	8.0E-81	A1251752.1	EST_HUMAN	qh80g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1854298 3'
11033	23547	36582	6.13	8.0E-81	BE394525.1	EST_HUMAN	601310531F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3632070 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7299	19827	32686	3.19	7.0E-81	A1822115.1	EST_HUMAN	zab1c08.x5 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:299918 3'
4476	17061	29510	4.95	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
4476	17061	29511	4.95	6.0E-81	BE256829.1	EST_HUMAN	601111970F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352840 5'
5487	18121	30528	1.71	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
5487	18121	30529	1.71	6.0E-81	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
9162	21697	34841	1.22	6.0E-81	AA360017.1	EST_HUMAN	EST169129 Fetal lung II Homo sapiens cDNA 5' end
12240	24453	30955	2.16	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
12240	24453	30956	2.16	6.0E-81	BF679022.1	EST_HUMAN	602153666F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294601 5'
2258	14832	27410	2.66	5.0E-81	BE268042.1	EST_HUMAN	601125505F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3345480 5'
8351	20892	33813	1.42	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
8351	20892	33814	1.42	5.0E-81	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9568	22068	35025	1.28	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
9568	22068	35026	1.28	5.0E-81	M60316.1	NT	Human transforming growth factor-beta (tgf-beta) mRNA, complete cds
11455	23905	36972	2.66	5.0E-81	9506634	NT	Homo sapiens hypothetical protein (FLJ11045), mRNA
238	12898	25381	1.3	4.0E-81	AF252257.1	NT	Homo sapiens CRP2 binding protein mRNA, partial cds
731	13351	25846	1.34	4.0E-81	A1521435.1	EST_HUMAN	th60e12.x1 NCI_CGAP_OV23 Homo sapiens cDNA clone IMAGE:2122702 3' similar to TR:Q85560 Q85560
3208	15818	28294	4.76	4.0E-81	AB037766.1	NT	Homo sapiens mRNA for KIAA1345 protein, partial cds
3690	16291	28760	0.98	4.0E-81	AW004608.1	EST_HUMAN	ws90h03.x1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:2505269 3' similar to TR:O43815 O43815
4240	16828	29277	2.39	4.0E-81	AF263306.1	NT	STRIATIN. ;
4240	16828	29278	2.39	4.0E-81	AF263306.1	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
4481	17066	29516	1.08	4.0E-81	8923209	NT	Homo sapiens rab3 interacting protein variant 2 mRNA, partial cds
7321	19848	32708	0.95	4.0E-81	4757893	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
8229	20770	33689	1.71	4.0E-81	X06989.1	NT	Homo sapiens calcium channel, voltage-dependent, L type, alpha 2/delta subunit (CACNA2) mRNA
8482	21021	33936	3.39	4.0E-81	U20197.1	NT	Human mRNA for amyloid A4(751) protein
8482	21021	33937	3.39	4.0E-81	U20197.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
9153	21688	34632	4.78	4.0E-81	AB018001.1	NT	Human cone photoreceptor cGMP-phosphodiesterase alpha' subunit gene, exons 2 and 3
10012	22507	35498	1.79	4.0E-81	11425281	NT	Homo sapiens mRNA for Death-associated protein kinase 2, complete cds
10075	22570	35564	0.57	4.0E-81	11439085	NT	Homo sapiens ligase I, DNA, ATP-dependent (LIG1), mRNA
10075	22570	35565	0.57	4.0E-81	11439085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11063	23575	36812	2.85	4.0E-81	4759085	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11063	23575	36813	2.85	4.0E-81	4759085	NT	Homo sapiens vesicle trafficking protein sec22b (SEC22B) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11708	24981	30834	11.8	4.0E-81	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11708	24981	30835	11.8	4.0E-81	11417882	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12277	24481	30938	2.13	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12277	24481	30939	2.13	4.0E-81	11417871	NT	Homo sapiens beta-ureidopropionase (LOC51733), mRNA
12430	24572	30912	4.2	4.0E-81	11417874	NT	Homo sapiens transferrin II; macrocytic anemia (TCN2), mRNA
1310	13904	26422	9.81	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
1310	13904	26423	9.81	3.0E-81	Y18000.1	NT	Homo sapiens NF2 gene
2409	14977	27551	1.66	3.0E-81	AF077188.1	NT	Homo sapiens cullin 4A (CUL4A) mRNA, complete cds
3020	15636	28112	5.8	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
3020	15636	28113	5.8	3.0E-81	4506280	NT	Homo sapiens pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1) (PTN) mRNA
5143	17714	27953	2.95	3.0E-81	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
2859	15478	27954	2.07	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5'
2859	15478	27954	2.07	2.0E-81	BE784636.1	EST_HUMAN	601474072F1 NIH_MGC 68 Homo sapiens cDNA clone IMAGE:3877121 5'
3841	16440	28902	0.75	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
12591	16440	28902	2.77	2.0E-81	AW611542.1	EST_HUMAN	hg85c01.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2952384 3'
1468	14060	26595	0.92	1.0E-81	W26539.1	EST_HUMAN	33f3 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4613	17196	29642	1.81	1.0E-81	AA040370.1	EST_HUMAN	2k45h09.r1 Soares pregnant uterus_NbHPU Homo sapiens cDNA clone IMAGE:485825 5' similar to
4750	17331	29774	8.65	1.0E-81	BE047096.1	EST_HUMAN	PIR:S52437 S52437 CDP-diacylglycerol synthase - fruit fly
5049	17622	30067	1.14	1.0E-81	AW192426.1	EST_HUMAN	tz45c04.y1 NCI_CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2291526 5'
5446	18017	37139	3.85	1.0E-81	U87928.1	NT	422a03.x1 Soares_NFL_T_GBC S1 Homo sapiens cDNA clone IMAGE:2659852 3'
5556	18188	30603	3.58	1.0E-81	11432968	NT	Human aconitate hydratase (ACO2) gene, exon 3
5556	18188	30604	3.58	1.0E-81	11432968	NT	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5983	18319	30818	0.77	1.0E-81	AA255569.1	EST_HUMAN	Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
5935	18459	31180	3.92	1.0E-81	U62351.1	NT	z65c06.r1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:682475 5' similar to SW:PRI2_HUMAN
5935	18459	31181	3.92	1.0E-81	U62351.1	NT	P49643 DNA PRIMASE 58 KD SUBUNIT
6295	18903	31574	1.82	1.0E-81	BF674641.1	EST_HUMAN	Homo sapiens arm-repeat protein NPRAP/neurexigin (CTNND2) mRNA, partial cds
6836	19428	32242	0.73	1.0E-81	AJ133269.1	NT	Homo sapiens arm-repeat protein NPRAP/neurexigin (CTNND2) mRNA, partial cds
7748	20256	33151	7.93	1.0E-81	11432968	NT	Homo sapiens arm-repeat protein NPRAP/neurexigin (CTNND2) mRNA, partial cds
7762	20270	33168	0.72	1.0E-81	AJ250408.1	NT	602137804F1 NIH_MGC_63 Homo sapiens cDNA clone IMAGE:4274536 5'
							Homo sapiens caveolin-1/-2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
							Homo sapiens polymerase (DNA directed), gamma (POLG), mRNA
							Homo sapiens GLI3 gene for GLI3 protein

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9691	22190	35163	13.75	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9691	22190	35164	13.75	1.0E-81	BE958278.1	EST_HUMAN	601645051F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930228 5'
9679	22376	35353	4.13	1.0E-81	BE564367.1	EST_HUMAN	601343180F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685483 5'
							ac114d06.s1 Strategene HeLa cell s3 937218 Homo sapiens cDNA clone IMAGE:856427 3' similar to SW:YB36_YEAST P38128 HYPOTHETICAL 60.5 KD PROTEIN IN RPS101-RPS13 INTERGENIC REGION.1
10014	22509	35500	1.16	1.0E-81	AA630784.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10016	22511	35502	2.64	1.0E-81	BE744545.1	EST_HUMAN	601577339F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3838280 5'
10016	22511	35503	2.64	1.0E-81	BE744545.1	EST_HUMAN	CM3-NN0059-140400-147-a12 NN0059 Homo sapiens cDNA
10402	22896	35892	1.47	1.0E-81	AW897550.1	EST_HUMAN	NR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
10967	23482	36508	2.02	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
10967	23482	36509	2.02	1.0E-81	AW844986.1	EST_HUMAN	MR0-CT0006-250599-019 CT0006 Homo sapiens cDNA
10971	23486	36514	1.57	1.0E-81	AW798167.1	EST_HUMAN	RC3-JM0046-290200-011-906 UM0046 Homo sapiens cDNA
10971	23486	36515	1.57	1.0E-81	AW798167.1	EST_HUMAN	RC3-JM0046-290200-011-906 UM0046 Homo sapiens cDNA
11152	18027	30489	2.07	1.0E-81	AW960658.1	EST_HUMAN	EST372729 MAGE resequences, MAGF Homo sapiens cDNA
11398	23850	36916	2.34	1.0E-81	BF204253.1	EST_HUMAN	601867714F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110459 5'
11920	24266	31012	3.39	1.0E-81	11418138	NT	Homo sapiens phorbol (similar to apolipoprotein B mRNA editing protein) (DJ742C19.2), mRNA
14	12693	25149	13.13	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
111	12693	25149	6.9	8.0E-82	AF161406.1	NT	Homo sapiens HSPC288 mRNA, partial cds
285	12941	25427	1.89	8.0E-82	U09888.1	NT	Human CRFB4 gene, partial cds
847	13463	25971	2.2	8.0E-82	U09888.1	NT	Human CRFB4 gene, partial cds
920	13533	26051	1.5	8.0E-82	U09888.1	NT	Human CRFB4 gene, partial cds
1537	14128	26665	1.12	8.0E-82	AB037748.1	NT	Homo sapiens mRNA for KIAA1327 protein, partial cds
1697	14280	26828	1.42	8.0E-82		NT	Homo sapiens glutathione peroxidase 5 (epididymal androgen-related protein) (GPX5), transcript variant 2, mRNA
4328	16914	28358	0.77	8.0E-82	8923432	NT	Homo sapiens hypothetical protein FLJ20461 (FLJ20461), mRNA
1499	14091		1.45	7.0E-82	BF035327.1	EST_HUMAN	601456531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862088 5'
2794	15347	27816	1.21	7.0E-82	AU144050.1	EST_HUMAN	AU144050 HEMBA1 Homo sapiens cDNA clone HEMBA1000752 3'
12395	24555		1.37	7.0E-82	AA515512.1	EST_HUMAN	m89e1.1 s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:925196 3'
1710	14303	26840	20.15	4.0E-82	AF081484.1	NT	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds
5688	18314	30812	0.83	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-708 HT0540 Homo sapiens cDNA
5688	18314	30813	0.83	4.0E-82	BF351691.1	EST_HUMAN	QV2-HT0540-120900-362-708 HT0540 Homo sapiens cDNA
11563	24010	37080	5.53	4.0E-82	AI937300.1	EST_HUMAN	wp75609.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2467824 3' similar to TR:075276 O75276 PKD1
12178	24415		5.98	4.0E-82	AF029701.2	NT	Homo sapiens presenilin-1 gene, exons 1 and 2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
299	12955	25444	14.77	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
732	13352	25847	2.11	3.0E-82	BE005705.1	EST_HUMAN	RC2-BN0120-010400-013-02 BN0120 Homo sapiens cDNA
820	13437	25944	8.87	3.0E-82	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
803	13517	26035	3.37	3.0E-82	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1099	13704		39.06	3.0E-82	AA725848.1	EST_HUMAN	ai23605.31 Soares_testis_NHT Homo sapiens cDNA clone 1343648 3'
1399	13993	26522	1.11	3.0E-82	AW875073.1	EST_HUMAN	RC6-PT0001-190100-021-B02 PT0001 Homo sapiens cDNA
1515	14107	26643	2.15	3.0E-82	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1945	14528	27085	1.59	3.0E-82	BE813232.1	EST_HUMAN	RC1-BN0005-260700-018-g04 BN0005 Homo sapiens cDNA
2050	14631	27202	1.18	3.0E-82	4501922	NT	Homo sapiens adenylate cyclase activating polypeptide 1 (pituitary) receptor type I (ADCYAP1R1) mRNA
3310	15921		2.54	3.0E-82	5453811	NT	Homo sapiens neurotrophic tyrosine kinase, receptor, type 2 (NTRK2) mRNA
5047	17620	30065	0.92	3.0E-82	AA135979.1	EST_HUMAN	zr63b04.r1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565711 5' similar to SW:PAGT_BOVIN Q07537 POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE ;
8093	20634	33546	2.5	3.0E-82	11425206	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8491	21030	33949	0.82	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
8491	21030	33950	0.82	3.0E-82	11432889	NT	Homo sapiens contactin 6 (CNTN6), mRNA
9738	22236	35215	5.16	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
9738	22236	35216	5.16	3.0E-82	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
623	13250	25723	2.46	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
623	13250	25724	2.46	2.0E-82	AB023216.1	NT	Homo sapiens mRNA for KIAA0999 protein, partial cds
1724	14315	26857	1.52	2.0E-82	AL046390.1	EST_HUMAN	DKFZp434M117_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434M117 5'
3837	16436	28898	1.47	2.0E-82	M86878.1	NT	H sapiens plasminogen-apolipoprotein (a) gene family, exon for 1st kring 4 repeat
3913	16511	28973	1.03	2.0E-82	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4095	16690	29146	0.62	2.0E-82	U76833.1	NT	Human integral membrane serine protease Seprase mRNA, complete cds
4317	16903	29347	0.66	2.0E-82	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4656	17236	29693	1.38	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
4656	17236	29694	1.38	2.0E-82	AB029019.1	NT	Homo sapiens mRNA for KIAA1098 protein, partial cds
4995	17569	30013	2.59	2.0E-82	AF045555.1	NT	Homo sapiens wbscr1 (WBSGR1) and wbscr5 (WBSGR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
5239	17803	30223	1.36	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA
5239	17803	30224	1.36	2.0E-82	4507580	NT	Homo sapiens tumor necrosis factor receptor superfamily, member 5 (TNFRSF5) mRNA

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5320	17882	30301	1.3	2.0E-82	4502508	NT	Homo sapiens complement component 5 (C5) mRNA
5662	18289	30787	3.76	2.0E-82	AB018270.1	NT	Homo sapiens mRNA for KIAA0727 protein, partial cds
6322	18929	31705	4.77	2.0E-82	AF234882.1	NT	Homo sapiens FAM44A1 splice variant a (FAM44A1) mRNA, complete cds
7673	25121		1.02	2.0E-82	AI478428.1	EST_HUMAN	hm21g05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157272 3'
7771	20280	33177	0.71	2.0E-82	8923130	NT	Homo sapiens hypothetical protein FLJ20128 (FLJ20128), mRNA
8247	20798	33707	1.82	2.0E-82	11321570	NT	Homo sapiens slit (Drosophila) homolog 3 (SLIT3), mRNA
10018	22513	35505	1.45	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10018	22513	35506	1.45	2.0E-82	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
11149	23657	36699	1.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11149	23657	36700	1.95	2.0E-82	11417191	NT	Homo sapiens leucylcystinyl aminopeptidase (LNPEP), mRNA
11155	23662	36707	2.35	2.0E-82	11417105	NT	Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A reductase (HMGCR), mRNA
11188	23693	36741	8.98	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11188	23693	36742	8.98	2.0E-82	U80738.1	NT	Homo sapiens CAGF9 mRNA, partial cds
11737	24140		4.92	2.0E-82	N94650.1	EST_HUMAN	zb31d10.s1 Soares_parathyroid tumor_NbHPA Homo sapiens cDNA clone IMAGE:305203 3'
12299	24496		2.45	2.0E-82	AA011278.1	EST_HUMAN	201g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
618	13245	25718	1.59	1.0E-82	11545921	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
1250	13847		1.25	1.0E-82	BE885106.1	EST_HUMAN	601510859F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912207 5'
1329	13923	26443	2.7	1.0E-82	BE064386.1	EST_HUMAN	RC4-BT0310-110300-015-f10 BT0310 Homo sapiens cDNA
1330	13924	26444	0.84	1.0E-82	AB011110.2	NT	Homo sapiens mRNA for KIAA0538 protein, partial cds
8872	21411	34334	1.31	1.0E-82	AB037839.1	NT	Homo sapiens mRNA for KIAA1417 protein, partial cds
9571	22071	35032	0.48	1.0E-82	AB014562.1	NT	Homo sapiens mRNA for KIAA0662 protein, partial cds
10143	22638		1.19	1.0E-82	BF515938.1	EST_HUMAN	UIH-BW1-aaa-f03-Q-UI.s1 NCL_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084053 3'
10824	23156	39169	2.41	1.0E-82	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
10887	23408	36425	1.55	1.0E-82	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8649	21198	34106	4.39	9.0E-83	BF672220.1	EST_HUMAN	602150403F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291561 5'
10175	22870	35684	0.78	9.0E-83	BE255347.1	EST_HUMAN	60111760F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3357734 5'
1459	14051	26583	4.53	8.0E-83	BE383973.1	EST_HUMAN	601273349F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614362 5'
1721	15394	26852	2.5	8.0E-83	N66951.1	EST_HUMAN	zz48f12.s1 Soares_fetal_liver_spleen_1NFLS Homo sapiens cDNA clone IMAGE:295823 3'
1401	13995	26523	1	7.0E-83	AW385529.1	EST_HUMAN	QV4-LT0016-271299-068-h11 LT0016 Homo sapiens cDNA
2890	15507		1.75	7.0E-83	AA584655.1	EST_HUMAN	no12h01.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100497 3' similar to contains Alu repetitive element
4940	17515		6.94	7.0E-83	BF221813.1	EST_HUMAN	7p37a07.x1 NCL_CGAP_P28 Homo sapiens cDNA clone IMAGE:3647893 3' similar to TR:Q9Y316 Q9Y316
6202	18812	31582	0.69	7.0E-83	11426657	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
428	13061	25555	3.97	6.0E-83	M33320.1	NT	Human platelet Glycoprotein IIb (GPIIb) gene, exons 2-29
1822	14411	26956	2.07	6.0E-83	AW573098.1	EST_HUMAN	h31h03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2933525 3' similar to
3087	15702		0.81	6.0E-83	AF231919.1	NT	SW:YBEB_HAEIN_P44471 HYPOTHETICAL PROTEIN H10034.1
3619	16222	28700	1.18	6.0E-83	11430241	NT	Homo sapiens chromosome 21 unknown mRNA
5497	18131	30539	2.35	6.0E-83	4507868	NT	Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A (33kD) (VAPA) mRNA, and translated products
6174	18785	31553	1.18	6.0E-83	AJ010770.1	NT	Homo sapiens hyperion gene, exons 1-50
7613	20034	32900	1.98	6.0E-83	11420204	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA
9594	22094	35058	3.97	6.0E-83	4505314	NT	Homo sapiens myomesin (M-protein) 2 (185kD) (MYOM2), mRNA
9684	22183	35157	2.77	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Pp18 (PRP18), mRNA
9684	22183	35158	2.77	6.0E-83	11430647	NT	Homo sapiens pre-mRNA splicing factor similar to S. cerevisiae Pp18 (PRP18), mRNA
11405	23856		6.64	8.0E-83	AA486105.1	EST_HUMAN	ab14e10.s1 Stralagene lung (#837210) Homo sapiens cDNA clone IMAGE:840810 3' similar to contains THR12 THR repetitive element
11685	24102		5.62	6.0E-83	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
982	13594		10.4	5.0E-83	U17883.1	NT	Human succinate dehydrogenase iron-protein subunit (sdhB) gene, exon 5
2084	15397		1.12	5.0E-83	AF006305.1	NT	Homo sapiens 26S proteasome regulatory subunit (SUG2) mRNA, complete cds
3700	16301	28769	0.98	5.0E-83	AL133207.2	NT	Novel human gene mapping to chromosome X
3977	16575	29045	0.84	5.0E-83	4885190	NT	Homo sapiens deoxyribonuclease I (DNAse1), mRNA
4527	17111	29555	0.6	5.0E-83	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
5238	17802	30221	13.17	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
5238	17802	30222	13.17	5.0E-83	4557013	NT	Homo sapiens catalase (CAT) mRNA
668	13292	26773	1.34	4.0E-83	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
3564	16168	28650	1.07	4.0E-83	BE888078.1	EST_HUMAN	601511580F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913195 5'
1035	13645		3.47	3.0E-83	AA368311.1	EST_HUMAN	EST79542 Placenta 1 Homo sapiens cDNA similar to similar to endogenous retrovirus ERV9
6602	19288		0.68	3.0E-83	A1217223.1	EST_HUMAN	q173d08.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1755682 3'
1835	14423	26973	1.31	2.0E-83	AA983492.1	EST_HUMAN	q164q05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1621592 3' similar to TR:Q92614
1835	14423	26974	1.31	2.0E-83	AA983492.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216.1
1969	14553	27109	2.88	2.0E-83	AG6951.1	EST_HUMAN	Q92614 MYELOBLAST KIAA0216.1
2876	15494	27964	1.08	2.0E-83	BE828894.1	EST_HUMAN	z948f12.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295823 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3307	15918		2.53	2.0E-83	11430834	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3942	16441		0.78	2.0E-83	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4428	17015	28457	4.01	2.0E-83	AF202879.1	NT	Homo sapiens hematopoietic progenitor cell antigen CD34 precursor (CD34) mRNA, partial cds
4756	17337	29781	4.54	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
4768	17337	29782	4.54	2.0E-83	7706398	NT	Homo sapiens ankyrin repeat-containing protein ASB-2 (LOC51676), mRNA
5475	18109	30518	0.8	2.0E-83	U06678.1	NT	Human carcinoembryonic antigen gene family member 18 (CGM18), mRNA
6119	18735	31488	1.28	2.0E-83	BE805401.1	EST_HUMAN	601507482F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909068 5'
7462	19985	32850	6.08	2.0E-83	AF129533.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
7784	20327	33232	0.53	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7784	20327	33233	0.53	2.0E-83	AB001025.1	NT	Homo sapiens mRNA for brain ryanodine receptor, complete cds
7928	20470	33379	1.54	2.0E-83	U066707.1	NT	Rattus norvegicus densin-180 mRNA, complete cds
8256	20797	33714	2.17	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8256	20797	33715	2.17	2.0E-83	AF011920.1	NT	Homo sapiens protein kinase CK2 catalytic subunit alpha gene, exon 1
8797	22285	35278	0.65	2.0E-83	BF128748.1	EST_HUMAN	60181127F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4053894 5'
8947	22442	35419	2.41	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
8947	22442	35420	2.41	2.0E-83	M22094.1	NT	Human neural cell adhesion molecule (N-CAM) secreted isoform mRNA, 3' end
10025	22520	35516	1.12	2.0E-83	AU117659	EST_HUMAN	AU117659 HEMBA1 Homo sapiens cDNA clone HEMBA1001910 5'
10092	22587	35580	0.78	2.0E-83	AW505600.1	EST_HUMAN	UI-HF-BND-amd-H-07-O-J1, r1 NIH_MGC 50 Homo sapiens cDNA clone IMAGE:3081852 5'
10728	23255	36271	4.96	2.0E-83	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
10806	23329	36340	1.95	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547J135 5'
10808	23328	36341	1.95	2.0E-83	AL134452.1	EST_HUMAN	DKFZp547J135_r1 547 (synonym: hfbt1) Homo sapiens cDNA clone DKFZp547J135 5'
12342	24523		4.52	2.0E-83	AB011398.1	NT	Homo sapiens gene for AF-6, complete cds
1457	14049	26580	2.83	1.0E-83	4504326	NT	Homo sapiens hydroxycyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1457	14049	26581	2.83	1.0E-83	4504326	NT	Homo sapiens hydroxycyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit (HADHB) mRNA
1506	14098	26635	15.46	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
1506	14098	26636	15.46	1.0E-83	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
2064	14644	27218	1.11	1.0E-83	4503852	NT	Homo sapiens fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1) mRNA
2681	15239	27807	1.06	1.0E-83	BE883690.1	EST_HUMAN	601507375F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908754 5'
3217	15829	28308	0.69	1.0E-83	7662349	NT	Homo sapiens cell recognition molecule Caspr2 (KIAA0868), mRNA
3936	16534	29000	5.6	1.0E-83	AF053768.1	NT	Rattus norvegicus brain specific contactin-binding protein CBP90 mRNA, partial cds
4328	16915	29359	2.45	1.0E-83	725822.1	NT	H. sapiens gene for mitochondrial dodecanoyl-CoA delta-isomerase, exon 3

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6797	19388	32204	1.58	1.0E-83	A027814.1	EST_HUMAN	α99b08.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1645431 3' similar to gb:M64241 QM PROTEIN (HUMAN);
3884	16482	28928	3.57	7.0E-84	BE901209.1	EST_HUMAN	601876023F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:395883 5'
1338	13932	26451	3.5	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200800-011-g05 FN0119 Homo sapiens cDNA
1338	13932	26452	3.5	6.0E-84	BE838864.1	EST_HUMAN	RC2-FN0119-200800-011-g05 FN0119 Homo sapiens cDNA
2441	15008	27580	21.62	6.0E-84	AA776574.1	EST_HUMAN	ae86a03.s1 Strategene schizo brain S11 Homo sapiens cDNA clone IMAGE:971020 3'
5449	18019		2.84	6.0E-84	AL042803.2	EST_HUMAN	DKFZp434H0322_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434H0322 5'
5709	18335	30840	1.74	6.0E-84	AA897339.1	EST_HUMAN	al47g03.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1460500 3' similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN);
5841	18485	31189	1.06	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC); mRNA
5841	18485	31190	1.06	6.0E-84	11426718	NT	Homo sapiens acetyl LDL receptor; SREC=scavenger receptor expressed by endothelial cells (SREC); mRNA
7489	20012	32878	3.2	6.0E-84	BE810371.1	EST_HUMAN	PM0-LT0019-190600-004-F02 LT0019 Homo sapiens cDNA
7679	20180	33079	0.93	6.0E-84	AF038391.1	NT	Homo sapiens pre-mRNA splicing factor (PRP16) mRNA, complete cds
8018	20560	33481	1.85	6.0E-84	BE770199.1	EST_HUMAN	PM4-FT0054-160800-004-s10 FT0054 Homo sapiens cDNA
11409	23860		2	6.0E-84	AW368812.1	EST_HUMAN	IL0-BT0168-091199-139-e06 BT0168 Homo sapiens cDNA
743	13363	25858	0.69	5.0E-84	AA392811.1	EST_HUMAN	EST196094 Testis 1 Homo sapiens cDNA 5' end
3048	15684		1.4	5.0E-84	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
11419	23870	36931	2.7	5.0E-84	11428740	NT	Homo sapiens regulatory factor X, 3 (influences HLA class II expression) (RFX3), mRNA
11506	23955	37024	1.95	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
11506	23955	37025	1.95	5.0E-84	AB032957.1	NT	Homo sapiens mRNA for KIAA1131 protein, partial cds
1456	14048	26579	2.3	4.0E-84	AI685321.1	EST_HUMAN	wa76a04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2302086 3' similar to SW:NRDC_HUMAN_043847 NARDILYSIN PRECURSOR;
5095	17658	30099	0.70	4.0E-84	4505928	NT	Homo sapiens polymerase (DNA-directed), alpha (70kD) (POLA2), mRNA
5096	17659	30100	1.62	4.0E-84	AF09601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
5751	18377	31087	1.42	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
5751	18377	31088	1.42	4.0E-84	11386168	NT	Homo sapiens protein tyrosine phosphatase, receptor type, G (PTPRG), mRNA
6414	19017	31800	2.16	4.0E-84	AF056650.1	NT	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds
7643	20155	33041	13.58	4.0E-84	11421326	NT	Homo sapiens KIAA0783 gene product (KIAA0783), mRNA
8842	21381	34305	1.06	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8842	21381	34306	1.06	4.0E-84	4557528	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
10798	23321	36331	5.76	4.0E-84	AB032956.1	NT	Homo sapiens mRNA for KIAA1130 protein, partial cds
338	12890	25477	1.97	3.0E-84	AF026200.1	NT	Homo sapiens Bact1 protein homolog mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1194	13795	26304	0.86	3.0E-84	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2003	14585	27144	1.93	3.0E-84	5453855	NT	Homo sapiens pericentriolar material 1 (PCM1) mRNA
2051	14632	27203	1.94	3.0E-84	AL096880.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
3812	16411	28876	5.94	3.0E-84	AF014459.1	NT	Homo sapiens X-linked juvenile retinoschisis precursor protein (XLR51) mRNA, complete cds
10758	23282		10.76	3.0E-84	AI983801.1	EST_HUMAN	wu20d05.x1 Soares Dieckgraebe colon NHQD Homo sapiens cDNA clone IMAGE:2520585 3' similar to
2153	14730	27304	6.66	2.0E-84	BE695397.1	EST_HUMAN	gb:LO5093 60S RIBOSOMAL PROTEIN L18A (HUMAN);
2153	14730	27305	6.66	2.0E-84	BE695397.1	EST_HUMAN	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2970	15586	28088	11.6	2.0E-84	AF036943.1	NT	CM1-BT0795-190600-272-508 BT0795 Homo sapiens cDNA
2989	15605	28085	1.3	2.0E-84	X89211.1	NT	Homo sapiens myelin transcription factor 1-like (MYT1-L) mRNA, complete cds
5717	18343	30849	1.02	2.0E-84	BF511575.1	EST_HUMAN	H. sapiens DNA for endogenous retroviral like element
5717	18343	30850	1.02	2.0E-84	BF511575.1	EST_HUMAN	UI-H-B14-ache-02-0-UI.st NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
6748	19341	32148	1.04	2.0E-84	H63370.1	EST_HUMAN	UI-H-B14-ache-02-0-UI.st NCI CGAP Sub8 Homo sapiens cDNA clone IMAGE:3084963 3'
8001	20543		1.51	2.0E-84	AI298674.1	EST_HUMAN	yf56e11.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:209324 3'
9269	21795	34744	0.89	2.0E-84	AU120280.1	EST_HUMAN	gm87c09.x1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1895728 3'
9647	22146	35117	0.55	2.0E-84	H22841.1	EST_HUMAN	AU120280 HEMBB1 Homo sapiens cDNA clone HEMBB1000339 5'
11954	24279	31021	1.69	2.0E-84	BF448000.1	EST_HUMAN	ym49e11.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:51383 5' similar to SP-APOH_RAT
11954	24279	31022	1.69	2.0E-84	BF448000.1	EST_HUMAN	P26844 BETA-2-GLYCOPROTEIN I ;
334	12986	25473	1.61	1.0E-84	AF114488.1	NT	nae30a02.x1 Lupskl sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
575	13205	25685	7.74	1.0E-84	4507952	NT	TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
749	13369		4	1.0E-84	11427631	NT	nae30a02.x1 Lupskl sympathetic trunk Homo sapiens cDNA clone IMAGE:4090251 3' similar to
1336	13930	26449	3.89	1.0E-84	AA984379.1	EST_HUMAN	TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
2098	14678	27248	2.49	1.0E-84	BE392197.1	EST_HUMAN	TR:Q9UGS3 Q9UGS3 DJ756G23.1 ;
2265	14839	27415	1.21	1.0E-84	11427197	NT	Homo sapiens interseitin short isoform (ITSN) mRNA, complete cds
2945	15581	28035	1.09	1.0E-84	4507848	NT	Homo sapiens tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide (YWHAZ) mRNA
2945	15581	28036	1.09	1.0E-84	4507848	NT	Homo sapiens complement component 5 (C5). mRNA
3814	16414	28878	2.92	1.0E-84	AA720851.1	EST_HUMAN	sm85b11.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1628885 3'
4508	17092	28539	6.06	1.0E-84	AJ229041.1	NT	601308006F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3626257 5'
4809	17387	29837	3.09	1.0E-84	AL043314.2	EST_HUMAN	Homo sapiens pericentriolar material 1 (PCM1) mRNA
4809	17387	29838	3.09	1.0E-84	AL043314.2	EST_HUMAN	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
							Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13) mRNA
							hw12e06.s1 NCI CGAP SS1 Homo sapiens cDNA clone IMAGE:1239106 3'
							Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22: segment 1/3
							Homo sapiens 659 kb contig between AML1 and CBR1 on chromosome 21q22: segment 1/3
							DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
							DKFZp434N0323_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5037	17092	29539	3.8	1.0E-84	AJ229041.1	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22, segment 1/3
6079	18696	31443	0.81	1.0E-84	11434422	NT	Homo sapiens speckle-type POZ protein (SPOP), mRNA
6337	18943	31722	1.46	1.0E-84	S73492.1	NT	uterine water channel=28 kda erythrocyte integral membrane protein homolog [human, uterus, mRNA, 1340 nt]
6961	19538	32361	1.63	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
6961	19538	32362	1.63	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7162	19694	32540	2.39	1.0E-84	AL049784.1	NT	Novel human gene mapping to chromosome 13
7486	20009	32875	3.27	1.0E-84	8393994	NT	Homo sapiens polymerase (DNA directed), alpha (POLA), mRNA
7565	20082	32958	1.18	1.0E-84	11430846	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
7598	20082	32958	2.45	1.0E-84	11430846	NT	Homo sapiens NGFI-A binding protein 1 (ERG1 binding protein 1) (NAB1), mRNA
8454	21980	35159	4.5	1.0E-84	5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15), mRNA
9685	22184	35159	0.58	1.0E-84	AF224511.1	NT	Homo sapiens Cdz-binding protein CABP3 (CABP3) gene, exon 8 and partial cds
9708	15561	28035	2.37	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
9708	15561	28036	2.37	1.0E-84	4507848	NT	Homo sapiens ubiquitin specific protease 13 (isopeptidase T-3) (USP13), mRNA
11833	24198	28036	2.44	1.0E-84	11417812	NT	Homo sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
11943	24274	31017	3.97	1.0E-84	11418185	NT	Homo sapiens acinifase 2, mitochondrial (ACO2), mRNA
1002	13613	28224	4.54	9.0E-85	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
1111	13715	28224	6.28	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1111	13715	28225	6.29	9.0E-85	U51432.1	NT	Homo sapiens nuclear protein Skip mRNA, complete cds
1424	14017	28546	1.35	9.0E-85	4758869	NT	Homo sapiens leupadin (LDPL), mRNA
1622	14215	28746	9.44	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1622	14215	28747	9.44	9.0E-85	M33282.1	NT	Human plasminogen gene, exon 7
1714	14308	28845	2.45	9.0E-85	7657020	NT	Homo sapiens DKFZP434P211 protein (DKFZP434P211), mRNA
4338	16925	28366	0.97	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
5006	17579	30023	0.96	9.0E-85	5901979	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
5038	17611	30055	1.02	9.0E-85	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C068
1175	13777	26287	10.28	7.0E-85	L05084.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds
11469	23948		11.38	7.0E-85	AF113210.1	NT	Homo sapiens MSTP030 mRNA, complete cds
11284	23748	36803	3.15	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
11284	23748	36804	3.15	6.0E-85	11438573	NT	Homo sapiens DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase) (DDX10), mRNA
2371	14941	27514	1.09	5.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4525	17109		0.59	5.0E-85	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
5642	18271	30744	1.42	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862402 5'
5642	18271	30745	1.42	5.0E-85	BF035674.1	EST_HUMAN	601458646F1 NIH_MGC 66 Homo sapiens cDNA clone IMAGE:3862402 5'
10998	23512	36545	1.95	5.0E-85	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12589	17109		3.17	5.0E-85	AF211188.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1I-a isoform (CACNA1I) mRNA, complete cds
6297	18905	31675	1.63	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
6297	18905	31676	1.63	4.0E-85	BF677910.1	EST_HUMAN	602084730F1 NIH_MGC 83 Homo sapiens cDNA clone IMAGE:4249087 5'
10484	22958		1.64	4.0E-85	BE079263.1	EST_HUMAN	RC1-BT0623-120200-011-c07 BT0623 Homo sapiens cDNA
1342	13937	26458	0.88	3.0E-85	AF098157.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 6
1816	14408	26950	5.06	3.0E-85	T97495.1	EST_HUMAN	ye53g08.r1 Soares fetal liver spleen 1N1LS Homo sapiens cDNA clone IMAGE:121504 5'
4405	16980	29434	0.93	3.0E-85	BE287189.1	EST_HUMAN	601189704F2 NIH_MGC 7 Homo sapiens cDNA clone IMAGE:3533616 5'
5025	17599	30043	1.44	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
5025	17599	30044	1.44	3.0E-85	11024695	NT	Homo sapiens F-box only protein 24 (FBXO24), mRNA
6283	18891	31659	6.49	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
6283	18891	31660	6.49	3.0E-85	7662309	NT	Homo sapiens KIAA0793 gene product (KIAA0793), mRNA
7032	19568		7.22	3.0E-85	AJ404488.1	NT	Homo sapiens mRNA for dynein heavy chain (DNAH9 gene)
7428	19952	32817	0.95	3.0E-85	11416870	NT	Homo sapiens GTPase regulator associated with the focal adhesion kinase pp125(FAK); KIAA0621 protein (KIAA0621), mRNA
7813	20356	33264	1.55	3.0E-85	U44953.1	NT	Homo sapiens DENN mRNA, complete cds
8445	20985	33900	0.78	3.0E-85	11525829	NT	Homo sapiens CGI-81 protein (LOC51108), mRNA
8908	21447	34369	3.75	3.0E-85	11430899	NT	Homo sapiens phospholipase C, epsilon (PLCE), mRNA
9230	21952	34901	1.32	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB2), mRNA
9230	21952	34902	1.32	3.0E-85	11421422	NT	Homo sapiens small nuclear ribonucleoprotein polypeptide B' (SNRNPB2), mRNA
10377	22871	35864	0.81	3.0E-85	AF098642.1	NT	Homo sapiens phospholipid scramblase mRNA, complete cds
11390	23832	36895	2.25	3.0E-85	5031660	NT	Homo sapiens EGF-like repeats and discodin 1-like domains 3 (EDIL3), mRNA
12470	24595		2.19	3.0E-85	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
998	13609	26124	3.12	2.0E-85		NT	Homo sapiens KIAA0929 protein Mst2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1078	13683	26194	2.1	2.0E-85	AF248540.1	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1450	14042	26570	3.85	2.0E-85		NT	Homo sapiens CGI-201 protein (LOC51340), mRNA
1465	14057	26590	32.65	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1465	14057	26591	32.65	2.0E-85	5174775	NT	Homo sapiens apolipoprotein C-II (APOC2) mRNA
2274	14848	27424	2.27	2.0E-85	U10525.1	NT	Human DNA polymerase beta gene, exons 12 and 13
2850	13976		8.53	2.0E-85	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3057	15873	28149	1.18	2.0E-85	M30838.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
4427	17013	29455	7.95	2.0E-85	4505880	NT	Homo sapiens plasminogen (PLG) mRNA
4684	17246	29700	8.24	2.0E-85	4826977	NT	Homo sapiens retin (RELN) mRNA
5036	17610	30054	1.19	2.0E-85	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5313	17875	30297	1.73	2.0E-85	4502212	NT	Homo sapiens arginase, liver (ARG1) mRNA
9197	21714	34658	1.33	2.0E-85	A1760820.1	EST_HUMAN	w167h08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398431 3' similar to contains element
9567	22067	35027	0.84	2.0E-85	A1614459.1	EST_HUMAN	MSR1 repetitive element;
10163	22658	35654	1.38	2.0E-85	A186384.1	EST_HUMAN	wd49d03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331461 3'
2326	14997		2.43	1.0E-85	BE794306.1	EST_HUMAN	wm94d12.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2443607 3'
2437	15004	27576	8.29	1.0E-85	BE618392.1	EST_HUMAN	601591416F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945818 5'
2437	15004	27577	8.29	1.0E-85	BE618392.1	EST_HUMAN	601482817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
9696	22195	35168	2.03	1.0E-85	BE267917.1	EST_HUMAN	601482817F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3866021 5'
10804	23327	36337	2.87	1.0E-85	AA778785.1	EST_HUMAN	601109738F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350553 5'
10876	23397	36413	2.59	1.0E-85	BF311552.1	EST_HUMAN	z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10876	23397	36414	2.59	1.0E-85	BF311552.1	EST_HUMAN	z45f03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:453245 3'
10943	23458	36482	2.48	1.0E-85	Y00052.1	NT	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
11605	24048	37114	2.17	1.0E-85	A1198420.1	EST_HUMAN	601897003F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126440 5'
11838	24363	30969	4.42	1.0E-85	11417862	NT	Human mRNA for T-cell cyclophilin
12098	24363	30969	5.48	1.0E-85	11417862	NT	qi56a07.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:1860468 3'
1475	14067		17.55	9.0E-86	BE274217.1	EST_HUMAN	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
6275	18983	31651	1.65	8.0E-86	11424140	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11543	23991	37053	1.65	8.0E-86	4503224	NT	601120778F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967680 5'
244	12903	25384	0.68	7.0E-86	7662247	NT	Homo sapiens similar to CDC28 protein kinase 1 (H. sapiens) (LOC63041), mRNA
972	13583	26096	1.06	7.0E-86	AA80801.1	EST_HUMAN	Homo sapiens cytochrome P450, subfamily IIF, polypeptide 1 (CYP2F1) mRNA
972	13583	26096	1.06	7.0E-86	AA80801.1	EST_HUMAN	Homo sapiens KIAA0680 gene product (KIAA0680), mRNA
6343	18949	31728	1.01	7.0E-86	9968886	NT	aj88f08.s1 Soares_parathyroid_tumor_NbH-PA Homo sapiens cDNA clone IMAGE:1403559 3'
6343	18949	31727	1.01	7.0E-86	9968886	NT	aj88f08.s1 Soares_parathyroid_tumor_NbH-PA Homo sapiens cDNA clone IMAGE:1403559 3'
7053	18072	30463	5.8	7.0E-86	11421737	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
8679	21218	34138	3.41	7.0E-86	L39557.1	NT	Homo sapiens tumor endothelial marker 7 precursor (TEM7), mRNA
							Homo sapiens T-cell leukemia virus type 1 binding protein 1 (TAX1BP1), mRNA
							Homo sapiens galactose oxidase (GALC) gene, exon 15

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9616	22116		1.53	7.0E-86	5453987	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9673	22172	35148	1.82	7.0E-86	11526307	NT	Homo sapiens DiGeorge syndrome critical region gene 6 (DGCR6), mRNA
10841	23362	36377	2.38	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
10841	23362	36378	2.38	7.0E-86	11417012	NT	Homo sapiens similar to transcription factor CA150 (H. sapiens) (LOC63170), mRNA
11638	24077	37137	2.7	7.0E-86	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1337	13831	26450	2.34	6.0E-86	4505492	NT	Homo sapiens oxoglutarate dehydrogenase (lipoamide) (OGDH), mRNA
226	12886	25373	2.46	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
6185	18795	31563	10.86	4.0E-86	BE295843.1	EST_HUMAN	601176865F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531953 5'
11120	12886	25373	1.86	4.0E-86	BE547173.1	EST_HUMAN	601072594F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458830 5'
4377	16984	29410	0.64	3.0E-86	BE867703.1	EST_HUMAN	601443262F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847455 5'
5782	18407	31123	6.23	3.0E-86	AW340946.1	EST_HUMAN	x282h12.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2871719 3'
8205	20748	33658	1.15	3.0E-86	AV722329.1	EST_HUMAN	AV722329 HTB Homo sapiens cDNA clone HTBBS004 5'
10121	22616	35606	3.12	3.0E-86	BE86479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
10121	22616	35607	3.12	3.0E-86	BE86479.1	EST_HUMAN	601509696F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911303 5'
11312	23010	36018	10.63	3.0E-86	AI659240.1	EST_HUMAN	tu18b02.x1 NCL CGAP_P28 Homo sapiens cDNA clone IMAGE:2251371 3'
11808	24893		3.18	3.0E-86	BE410354.1	EST_HUMAN	601302333F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636753 5'
288	12944	25429	2.06	2.0E-86	AA306284.1	EST_HUMAN	EST177232 Jurkat T-cells V1 Homo sapiens cDNA 5' end
439	13072		2.33	2.0E-86	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
1232	13631	26345	2.16	2.0E-86	N58977.1	EST_HUMAN	yz19a08.r1 Soares multiple sclerosis_2NBHMSF Homo sapiens cDNA clone IMAGE:283478 5'
2233	14808	27381	1.95	2.0E-86	9635487	NT	Human endogenous retrovirus, complete genome
3462	16069	28542	1.38	2.0E-86	AW966142.1	EST_HUMAN	EST378215 IMAGE resequences, MAGI Homo sapiens cDNA
3809	16403	28872	2.89	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3809	16408	28873	2.89	2.0E-86	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
4113	16707	29937	3.01	2.0E-86	AW515742.1	EST_HUMAN	hd87g08.x1 NCL CGAP_G08 Homo sapiens cDNA clone IMAGE:2816542 3'
4904	17479	31392	3.25	2.0E-86	AF056480.1	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
6032	18651	31392	1.55	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
6032	18651	31393	1.55	2.0E-86	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
						NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
7134	24773	32284	0.86	2.0E-86	11419429	NT	Human Chediak-Higashi syndrome protein short isoform (LYST) mRNA, complete cds
7952	20494	33403	0.6	2.0E-86	U84744.1	NT	Homo sapiens chromosome 21 segment HS21C027
8453	20963		0.54	2.0E-86	AL163227.2	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8509	21048	33969	2.19	2.0E-86	11437135	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8509	21048	33970	2.19	2.0E-86	11437135	NT	Homo sapiens butyrobetaine (gamma), 2-oxoglutarate dioxygenase (gamma-butyrobetaine hydroxylase) (BBOX), mRNA
8834	21373	34298	1.29	2.0E-86	10863876	NT	Homo sapiens phospholipid scramblase 1 (PLSCR1), mRNA
9242	21768	34717	2.06	2.0E-86	11422084	NT	Homo sapiens chromosome segregation 1 (yeast homolog)-like (CSE1L), mRNA
10344	22838	35833	2.82	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10344	22838	35834	2.82	2.0E-86	11545846	NT	Homo sapiens basic-helix-loop-helix-PAS protein (NPAS3), mRNA
10347	22841	35837	1.85	2.0E-86	11417120	NT	Homo sapiens hypothetical protein FLJ20125 (FLJ20125), mRNA
10397	22891	35885	0.85	2.0E-86	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
10784	23308	36315	1.94	2.0E-86	4759051	NT	Homo sapiens ribosomal protein S6 kinase, 90kD, polypeptide 5 (RPS9KA5), mRNA
12269	24478	30935	3.82	2.0E-86	11418169	NT	Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
12452	24586		3.36	2.0E-86	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
1641	14233	26767	1.33	1.0E-86	4828855	NT	Homo sapiens NADH dehydrogenase (ubiquinone) Fe-S protein 1 (75kD) (NADH-coenzyme Q reductase) (NDUFS1), mRNA
3198	15910	28283	1.54	1.0E-86	5453649	NT	Homo sapiens fibulin 5 (FBLN5), mRNA
3272	15984	28366	3.1	1.0E-86	L20492.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
3335	15945	28420	1.24	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
3335	15945	28421	1.24	1.0E-86	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4018	16616	29090	0.98	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4018	16616	29091	0.98	1.0E-86	7706161	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
4351	16938	29380	5.98	1.0E-86	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
5042	17615	30059	0.9	1.0E-86	AF100751.1	NT	Homo sapiens FK506-binding protein FKBP23 isoform mRNA, complete cds
5741	18367	31074	1.62	1.0E-86	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5559	18191		1.72	9.0E-87	AI150703.1	EST_HUMAN	SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
7472	19894	32657	1.78	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
7472	19894	32658	1.78	9.0E-87	4757721	NT	Homo sapiens a disintegrin and metalloproteinase domain 22 (ADAM22), mRNA
505	13137	25625	84.06	8.0E-87	X62245.1	NT	O. curticulus mRNA for elongation factor 1 alpha
2335	14908	27477	2.29	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
2335	14908	27478	2.29	7.0E-87	BF063211.1	EST_HUMAN	7h85f02.x1 NCI CGAP_Co16 Homo sapiens cDNA clone IMAGE:3322779 3'
6533	19133	31928	0.86	7.0E-87	AF080336.1	EST_HUMAN	MRO-NT0038-020500-004-a11 NT0039 Homo sapiens cDNA
8130	20671	33581	2.87	7.0E-87	BF352778.1	EST_HUMAN	IL3-HT0619-060700-198-D10 HT0619 Homo sapiens cDNA
9375	20314	33216	0.87	7.0E-87	BE712861.1	EST_HUMAN	IL5-HT0702-160800-103-d06 HT0702 Homo sapiens cDNA
9983	22478	35460	3.7	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'
9983	22478	35461	3.7	7.0E-87	AL043314.2	EST_HUMAN	DKFZp434N0323_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434N0323 5'

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10770	23294	36299	11	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
10770	23294	36300	11	7.0E-87	K03002.1	NT	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A
3579	19183	28665	0.82	6.0E-87	7657213	NT	Human sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5553	19151	31947	1.54	6.0E-87	AB023004.1	NT	Human sapiens mRNA for KIAA1081 protein, partial cds
10603	23137		6.8	6.0E-87	11432444	NT	Human sapiens similar to SET translocation (myeloid leukemia-associated) (H. sapiens) (LOC63102), mRNA
1200	13801	26313	2.58	5.0E-87	AA382811.1	EST_HUMAN	EST196094 Testis 1 Homo sapiens cDNA 5' end
12100	13801	26313	2.47	5.0E-87	AA382811.1	EST_HUMAN	EST196094 Testis 1 Homo sapiens cDNA 5' end
1001	13612	26126	0.85	4.0E-87	AL163210.2	NT	Human sapiens chromosome 21 segment HS21C010
1214	13814	26328	11.73	4.0E-87	AB037835.1	NT	Human sapiens mRNA for KIAA1414 protein, partial cds
1476	14068	26605	3.14	4.0E-87	R78133.1	EST_HUMAN	y80f10.r1 Scores placenta Nb2HP Homo sapiens cDNA clone IMAGE:145579 5' similar to contains Alu repetitive element
2466	15033	27599	2.57	4.0E-87	7706299	NT	Human sapiens CGI-60 protein (LOC51626), mRNA
2466	15033	27600	2.57	4.0E-87	7706299	NT	Human sapiens CGI-60 protein (LOC51626), mRNA
3511	16116	28595	1.82	4.0E-87	5174574	NT	Human sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
5439	17894		0.92	4.0E-87	AL163281.2	NT	Human sapiens chromosome 21 segment HS21C081
5637	18266	30738	11.09	4.0E-87	O00321	SWISSPROT	ETS-RELATED PROTEIN 71 (ETS TRANSLLOCATION VARIANT 2)
5925	18547	31273	0.72	4.0E-87	U85426.1	NT	Human transcription factor NFATx3 mRNA, complete cds
6198	18808	31575	4.42	4.0E-87	BE247284.1	EST_HUMAN	TCBAP1E4051 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4051
11044	23558	36594	5.04	4.0E-87	M60676.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
11623	24085	37130	2.12	4.0E-87	11417339	NT	Human sapiens similar to heat shock 70kD protein 9B (mortalin-2) (H. sapiens) (LOC63184), mRNA
12202	24947	30623	1.81	4.0E-87	11417862	NT	Human sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12202	24947	30624	1.81	4.0E-87	11417862	NT	Human sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12371	24541		17.18	4.0E-87	11417812	NT	Human sapiens purinergic receptor P2X-like 1, orphan receptor (P2RXL1), mRNA
2805	15357	27924	2.34	2.0E-87	4885420	NT	Human sapiens high-mobility group (nonhistone chromosomal) protein 4 (HMG4) mRNA
2875	15591		1.1	2.0E-87	BF327920.1	EST_HUMAN	QVQ-BN0148-050600-254-a03 BN0148 Homo sapiens cDNA
3852	18480	28913	0.78	2.0E-87	AU116935.1	EST_HUMAN	AU116935 HEMBA1 Homo sapiens cDNA clone HEMBA1000307 5'
5039	17612	30055	0.6	2.0E-87	BF376311.1	EST_HUMAN	CMO-TN0038-150900-552-h08 TN0038 Homo sapiens cDNA
5942	18468	31191	12.69	2.0E-87	BE734180.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730 5'
5942	18468	31192	12.69	2.0E-87	BE734180.1	EST_HUMAN	601569041F1 NIH_MGC 21 Homo sapiens cDNA clone IMAGE:3843730 5'
6468	19069		6.41	2.0E-87	BE667193.1	EST_HUMAN	601341383F1 NIH_MGC 53 Homo sapiens cDNA clone IMAGE:3683348 5'
6800	19391	32206	2.12	2.0E-87	N48128.1	EST_HUMAN	y21e07.r1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243396 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6877	19811	32444	0.93	2.0E-87	AV654143.1	EST_HUMAN	AV654143 GLC Homo sapiens cDNA clone GLCDSG04 3'
7225	19756	32611	1.43	2.0E-87	BE294432.1	EST_HUMAN	601178032F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531511 5'
7277	19805	32664	0.76	2.0E-87	11433046	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
7476	19998	32863	31.97	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
7676	20187	33075	33.12	2.0E-87	N48128.1	EST_HUMAN	yv21e07.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243398 5'
8334	20875	33797	15.53	2.0E-87	X52851.1	NT	Human cyclophilin gene for cyclophilin (EC 5.2.1.8)
9700	22199		5.14	2.0E-87	BE531136.1	EST_HUMAN	601278315F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610539 5'
1224	15392		1.66	1.0E-87	7705683	NT	Homo sapiens putative glycolipid transfer protein (LOC51054), mRNA
1478	14070	26607	1.21	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
1478	14070	26608	1.21	1.0E-87	AW361977.1	EST_HUMAN	PM2-CT0265-141099-001-g04 CT0265 Homo sapiens cDNA
3772	16373	28838	6.15	1.0E-87	Y00052.1	NT	Human mRNA for T-cell cyclophilin
3796	16396	28861	2.65	1.0E-87	4758627	NT	Homo sapiens neuroxin III (NRXN3) mRNA
5283	17845	30272	1.14	1.0E-87	U50949.1	NT	Rattus norvegicus taste bud receptor protein TB 641 (TB 641) gene, complete cds
6374	18978	31756	2.17	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
6374	18978	31757	2.17	1.0E-87	AF073371.1	NT	Homo sapiens growth factor receptor-bound protein 10 (GRB10) gene, exon 8
7228	19760	32615	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotropin-releasing factor type 1 receptor gene, exon 8
7228	19760	32616	0.72	1.0E-87	AF039517.1	NT	Homo sapiens corticotropin-releasing factor type 1 receptor gene, exon 8
7235	19765	32621	1	1.0E-87	4508768	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
7430	19984	32819	1.18	1.0E-87	11431560	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
8059	20601	33511	10.74	1.0E-87	AF214562.1	NT	Homo sapiens tracheal epithelium enriched protein (PLUNC) gene, complete cds
8840	21379	34302	1.01	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
8840	21379	34303	1.01	1.0E-87	AB022918.1	NT	Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds
9551	22051	35013	3.71	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0278-050700-012-E02 BN0278 Homo sapiens cDNA
9551	22051	35014	3.71	1.0E-87	BE818183.1	EST_HUMAN	RC6-BN0278-050700-012-E02 BN0278 Homo sapiens cDNA
10275	22770	35758	0.89	1.0E-87	M34428.1	NT	Human L-plastin mRNA, 5' end
10611	23144	36155	2.84	1.0E-87	5728967	NT	Homo sapiens hec domain and RLD 2 (HERC2), mRNA
10878	23398		1.82	1.0E-87	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
12198	25096		2.92	1.0E-87	7657632	NT	Homo sapiens sulfotransferase-related protein (SULTX3), mRNA
955	13587	26081	5.21	9.0E-88	5463887	NT	Homo sapiens protease inhibitor 4 (kallistatin) (P14) mRNA
1145	13748	26257	8.79	9.0E-88	AF167465.1	NT	Homo sapiens double stranded RNA activated protein kinase (PKR) gene, exon 12
1393	13987	26514	2.74	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1398 protein, partial cds
1393	13987	26515	2.74	9.0E-88	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
3689	16290	28759	1.7	9.0E-88	AL103209.2	NT	Homo sapiens chromosome 21 segment HS21C009
4358	16843	29385	3.11	9.0E-88	X91928.1	NT	H. sapiens ECE-1 gene (exon 9)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4356	16943	28386	3.11	9.0E-88	X01929.1	NT	H. sapiens ECE-1 gene (exon 9)
5146	17718	30147	1.11	9.0E-88	AB028898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
8951	21489	34412	3.16	6.0E-88	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
1868	14454		0.96	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
2666	15224	27797	2.31	5.0E-88	N89399.1	EST_HUMAN	X9719F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone K9719 5' similar to ZINC FINGER PROTEIN HZF1
3031	15647	28125	0.77	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3044	15660	28140	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3044	15660	28141	0.91	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
3436	16044		2.91	5.0E-88	AI693217.1	EST_HUMAN	wf68h08.x1 NCL_OGAP_Lu24 Homo sapiens cDNA clone IMAGE:2336799 3' similar to contains Alu repetitive element contains element MER22 MER22 repetitive element ;
3598	16192	28676	0.76	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
4843	17421	28874	0.79	5.0E-88	AF114488.1	NT	Homo sapiens intersecin short isoform (ITSN) mRNA, complete cds
6868	19602	32434	2.99	5.0E-88	H10932.1	EST_HUMAN	ym08b10.r1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:47129 5'
7870	20412	33318	1.73	5.0E-88	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
9236	21762	34708	0.54	5.0E-88	BF680206.1	EST_HUMAN	602154958F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295775 5'
11942	14454		1.37	5.0E-88	7661887	NT	Homo sapiens KIAA0063 gene product (KIAA0063), mRNA
1374	13968	26495	1.93	4.0E-88	BF091228.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
1374	13968	26496	1.93	4.0E-88	BF091229.1	EST_HUMAN	PM1-TN0028-050900-004-f10 TN0028 Homo sapiens cDNA
7292	19820	32679	2.25	4.0E-88	11416586	NT	Homo sapiens transforming growth factor, beta-induced, 68kD (TGFBI), mRNA
10789	23312	36320	1.83	4.0E-88	4502694	NT	Homo sapiens cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10) mRNA
11362	23814	36874	2.42	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
11362	23814	36875	2.42	4.0E-88	7661947	NT	Homo sapiens KIAA0152 gene product (KIAA0152), mRNA
781	13380	25877	0.96	3.0E-88	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
1848	14436		2.59	3.0E-88	4508020	NT	Homo sapiens zinc finger protein 259 (ZNF259) mRNA
2874	15590	28073	4.76	3.0E-88	N66851.1	EST_HUMAN	za48f12.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:295823 3'
4325	18911	28352	0.64	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4325	18911	28353	0.64	3.0E-88	4501912	NT	Homo sapiens a disintegrin and metalloproteinase domain 23 (ADAM23) mRNA
4576	17159		4.33	3.0E-88	11429300	NT	Homo sapiens hypothetical protein FLJ20220 (FLJ20220), mRNA
5502	18136	30546	2.95	3.0E-88	11429567	NT	Homo sapiens valosin-containing protein (VCP), mRNA
5773	18398	31112	4.24	3.0E-88	9866888	NT	Homo sapiens polycythemia rubra vera 1; cell surface receptor (PRV1), mRNA
5882	18504	31230	3.86	3.0E-88	11420697	NT	Homo sapiens v-rat simian leukemia viral oncogene homolog A (ras related) (RALA), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6309	18916	31690	1.3	3.0E-88	11417370	NT	Homo sapiens interleukin 13 (IL13), mRNA
6545	24764	31938	0.99	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
6545	24764	31939	0.99	3.0E-88	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7125	19485	32283	15.2	3.0E-88	AF279265.1	NT	Homo sapiens putative anion transporter 1 mRNA, complete cds
7546	20066	32940	5.75	3.0E-88	11436400	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
7861	20403	33310	9.25	3.0E-88	11421728	NT	Homo sapiens growth differentiation factor 5 (cartilage-derived morphogenetic protein-1) (GDF5), mRNA
8137	20678	33589	1.57	3.0E-88	AF034374.1	NT	Homo sapiens myoblast fusion factor biosynthesis protein A and myoblast fusion factor biosynthesis protein C mRNA, complete cds
9355	20284	33183	2.09	3.0E-88	11528262	NT	Homo sapiens v-src avian erythroblastosis virus E26 oncogene related (ERG), mRNA
9841	22339	35320	0.67	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9841	22339	35321	0.67	3.0E-88	AB015228.1	NT	Homo sapiens mRNA for RALDH2-T, complete cds
9867	22364	35343	0.89	3.0E-88	11439065	NT	Homo sapiens acyl-Coenzyme A dehydrogenase family, member 8 (ACAD8), mRNA
11928	24263	30828	5.36	3.0E-88	11417974	NT	Homo sapiens transcobalamin II; macrocytic anemia (TON2), mRNA
11944	24954	30828	1.26	3.0E-88	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12668	24738	30828	1.41	3.0E-88	11528140	NT	Homo sapiens protease, serine, 7 (enterokinase) (PRSS7), mRNA
1074	13679	26188	1.87	2.0E-88	7305198	NT	Homo sapiens Calsenilin, presenilin-binding protein, EF hand transcription factor (CSEN), mRNA
1685	14258	26792	1.57	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
1798	14376	26920	4.58	2.0E-88	AF246219.1	NT	Homo sapiens SNARE protein kinase SNAK mRNA, complete cds
4518	17100	29547	2.07	2.0E-88	5031668	NT	Homo sapiens dynein, axonemal, light polypeptide 4 (DNAL4), mRNA
6070	18687	31430	5.11	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aea-d-04-0-U1.s1 NCL CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6070	18687	31431	5.11	1.0E-88	AW139565.1	EST_HUMAN	UI-H-B11-aea-d-04-0-U1.s1 NCL CGAP Sub3 Homo sapiens cDNA clone IMAGE:2718750 3'
6753	19346	32153	22.7	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
6753	19346	32154	22.7	1.0E-88	AB007877.1	NT	Homo sapiens KIAA0417 mRNA, complete cds
7176	19708	32556	1.3	1.0E-88	AI969034.1	EST_HUMAN	wg70a12.x1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:2478606 3'
7236	19766	32622	4.05	1.0E-88	AA488981.1	EST_HUMAN	aa54a11.s1 NCL CGAP GC8 Homo sapiens cDNA clone IMAGE:824732 3' similar to WP:B0272.2 CE00851
9166	21743	34696	0.9	1.0E-88	AA190388.1	EST_HUMAN	zp87c02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:827170 5' similar to SW:POL.1_HUMAN P10266 RETROVIRUS-RELATED POL POLYPROTEIN
9499	21999	34956	3.09	1.0E-88	AL043314.2	EST_HUMAN	DKFZP434N0323_11 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZP434N0323 5'
11319	23017	36026	6.14	1.0E-88	AA991479.1	EST_HUMAN	os91g03.s1 NCL CGAP GC3 Homo sapiens cDNA clone IMAGE:1612756 3' similar to gb:M16342 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2 (HUMAN);
12160	24400		5.36	1.0E-88	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
10830	23351	36366	3.56	9.0E-89	11421238	NT	Homo sapiens transgelin 2 (TAGLN2), mRNA

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2763	15317	27884	1.05	8.0E-89	BE311557.1	EST_HUMAN	601142409F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506186 5'
7012	19510	32331	1.07	8.0E-89	11421514	NT	Homo sapiens similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A (H. sapiens) (LOC83232), mRNA
458	13092	25585	1.26	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
458	13092	25586	1.26	7.0E-89	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
5012	17586	30028	2.51	7.0E-89	4557390	NT	Homo sapiens complement component 8, beta polypeptide (C8B), mRNA
5094	17637	30080	6.15	7.0E-89	AL045748.1	EST_HUMAN	DKFZp434E246 r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434E246 5'
5623	18252	30720	1.26	7.0E-89	X98832.1	NT	H. sapiens CLN3 gene, complete cds
5623	18252	30721	1.26	7.0E-89	X98832.1	NT	H. sapiens CLN3 gene, complete cds
6483	19084	31865	1.06	7.0E-89	7549808	NT	Homo sapiens plastin 3 (T isoform) (PLS3), mRNA
6483	19084	31866	1.06	7.0E-89	7549808	NT	Homo sapiens plastin 3 (T isoform) (PLS3), mRNA
7510	20031	32886	1.86	7.0E-89	11420754	NT	Homo sapiens actin related protein 2/3 complex, subunit 1A (41 kD) (ARPC1A), mRNA
7820	20362	33266	0.51	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
7820	20362	33270	0.51	7.0E-89	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
8415	20955	33872	0.83	7.0E-89	J02923.1	NT	Human 65-kilodalton phosphoprotein (p65) mRNA, complete cds
10423	22917	35917	1.3	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10423	22917	35918	1.3	7.0E-89	X62048.1	NT	H. sapiens Wee1 hu gene
10440	22934	35942	0.97	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
10440	22934	35943	0.97	7.0E-89	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
12604	24905		1.86	7.0E-89	J05235.1	NT	Human gamma-glutamyl transpeptidase mRNA, complete cds
1081	13666	26177	1.41	6.0E-89	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (IMMT), mRNA
2254	14828	27404	1.24	6.0E-89	4506124	NT	Homo sapiens serine/threonine-protein kinase PRP4 homolog (PRP4) mRNA
2477	15044	27611	1.37	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
2477	15044	27612	1.37	6.0E-89	4507788	NT	Homo sapiens ubiquitin-conjugating enzyme E2L 3 (UBE2L3) mRNA
3577	16181	28663	0.91	6.0E-89	7661817	NT	Homo sapiens HSPC159 protein (HSPC159), mRNA
4743	17324	29765	3	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
4743	17324	29766	3	6.0E-89	AB007866.2	NT	Homo sapiens mRNA for KIAA0408 protein, partial cds
5366	17926	30340	0.62	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5366	17926	30341	0.62	6.0E-89	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
5234	17798	30216	2.68	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
5234	17798	30217	2.68	5.0E-89	BE244323.1	EST_HUMAN	TCBAP2E0383 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP0383
7587	20102	32977	0.91	4.0E-89	BE762749.1	EST_HUMAN	QV3-NT0022-080600-219-g03 NT0022 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11020	23534	36570	1.69	4.0E-89	AI798672.1	EST_HUMAN	w691c03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2348452 3'
2901	15518	27988	2.21	3.0E-89	AW078181.1	EST_HUMAN	EST388290 IMAGE resequences, MAGN Homo sapiens cDNA
7194	19725	32575	1.5	3.0E-89	AI217359.1	EST_HUMAN	qh17b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844915 3'
10678	23210	36221	2.24	3.0E-89	N57357.1	EST_HUMAN	yw86e11.1 Soares placenta_8to9weeks_2Nbl-IP8c9W Homo sapiens cDNA clone IMAGE:259148 5'
12270	24840	30799	2.82	3.0E-89	AV708431.1	EST_HUMAN	similar to SW_P14K_HUMAN P42356 PHOSPHATIDYLINOSITOL 4-KINASE ALPHA ;
12364	24537	30902	1.32	3.0E-89	AV705749.1	EST_HUMAN	AV708431 ADC Homo sapiens cDNA clone ADCARE02 5'
132	13066	25561	0.74	2.0E-89	7706670	NT	AV705749 ADB Homo sapiens cDNA clone ADBBGA01 5'
132	13066	25562	0.74	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
433	13066	25561	0.65	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
433	13066	25562	0.65	2.0E-89	7706670	NT	Homo sapiens PXR2b protein (PXR2b), mRNA
1826	14415	26962	1.71	2.0E-89	AJ238277.1	NT	Homo sapiens mRNA for cancer-testis-associated protein (CTP11) gene
2905	15522	27992	1.84	2.0E-89	A1222095.1	EST_HUMAN	qg96c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131
3608	18212	28691	0.67	2.0E-89	AA759149.1	EST_HUMAN	GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN)/contains Alu repetitive element;
3608	18212	28692	0.67	2.0E-89	AA759149.1	EST_HUMAN	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4226	18814	29261	1.18	2.0E-89	AF089897.1	NT	ah70e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1320988 3'
4233	18821	29271	5.23	2.0E-89	X58742.1	NT	Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds
4233	18821	29272	5.23	2.0E-89	X58742.1	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4441	17027	29467	0.7	2.0E-89	AL163203.2	NT	H.sapiens HCK gene for tyrosine kinase (PTK), exons 10-11
4596	17179	29628	1.52	2.0E-89	AJ007378.1	NT	Homo sapiens chromosome 21 segment HS21C003
5546	18178		1.07	2.0E-89	BE541744.1	EST_HUMAN	Homo sapiens GGT gene, exon 5
5672	18299	30780	3.13	2.0E-89	AB007546.1	NT	601065996F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452423 5'
5960	18582	31316	1.44	2.0E-89	U03985.1	NT	Homo sapiens gene for LECT2, complete cds
6358	18862	31739	0.7	2.0E-89	AL163285.2	NT	Human N-ethylmaleimide-sensitive factor mRNA, partial cds
7664	20176	33063	4.46	2.0E-89	U81004.1	NT	Homo sapiens chromosome 21 segment HS21C085
7875	20417	33325	3.22	2.0E-89	11428801	NT	Homo sapiens chromosome 21 segment HS21C085
8356	20898	33816	1	2.0E-89	AJ245503.1	NT	Homo sapiens solute carrier family 24 (sodium/potassium/calcium exchanger), member 2 (SLC24A2), mRNA
9177	21754	34701	0.69	2.0E-89	AB037754.1	NT	Homo sapiens partial mRNA for PEX5-related protein
9724	22222	35167	0.65	2.0E-89	AF170814.1	NT	Homo sapiens mRNA for KIAA1333 protein, partial cds
9724	22222	35168	0.65	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5
9724	22222	35168	0.65	2.0E-89	AF170814.1	NT	Homo sapiens CaBP5 (CABP5) gene, exon 5

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11252	23782	36838	2.58	2.0E-89	11434411	NT	Homo sapiens integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3), mRNA
11444	23804	36959	5.1	2.0E-89	11433673	NT	Homo sapiens cell adhesion molecule with homology to L1CAM (close homologue of L1) (CHL1), mRNA
11594	24011	37081	2.25	2.0E-89	U10692.1	NT	Human IMAGE:7 antigen (IMAGE7) pseudogene, complete cds
11448	23899	36965	6.8	1.0E-89	BF198052.1	EST_HUMAN	h181409.x1 NCI_CGAP_Ki611 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
11449	23898	36966	6.8	1.0E-89	BF198052.1	EST_HUMAN	h181409.x1 NCI_CGAP_Ki611 Homo sapiens cDNA clone IMAGE:3134897 3' similar to TR:054778 O54778 SOLUTE CARRIER FAMILY 22 -LIKE 2 PROTEIN ;
8169	20710	33626	1.59	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
8169	20710	33627	1.59	9.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1101	13706	26214	1.9	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1102	13706	26214	2.3	8.0E-90	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
1375	15439	26497	4.58	8.0E-90	BE670561.1	EST_HUMAN	7a36608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
1375	15439	26498	4.58	8.0E-90	BE670561.1	EST_HUMAN	7a36608.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3284583 3'
8495	21034	33955	0.68	8.0E-90	BE177830.1	EST_HUMAN	RC1-HT0598-120400-022-b08 HT0598 Homo sapiens cDNA
10579	23114	36127	1.61	8.0E-90	A1222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
10579	23114	36128	1.61	8.0E-90	A1222095.1	EST_HUMAN	q996c08.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYL TRANSPEPTIDASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
869	13484		4.48	7.0E-90	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
8363	20903		1.73	7.0E-90	AA782977.1	EST_HUMAN	ai63d08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1375503 3'
8896	21434	34357	1.47	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
8896	21434	34358	1.47	7.0E-90	BE962525.2	EST_HUMAN	601655837R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855824 3'
10042	22537	35533	2.15	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares_fetal_liver_spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP-C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10042	22537	35534	2.15	7.0E-90	H68849.1	EST_HUMAN	yr86e04.s1 Soares_fetal_liver_spleen 1NFLS Homo sapiens cDNA clone IMAGE:212190 3' similar to SP-C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
10352	22846	35840	0.89	7.0E-90	BF526089.1	EST_HUMAN	SP-C1TC_HUMAN P11586 C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC ;
3104	15719	28189	1.18	6.0E-90	X91926.1	NT	602071208FT NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4214257 5'
3104	15719	28190	1.18	6.0E-90	X91926.1	NT	H. sapiens ECE-1 gene (exon 6) H. sapiens ECE-1 gene (exon 6)

Table 4
Single Exon Probes Expressed In Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4311	18897	28341	8.68	5.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
4311	18897	28342	8.68	6.0E-90	8922398	NT	Homo sapiens hypothetical protein FLJ10388 (FLJ10388), mRNA
6137	18751	31508	3.08	6.0E-90	U77700.1	NT	Homo sapiens HsGDN1 mRNA, partial cds
6137	18751	31509	3.08	6.0E-90	U77700.1	NT	Homo sapiens HsGDN1 mRNA, partial cds
8269	20810	33730	3.18	6.0E-90	4504794	NT	Homo sapiens Insitol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
8269	20810	33731	3.18	6.0E-90	4504794	NT	Homo sapiens Insitol 1,4,5-triphosphate receptor, type 3 (ITPR3) mRNA
166	12828		24.29	5.0E-90	AB035344.1	NT	Homo sapiens TCL6 gene, exon 1-10b
1234	13833	28347	2.39	5.0E-90	U80226.1	NT	Human gamma-aminobutyric acid transaminase mRNA, partial cds
1858	14446	27002	2.57	5.0E-90	A122095.1	EST_HUMAN	q99608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
1858	14446	27003	2.57	5.0E-90	A122095.1	EST_HUMAN	q99608.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843022 3' similar to gb:J04131 GAMMA-GLUTAMYLTRANSFERASE 1 PRECURSOR (HUMAN); contains Alu repetitive element;
2591	15153	27720	4.06	5.0E-90	AF114487.1	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
4638	17220	28674	10.01	5.0E-90	4506354	NT	Homo sapiens pregnancy-zone protein (PZP) mRNA
4660	17242	29696	0.64	5.0E-90	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
5777	18402	31118	2.63	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
5871	18493	31220	1.13	5.0E-90	AB015617.1	NT	Homo sapiens ELKS mRNA, complete cds
5839	18402	31118	2.21	5.0E-90	Z16411.1	NT	H. sapiens mRNA encoding phospholipase c
7267	19795	32651	2.56	5.0E-90	AF113708.1	NT	Homo sapiens angiotensinogen 4 (ANG4) mRNA, partial cds
7267	19795	32652	2.56	5.0E-90	AF113708.1	NT	Homo sapiens angiotensinogen 4 (ANG4) mRNA, partial cds
7564	20081	32657	13.89	5.0E-90	4557258	NT	Homo sapiens adenylate cyclase 9 (ADCY9) mRNA
8234	20775	33697	4.57	5.0E-90	11345483	NT	Homo sapiens hypothetical protein FLJ13222 (FLJ13222), mRNA
9598	22098	35081	1.24	5.0E-90	11418429	NT	Homo sapiens similar to ectorucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC83214), mRNA
10181	22676	35669	0.71	5.0E-90	AF123303.1	NT	Homo sapiens calcium-binding transporter mRNA, partial cds
10311	22805	35797	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10311	22805	35798	0.53	5.0E-90	11417118	NT	Homo sapiens KIAA0433 protein (KIAA0433), mRNA
10343	22837	35832	8.78	5.0E-90	11433721	NT	Homo sapiens ATPase, aminophospholipid transporter-like, Class I, type 8A, member 2 (ATP8A2), mRNA
10399	22893	35887	0.51	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10399	22893	35888	0.51	5.0E-90	7682051	NT	Homo sapiens KIAA0317 gene product (KIAA0317), mRNA
10795	23318	36328	3.38	5.0E-90	D49387.1	NT	Human mRNA for NADP dependent leukotriene b4 12-hydroxydehydrogenase, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12421	24607		1.8	5.0E-90	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12471	24598		5.4	5.0E-90	AF523366.1	EST_HUMAN	ar78105.x1 Barleed aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2128761 3'
324	12878	25466	1.61	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
324	12878	25467	1.61	4.0E-90	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
1125	13728	26239	4.34	4.0E-90	4505316	NT	Homo sapiens myosin phosphatase, target subunit 1 (MYPT1), mRNA
1727	14318	26861	8.55	4.0E-90	X99033.1	NT	H sapiens gene encoding discoidin receptor tyrosine kinase, exon 16
3024	15640	28117	0.97	4.0E-90	AF007544.1	NT	Homo sapiens prostate-specific membrane antigen (PSM) gene, complete cds
4761	17342	29790	3.77	4.0E-90	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4915	17490	29944	2.2	4.0E-90	AB033070.1	NT	Homo sapiens mRNA for KIAA1244 protein, partial cds
4943	17518	29960	1.62	4.0E-90	M85967.1	NT	Human prothormone converting enzyme (NEC2) gene, exon 8
5096	17669		0.7	3.0E-90	A1370786.1	EST_HUMAN	qz8908.x1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:2041743 3' similar to gb:M31470 RAS-LIKE PROTEIN TC10 (HUMAN);
7794	20337	33244	1.07	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-O-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
7794	20337	33245	1.07	3.0E-90	BF516168.1	EST_HUMAN	UI-H-BW1-amy-b-04-O-UI.s1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3083839 3'
11491	23940	37011	33.84	3.0E-90	BE563833.1	EST_HUMAN	601335244F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689147 5'
230	12890	25376	4.32	2.0E-90	BE537913.1	EST_HUMAN	601067378F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3453834 5'
1215	13815	26329	16.29	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1215	13815	26330	16.29	2.0E-90	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
2420	14988		1.78	2.0E-90	4505052	NT	Homo sapiens lymphocyte antigen 75 (LY75) mRNA, and translated products
3912	16510	28972	2.37	2.0E-90	A1138213.1	EST_HUMAN	qc54c02.x1 Soares_placenta_8w6weeks_2NblHP8c9W Homo sapiens cDNA clone IMAGE:1713410 3'
4798	17376	29827	1.16	2.0E-90	AB006627.1	NT	similar to SW_OLF3_MOUSE P23275 OLFACTORY RECEPTOR OR3. ;
5035	17609	30053	10.95	2.0E-90	5729855	NT	Homo sapiens mRNA for KIAA0289 gene, partial cds
5948	18569	31300	0.72	2.0E-90	11525901	NT	Homo sapiens GRB2-related adaptor protein (GRAP) mRNA
5948	18569	31301	0.72	2.0E-90	11525901	NT	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
5955	18577	31311	4.78	2.0E-90	AW672686.1	EST_HUMAN	Homo sapiens Rap2 interacting protein 8 (RPIP8), mRNA
9705	22204	35176	8.36	2.0E-90	11427320	NT	ba494005.y3 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2898881 5' similar to TR:O75208 O75208 HYPOTHETICAL 35.5 KD PROTEIN. ;
9705	22204	35177	8.36	2.0E-90	11427320	NT	HYPOTHETICAL 35.5 KD PROTEIN. ;
9870	22367	35344	0.92	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
9870	22367	35345	0.92	2.0E-90	AU118985.1	EST_HUMAN	Homo sapiens similar to laminin receptor 1 (67KD, ribosomal protein SA) (H. sapiens) (LOC63484), mRNA
11345	23043	36053	4.12	2.0E-90	11024711	NT	AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
							AU118985 HEMBA1 Homo sapiens cDNA clone HEMBA1004795 5'
							Homo sapiens myosin, heavy polypeptide 4, skeletal muscle (MYH4), mRNA

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Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
298	12954	25443	3.2	1.0E-90	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
397	15386	25533	2.02	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
398	15386	25533	1.38	1.0E-80	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
724	13344	25835	1.49	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
724	13344	25836	1.49	1.0E-90	AJ237589.1	NT	Homo sapiens mRNA for T-box transcription factor (TBX20 gene), partial
759	13378	25874	13.32	1.0E-80	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
759	13378	25875	13.32	1.0E-80	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1149	13752		3.05	1.0E-90	4507828	NT	Homo sapiens Kruppel-like factor 7 (ubiquitous) (KLF7), mRNA
1349	13944	26487	2.46	1.0E-80	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1349	13944	26488	2.46	1.0E-80	AF098154.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 3
1707	14300		1.38	1.0E-90	BE379884.1	EST_HUMAN	60115963F2 NIH_MGC S3 Homo sapiens cDNA clone IMAGE.3511118 5'
1948	14530	27066	2.82	1.0E-80	11420514	NT	Homo sapiens similar to SALL1 (sal (Drosophila)-like (LOC57167), mRNA
2878	15496	27987	7.6	1.0E-90	6005720	NT	Homo sapiens chromosome 8 open reading frame 2 (C8ORF2), mRNA
3918	16516	28980	0.98	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
3918	16516	28981	0.98	1.0E-90	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
4514	17098	29545	1.64	1.0E-80	AF187340.1	NT	Homo sapiens soluble interleukin 1 receptor accessory protein (IL1RAP) gene, exon 8, alternative exons 9 and complete cds, alternatively spliced
5855	18478	31201	1.98	1.0E-80	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
6002	18622	31357	0.95	1.0E-90	11426910	NT	Homo sapiens KIAA0623 gene product (KIAA0623), mRNA
7133	19473	32293	0.68	1.0E-80	U91934.1	NT	Human retina-derived POU-domain factor-1 mRNA, complete cds
7665	20177	33064	2.52	1.0E-90	11426768	NT	Homo sapiens solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6 (SLC1A6), mRNA
8755	21294	34214	4.17	1.0E-90	11422098	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
9217	21734		0.97	1.0E-90	AF183864.1	NT	Homo sapiens SNCA isoform (SNCA) gene, complete cds, alternatively spliced
9239	21765	34712	1.33	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
9239	21765	34713	1.33	1.0E-90	11422109	NT	Homo sapiens CGI-15 protein (LOC51006), mRNA
4274	16860	29309	6.54	8.0E-91	D12234.1	EST_HUMAN	HU0005381 Liver HepG2 cell line, Homo sapiens cDNA clone s381 3'
8248	20789	33708	2.74	7.0E-91	11419234	NT	Homo sapiens makorin, ring finger protein, 1 (MKRN1), mRNA
10201	22696	35690	0.74	7.0E-91	AB04151.1	EST_HUMAN	GM-BT043-090299-075 BT043 Homo sapiens cDNA
3521	16128	28608	1.52	5.0E-91	AA702784.1	EST_HUMAN	z89b04.s1 Soares fetal_liver_spleen_INFLS S1 Homo sapiens cDNA clone IMAGE.448015 3'
4614	17197	29643	1.21	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4614	17197	29644	1.21	5.0E-91	AU143539.1	EST_HUMAN	AU143539 Y79AA1 Homo sapiens cDNA clone Y79AA1002087 5'
4931	17506	29952	0.66	5.0E-91	7110634	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4931	17506	29953	0.68	5.0E-91	7110834	NT	Homo sapiens chromosome 22 open reading frame 5 (C22ORF5), mRNA
6729	19323	32128	1.06	5.0E-91	A1879995.1	EST_HUMAN	au49f09.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518121 3' similar to SW:ASPG FLAME Q47898 N4(BETA-N-ACETYLGLUCOSAMINYL)-L-ASPARAGINASE PRECURSOR ;
8147	20688	33601	1.52	5.0E-91	BF314882.1	EST_HUMAN	601901824F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130933 5'
8695	21234	34155	1.4	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
8695	21234	34156	1.4	5.0E-91	AV649878.1	EST_HUMAN	AV649878 GLC Homo sapiens cDNA clone GLCBYF08 3'
12443	24579		1.78	5.0E-91	A1193568.1	EST_HUMAN	q970f11.x1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:1744365 3' similar to contains MIR.b2 MIR MIR repetitive element ;
3236	15848	28328	1.25	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
3236	15848	28329	1.25	4.0E-91	AF156776.1	NT	Homo sapiens lysophosphatidic acid acyltransferase-delta (LPAAT-delta) mRNA, complete cds
10810	23333	36346	3.96	4.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
11882	24229	31001	3.09	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
11882	24229	31047	3.09	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12181	24417	30947	1.36	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
12181	24417	30948	1.36	4.0E-91	M77994.1	EST_HUMAN	EST01579 Hippocampus, Striatum (cat. #936205) Homo sapiens cDNA clone HHCMC60 similar to Retrovirus-related gag polyprotein
1660	14253	26787	4.64	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
1660	14253	26788	4.64	3.0E-91	11430193	NT	Homo sapiens solute carrier family 4, anion exchanger, member 3 (SLC4A3), mRNA
3383	15992	28470	1.4	3.0E-91	AL163283.2	NT	Homo sapiens chromosome 21 segment HS21C083
3509	16114	28592	3.17	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3509	16114	28593	3.17	3.0E-91	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3856	16454	28918	1.2	3.0E-91	AF084530.1	NT	Homo sapiens cyclin-D binding Myo-like protein mRNA, complete cds
4693	17275	29722	4.36	3.0E-91	M30938.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
5115	17687	30124	1.19	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5115	17687	30125	1.19	3.0E-91	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
5865	18487	31211	1.5	3.0E-91	11434964	NT	Homo sapiens epidermal secretory protein (19.5kD) (HE1), mRNA
6446	19048		2.85	3.0E-91	4502740	NT	Homo sapiens cyclin-dependent kinase 6 (CDK6) mRNA
6697	19293	32097	4.48	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6697	19293	32098	4.48	3.0E-91	11497611	NT	Homo sapiens gamma-aminobutyric acid (GABA) B receptor, 1 (GABBR1), transcript variant 2, mRNA
7634	20146	33028	4.04	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNL1B1) gene, exons 10 and 11
7634	20146	33029	4.04	3.0E-91	U86959.1	NT	Human L-type calcium channel beta-1 subunit (CACNL1B1) gene, exons 10 and 11
7887	20429	33338	0.46	3.0E-91	6601589	NT	Homo sapiens ankyrin-like with transmembrane domains 1 (ANKTM1), mRNA
8708	21245	34168	2.6	3.0E-91	D16494.1	NT	Human mRNA for very low density lipoprotein receptor, complete cds
9212	21729	34672	0.8	3.0E-91	AB011168.1	NT	Homo sapiens mRNA for KIAA0504 protein, partial cds
12504	18025	30406	9.31	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
12504	18025	30407	9.31	3.0E-91	AF169555.1	NT	Homo sapiens beta-ureidopropionase (BUP1) gene, exon 6
52	12732	25199	2.37	1.0E-91	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
1288	13883	26408	6.6	1.0E-91	AW449748.1	EST_HUMAN	UI-H-B13-eks-d-01-U1 s1 NCI_CGAP_Sub55 Homo sapiens cDNA clone IMAGE:2735280 3'
5608	18237	30687	0.84	1.0E-91	11434402	NT	Homo sapiens hypothetical protein PRO1855 (PRO1855), mRNA
6930	19589	32419	1.76	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157804 5'
6930	19589	32420	1.76	1.0E-91	BF348182.1	EST_HUMAN	602022088F1 NCI_CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4157804 5'
1284	13880	26402	9.55	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
1284	13880	26403	9.55	9.0E-92	AJ001689.1	NT	Homo sapiens NKX2D gene, exon 10
5389	17947	30359	0.59	9.0E-92	AB020940.1	NT	Homo sapiens mRNA for KIAA0833 protein, partial cds
5654	18281	30760	4.15	9.0E-92	J03007.1	NT	Human Na ⁺ K ⁺ ATPase alpha-subunit mRNA, partial cds
5700	18415	31131	2.53	9.0E-92	11427149	NT	Homo sapiens hypothetical protein FLJ20260 (FLJ20260), mRNA
6581	19179	31979	4	9.0E-92	AF310105.1	NT	Homo sapiens NALP1 mRNA, complete cds
7798	20341	33249	0.75	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
7798	20341	33250	0.75	9.0E-92	AJ250566.1	NT	Homo sapiens partial TM4SF2 gene for tetraspanin protein, exon 5
8315	20856	33781	1.11	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8315	20856	33782	1.11	9.0E-92	AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
9198	21715	34659	1.84	9.0E-92	11422086	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
96	12772	25254	11	8.0E-92	W26367.1	EST_HUMAN	2673 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
307	12962	25451	6.03	8.0E-92	BE386363.1	EST_HUMAN	601273513F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3614667 5'
1860	14448	27005	1.03	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG), mRNA
1860	14448	27006	1.03	8.0E-92	11434722	NT	Homo sapiens diacylglycerol kinase, gamma (90KD) (DGKG), mRNA
4306	18892	29335	0.96	8.0E-92	AA809157.1	EST_HUMAN	om13e02 s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1540922 3' similar to contains L1.b2 L1 repetitive element
5265	17827	30251	2.02	8.0E-92	AW157571.1	EST_HUMAN	au83n08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782911 3' similar to TR:O60302 O60302 KIAA0555 PROTEIN, contains element MER22 repetitive element
5591	18222	30571	0.76	8.0E-92	AB046820.1	NT	Homo sapiens mRNA for KIAA1600 protein, partial cds

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5690	18316	30815	0.96	8.0E-92	AF284717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
6689	19262	32066	1.25	8.0E-92	AJ000976.1	NT	Homo sapiens MCP-4 gene
6689	19265	32069	0.72	8.0E-92	AF179426.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit variant 1 (REV3L) mRNA, complete cds
7747	20255	33149	5.06	8.0E-92	XG9536.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
7747	20255	33150	5.06	8.0E-92	XG9536.1	NT	H. sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exons 7-8
8035	20577		0.68	8.0E-92	11416981	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
8364	20904	33822	4.96	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8364	20904	33823	4.96	8.0E-92	L04193.1	NT	Human lens membrane protein (mp19) gene, exon 11
8461	21001	33918	0.67	8.0E-92	11426569	NT	Homo sapiens transcription termination factor, RNA polymerase II (TTF2), mRNA
8992	21530	34459	2.47	8.0E-92	AB014511.1	NT	Homo sapiens mRNA for KIAA0811 protein, partial cds
9839	22434	35410	1.76	8.0E-92	Y13829.1	NT	Homo sapiens mRNA for MBNL protein
10683	23214	36226	5.17	8.0E-92	AF074393.1	NT	Homo sapiens nuclear mitogen- and stress-activated protein kinase-1 (MSK1) mRNA, complete cds
11239	23770	36828	2.58	8.0E-92	4503340	NT	Homo sapiens dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST) mRNA
257	15411	25402	1.61	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
257	15411	25403	1.61	7.0E-92	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
617	13244		1.09	7.0E-92	AF007822.1	NT	Homo sapiens cytoplasmic Seprase truncated isoform mRNA, complete cds
1323	13917	28439	3.02	7.0E-92	4502394	NT	Homo sapiens B-cell CLL/lymphoma 7b (BCL7B) mRNA
2229	14804	27375	1.25	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2229	14804	27376	1.25	7.0E-92	5031570	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (ACTR2), mRNA
2599	15161	27729	1.45	7.0E-92	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
2751	15306	27870	2.14	7.0E-92	6005738	NT	Homo sapiens NRAS-related gene (D1S155E), mRNA
2781	15334	27604	1.03	7.0E-92	AB031007.1	NT	Homo sapiens DNA, MHC class I region, 7.1 ancestral haplotype
3389	18003	28474	0.65	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
3389	18003	28475	0.65	7.0E-92	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4687	17269	28718	1.08	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
4687	17269	28719	1.08	7.0E-92	S71824.1	NT	N-CAM=145 kDa neural cell adhesion molecule [human, small cell lung cancer cell line OS2-R, mRNA, 2960 nt]
5147	17717	30148	1.15	7.0E-92	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
5350	17910	30325	1.12	7.0E-92	4508118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
5466	18101	30419	4.93	7.0E-92	AA446206.1	EST_HUMAN	zw66d12.1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781175 5'

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1631	14223		1.18	5.0E-92	BE390882.1	EST_HUMAN	601283012F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605018 5'
2763	15346	27915	2.12	3.0E-92	BE909714.1	EST_HUMAN	601501242F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902839 5'
6036	18655	31397	7.84	3.0E-92	AA378338.1	EST_HUMAN	EST191020 Synovial sarcoma Homo sapiens cDNA 5' end similar to ribosomal protein S13
10645	23177	36189	2.66	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
10645	23177	36190	2.66	3.0E-92	X15804.1	NT	Human mRNA for alpha-actinin
12358	25103		1.76	3.0E-92	BF367138.1	EST_HUMAN	RC1-GN0021-240800-012-811 GN0021 Homo sapiens cDNA
28	12707	25164	1.57	2.0E-92	4501888	NT	Homo sapiens activin A receptor, type IIB (ACVR2B) mRNA
153	12816	25304	26.76	2.0E-92	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
191	12851	26334	3.47	2.0E-92		NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
191	12851	25335	3.47	2.0E-92	11422946	NT	Homo sapiens hypothetical protein dJ462023.2 (D.J462023.2), mRNA
779	13398	25900	12.47	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
779	13398	25901	12.47	2.0E-92	BE289180.1	EST_HUMAN	601118337F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028304 5'
1752	14342		1.42	2.0E-92	S78853.1	NT	mng=mes-related [human, Genomic, 2416 nt]
1980	14563	27122	4.27	2.0E-92	A1818119.1	EST_HUMAN	wk27407 x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
1980	14563	27123	4.27	2.0E-92	A1818119.1	EST_HUMAN	Q12844 BREAKPOINT CLUSTER REGION PROTEIN
2092	14672	27242	4.82	2.0E-92	4506860	NT	wk27407 x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2413549 3' similar to TR:Q12844
2683	15241	27809	21.03	2.0E-92	6912457	NT	Q12844 BREAKPOINT CLUSTER REGION PROTEIN
2857	14287	26823	1.16	2.0E-92	11418424	NT	Homo sapiens syndecan 4 (amphiglycan, ryudocan) mRNA
2857	14287	26824	1.16	2.0E-92	11418424	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
3673	18274	28740	1.13	2.0E-92	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3673	18274	28741	1.13	2.0E-92	AF231919.1	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
3749	18350	28818	6.13	2.0E-92	5803180	NT	Homo sapiens chromosome 21 unknown mRNA
4376	18963	29409	1.46	2.0E-92	M10976.1	NT	Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA
4868	17444	28895	0.75	2.0E-92	AF136523.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
5133	17705		4.94	2.0E-92	AL040437.1	EST_HUMAN	Homo sapiens bile salt export pump (BSEP) mRNA, complete cds
6444	19046		0.68	2.0E-92	4504756	NT	DKFZp434C0414.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434C0414 5'
6727	19321	32126	2.75	2.0E-92	AB028891.1	NT	Homo sapiens integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide) (ITGAL) mRNA
7489	20005		0.75	2.0E-92	U67780.1	NT	Homo sapiens mRNA for KIAA1068 protein, partial cds
8789	21328	34253	1.78	2.0E-92	AW340174.1	EST_HUMAN	Human NPY Y1-like receptor pseudogene mRNA, complete cds
							h02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711
							O02711 PRO-POL-DUTPASE POLYPROTEIN

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10639	23171	36182	6.96	2.0E-92	11434900	NT	Homo sapiens thyroid stimulating hormone receptor (TSHR), mRNA
10926	23444	36465	1.92	2.0E-92	5803103	NT	Homo sapiens male-specific lethal-3 (Drosophila)-like 1 (MSL3L1), mRNA
11022	23536	36571	1.64	2.0E-92	AW836260.1	EST_HUMAN	CMA-L10026-161289-062-g08 L10026 Homo sapiens cDNA
11022	23536	36572	1.64	2.0E-92	AW836260.1	EST_HUMAN	CMA-L10026-161289-062-g08 L10026 Homo sapiens cDNA
12248	24459	30960	2.99	2.0E-92	AB026016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12593	15241	27809	96.37	2.0E-92	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1890	14475	27034	1.6	1.0E-92	R78078.1	EST_HUMAN	y80a08.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
1890	14475	27035	1.6	1.0E-92	R78078.1	EST_HUMAN	y80a08.11 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:145574 5'
2118	14696	27265	10.49	1.0E-92	4506668	NT	Homo sapiens ribosomal protein, large, P1 (RPLP1) mRNA
8189	20730	33842	1.01	1.0E-92	BE436625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
							tg01b02.x1 NCI CGAP CLL1 Homo sapiens cDNA clone IMAGE:2107467 3' similar to SW:PTNF_HUMAN
8091	21627	34563	4.16	1.0E-92	A1360356.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element;
9091	21627	34564	4.16	1.0E-92	A1360356.1	EST_HUMAN	Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;contains Alu repetitive element;contains element MER17 repetitive element;
2076	14696	27228	3.52	9.0E-93	AU121681.1	EST_HUMAN	AU121681 MAMMA1 Homo sapiens cDNA clone MAMMA1000738 5'
2086	14697		10.76	9.0E-93	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2673	15231		1.18	9.0E-93	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
3674	16275	26742	1.02	9.0E-93	BE388571.1	EST_HUMAN	601281867F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3603832 5'
11501	23950		18.44	9.0E-93	11418528	NT	Homo sapiens ribosomal protein L10a (RPL10A), mRNA
6705	19300	32104	4.23	8.0E-93	BF036364.1	EST_HUMAN	601460521F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663908 5'
267	12924	25410	8.56	7.0E-93	AF231918.1	NT	Homo sapiens chromosome 21 unknown mRNA
3111	15728	26197	0.59	6.0E-93	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
6762	19373	32189	1.17	6.0E-93	A3033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
6996	19494	32315	1.37	6.0E-93	AF095771.1	NT	Homo sapiens PTH-responsive osteocalcin B1 protein (B1) mRNA, complete cds
1423	14016	26545	1.92	5.0E-93	A3014511.1	NT	Homo sapiens mRNA for KIAA0611 protein, partial cds
1453	14045	26574	6.35	5.0E-93	A1674184.1	EST_HUMAN	wc09c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1453	14045	26575	6.35	5.0E-93	A1674184.1	EST_HUMAN	wc09c08.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2314670 3'
1523	14115		0.97	5.0E-93	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
1862	15452	27008	0.9	5.0E-93	AJ297710.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 2
3270	15882	26364	2.6	5.0E-93	X04201.1	NT	Human skeletal muscle 1.3 kb mRNA for tropomyosin

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5967	18588	31323	0.93	5.0E-93	M22878.1	NT	Human somatic cytochrome c (Hc1) processed pseudogene, complete cds
6257	18668		1.49	5.0E-93	AF045555.1	NT	Homo sapiens wbscr1 (WBSOR1) and wbscr5 (WBSOR5) genes, complete cds, alternatively spliced and replication factor C subunit 2 (RFC2) gene, complete cds
7700	20209	33096	3.68	5.0E-93	AF067136.1	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 11, complete cds and alternatively spliced product
8541	21080	34000	0.68	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
8541	21080	34001	0.68	5.0E-93	4557526	NT	Homo sapiens discs, large (Drosophila) homolog 2 (chapsyn-110) (DLG2) mRNA
9541	22041	35002	2.28	5.0E-93	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9721	22219	35194	2.87	5.0E-93	5032156	NT	Homo sapiens TAR (HIV) RNA-binding protein 1 (TARBP1) mRNA
9982	22477	35459	1.58	5.0E-93	AF069313.2	NT	Homo sapiens WSB1 protein (WSB1) mRNA, complete cds
10705	23234	36247	2.14	5.0E-93	11439599	NT	Homo sapiens nucleobindin 2 (NUCB2) mRNA
12145	24731	30856	2.11	5.0E-93	11417877	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
91	12767		6.55	4.0E-93	AA459933.1	EST_HUMAN	z60c09.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:795688 3' similar to SW.CLPA_RAT P37397 CALPONIN, ACIDIC ISOFORM
470	13103	25595	1.56	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
470	13103	25598	1.56	4.0E-93	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
804	13421	25926	2.39	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1) mRNA
804	13421	25927	2.39	4.0E-93	7657454	NT	Homo sapiens pescadillo (zebrafish) homolog 1, containing BRCT domain (PES1) mRNA
1225	13824	26339	1.5	4.0E-93	8923658	NT	Homo sapiens hypothetical protein FLJ20731 (FLJ20731) mRNA
2020	14602	27167	5.25	4.0E-93	AF047677.1	NT	Homo sapiens dystrophin (DMD) gene, deletion breakpoints 1-3 in intron 5
2638	15197	27771	1.41	4.0E-93	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1) mRNA
3624	16227	28705	0.8	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8) mRNA
4122	16715	29171	2.14	4.0E-93	4504654	NT	Homo sapiens interleukin 18 receptor 1 (IL18R1) mRNA
5171	16227	28705	0.86	4.0E-93	7705396	NT	Homo sapiens tumor antigen SLP-8p (HCC8) mRNA
5825	18449	31172	5.27	4.0E-93	T46864.1	EST_HUMAN	y694c12.1 Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:78838 5' similar to similar to SP:A44391 A44391 SERUM RESPONSE ELEMENT-BINDING PROTEIN SRE-ZBP - HUMAN
11013	23527	36563	14.54	4.0E-93	AV692051.1	EST_HUMAN	AV692051 GKC Homo sapiens cDNA clone GKCDRF07 5'
3713	16314	28761	8.68	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
3713	16314	28762	8.68	3.0E-93	BF690630.1	EST_HUMAN	602246554F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4332036 5'
4319	16905		5.51	3.0E-93	AF225896.1	NT	Homo sapiens tensin mRNA, complete cds
6879	19275	32079	1.28	3.0E-93	11426182	NT	Homo sapiens GCN5 (general control of amino-acid synthesis, yeast, homolog)-like 2 (GCN5L2) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10680	23212	36223	4.85	3.0E-93	AB24829.1	EST_HUMAN	wb02d05.x1 NCL_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304489 3'
204	12865	25349	26.58	2.0E-93	AB015610.1	NT	Chlorocephus aethiops mRNA for ribosomal protein S4X, complete cds
204	12865	25350	26.58	2.0E-93	AB015610.1	NT	Chlorocephus aethiops mRNA for ribosomal protein S4X, complete cds
345	12897	25483	10.26	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
346	12987	25483	6.69	2.0E-93	AL163285.2	NT	Homo sapiens chromosome 21 segment HS21C085
1657	14250	26784	7.56	2.0E-93	AF25896.1	NT	Homo sapiens tensin mRNA, complete cds
2527	15091	27694	1.01	2.0E-93	BE252982.1	EST_HUMAN	601117686F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3358220 5'
5611	18240	30889	6.13	2.0E-93	AW064385.1	EST_HUMAN	EST376458 IMAGE resequences, MAGH Homo sapiens cDNA
5818	18442	31164	1.06	2.0E-93	11430039	NT	Homo sapiens hypothetical protein (LOC51318), mRNA
5832	18456	31177	0.76	2.0E-93	U74313.1	EST_HUMAN	HSU74313 Human chromosome 14 Homo sapiens cDNA clone 1-86
6785	19376		1.21	2.0E-93	AW50202.1	EST_HUMAN	UI-HF-BND-aks-g-09-O-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078329 5'
12032	24322		2.49	2.0E-93	AA126735.1	EST_HUMAN	229c10.s1 Scarses_pregnant_uterus_NbhPU Homo sapiens cDNA clone IMAGE:503346 3'
12119	24378		2.81	2.0E-93	L41825.1	NT	Homo sapiens CYP17 gene, 5' end
12404	24562		5.66	2.0E-93	BF035327.1	EST_HUMAN	60145653F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
107	12783	25265	33.31	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
107	12783	25266	33.31	1.0E-93	AF238997.1	NT	Homo sapiens CTR1 pseudogene
544	13175	25655	7.63	1.0E-93	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
626	13283	25727	3.51	1.0E-93	AI146755.1	EST_HUMAN	0164b08.x1 NCL_CGAP_OLL1 Homo sapiens cDNA clone IMAGE:1672503 3' similar to TR:Q62384 Q62384
905	13519	26037	5.19	1.0E-93	D87675.1	NT	ZINC FINGER PROTEIN ;
1280	13875	26395	6.4	1.0E-93	8923270	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
1280	13875	26396	6.4	1.0E-93	8923270	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
1389	13983	26509	1.09	1.0E-93	AB040783.1	NT	Homo sapiens hypothetical protein FLJ20291 (FLJ20291), mRNA
2375	14945	27518	1.57	1.0E-93	AF231981.1	NT	Homo sapiens mRNA for KIAA1563 protein, partial cds
2503	15087	27641	2.67	1.0E-93	AF055066.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
2849	13933	26453	1.93	1.0E-93	BE297396.1	EST_HUMAN	Homo sapiens MHC class 1 region
2849	13933	26454	1.93	1.0E-93	BE297396.1	EST_HUMAN	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
2860	15576	28055	1.99	1.0E-93	D87675.1	NT	601177686F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532965 5'
							Homo sapiens DNA for amyloid precursor protein, complete cds
3252	15864		1.51	1.0E-93	AF231981.1	NT	Homo sapiens long chain polyunsaturated fatty acid elongation enzyme (HELO1) mRNA, complete cds
4520	17104	29550	1.82	1.0E-93	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
5755	18381	31092	1.36	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E
5755	18381	31093	1.36	1.0E-93	U78509.1	NT	Homo sapiens glucocorticoid receptor (GRL) gene, intron D, exon 5, and intron E

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5938	18559	31288	0.99	1.0E-93	AF227138.1	NT	Homo sapiens candidate taste receptor T2R14 gene, complete cds
6074	18691	31437	9.26	1.0E-93	4557792	NT	Homo sapiens neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease) (NF1) mRNA
6344	18950	31728	1.02	1.0E-93	7682241	NT	Homo sapiens KIAA0672 gene product (KIAA0672), mRNA
6896	19621	32455	2.16	1.0E-93	11431590	NT	Homo sapiens protein kinase C, beta 1 (PRKCB1), mRNA
7297	19825	32684	5.6	1.0E-93	D42072.1	NT	Human mRNA for NF1 N-isoform-exon11, complete cds
8203	20744	33657	2.4	1.0E-93	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
8480	21018	33934	1.1	1.0E-93	Y10183.1	NT	H. sapiens mRNA for MEMD protein
8583	21122	34042	1.26	1.0E-93	AF182032.1	NT	Homo sapiens protein kinase inhibitor gamma (PKIG) mRNA, complete cds
9373	20312	33214	1.84	1.0E-93	AB040918.1	NT	Homo sapiens mRNA for KIAA1485 protein, partial cds
9377	20316	33218	1.26	1.0E-93	AF091395.1	NT	Homo sapiens T10 isoform mRNA, complete cds
9507	22007	34963	4.34	1.0E-93	X13474.1	NT	Human PrkA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9507	22007	34964	4.34	1.0E-93	X13474.1	NT	Human PrkA4 gene for Alzheimer's disease A4 amyloid protein precursor (exon 9)
9641	22141	35108	0.59	1.0E-93	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
10050	22545	35540	0.51	1.0E-93	11433846	NT	Homo sapiens ryanodine receptor 3 (RYR3), mRNA
11686	24822	30763	1.37	1.0E-93	AI268262.1	EST_HUMAN	qin03c12.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1980758 3' similar to WP:119B4.4 CE13742
12301	24496		2.08	1.0E-93	AJ230125.1	NT	Homo sapiens GGT1 gene, exon 1
12397	24557		5.43	1.0E-93	11417856	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2), mRNA
12568	24687	30874	1.72	1.0E-93	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12584	25080		2.21	1.0E-93	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
10484	22978		1.17	8.0E-94	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C009
4034	18632	29101	2.19	6.0E-94	AF142482.1	NT	Homo sapiens transcription enhancer factor-5 mRNA, complete cds
12524	24640		1.31	6.0E-94	11418331	NT	Homo sapiens mitogen-activated protein kinase 12 (MAPK12), mRNA
5570	18201	30650	3.71	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
5570	18201	30651	3.71	5.0E-94	AB014512.1	NT	Homo sapiens mRNA for KIAA0812 protein, partial cds
6199	18609	31578	6.6	5.0E-94	AA722434.1	EST_HUMAN	z987g06.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:409594 3'
7081	19653	32481	1.45	5.0E-94	AI015800.1	EST_HUMAN	af33d05.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1623369 3'
8573	21112	34031	0.78	5.0E-94	BF529115.1	EST_HUMAN	602042163F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4180023 5'
10852	23373	36391	1.97	5.0E-94	11423962	NT	Homo sapiens adenylylate kinase 2 (AK2), mRNA
10852	23373	36392	1.97	5.0E-94	11423962	NT	Homo sapiens adenylylate kinase 2 (AK2), mRNA
12010	25083	30517	4.36	5.0E-94	T89398.1	EST_HUMAN	y498b04.s1 Soares_fetal_liver_spleen_NFLS Homo sapiens cDNA clone IMAGE:116239 3'
1882	14468		9.28	4.0E-94	U05094.1	NT	Homo sapiens ribosomal protein L27 mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4827	17405	28859	3.19	4.0E-94	AB591312.1	EST_HUMAN	hw11f10.x1 NCL CGAP_Brn52 Homo sapiens cDNA clone IMAGE:2259403 3' similar to TR:Q15265 Q15265 PROTEIN TYROSINE PHOSPHATASE ;
6594	19191	31995	2.35	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6594	19191	31996	2.35	4.0E-94	11440670	NT	Homo sapiens solute carrier family 22 (organic cation transporter), member 1-like (SLC22A1L), mRNA
6992	19490		0.89	4.0E-94	L27386.1	NT	Homo sapiens huntingtin (HD) gene, exon 37
11328	23026	36035	1.8	4.0E-94	11545792	NT	Homo sapiens hypothetical protein FLJ12455 (FLJ12455), mRNA
11598	24041	37110	4	4.0E-94	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
639	13262	25738	3.74	3.0E-94	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
750	13370	25884	9.91	3.0E-94	4502506	NT	Homo sapiens complement component 5 (C5) mRNA
1776	14366	26910	1.19	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1776	14366	26911	1.19	3.0E-94	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1809	14398	26944	5.11	3.0E-94	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
5861	18493	31207	4.01	3.0E-94	11496288	NT	Homo sapiens zinc finger protein 277 (ZNF277), mRNA
6299	18907	31678	1.07	3.0E-94	AB011536.1	NT	Homo sapiens mRNA for MEGF2, partial cds
6579	19177	31977	5.19	3.0E-94	11526228	NT	Homo sapiens chromosome 21 open reading frame 18 (C21ORF18), mRNA
8140	20681	33593	0.89	3.0E-94	AF152308.1	NT	Homo sapiens protocadherin alpha 13 (PCDH-alpha13) mRNA, complete cds
8523	21082	33984	3.81	3.0E-94	AB014579.1	NT	Homo sapiens mRNA for KIAA0679 protein, partial cds
9511	22011	34970	7.24	3.0E-94	AF087942.1	NT	Homo sapiens glycogenin-1L mRNA, complete cds
10979	23493	36523	1.64	3.0E-94	4757821	NT	Homo sapiens axonal transport of synaptic vesicles (ATSV) mRNA
11527	23975	37045	1.62	3.0E-94	U26711.1	NT	Human chb-b truncated form 1 lacking leucine zipper mRNA, complete cds
9687	22166	35140	0.51	2.0E-94	AB010393.1	EST_HUMAN	w30h11.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2391813 3'
9687	22166	35141	0.51	2.0E-94	AB010393.1	EST_HUMAN	w30h11.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:2391813 3'
160	12823	25311	2.34	1.0E-94	BE295714.1	EST_HUMAN	601175762F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3125	15739	28207	1.98	1.0E-94	BE253433.1	EST_HUMAN	601111698F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
3125	15739	28208	1.98	1.0E-94	BE253433.1	EST_HUMAN	601111698F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352559 5'
4450	17036	29480	1.14	1.0E-94	9506692	NT	Homo sapiens hypothetical protein (FLJ20746), mRNA
6223	18832	31608	1.21	1.0E-94	AE000269.1	NT	Escherichia coli K-12 MG1655 section 159 of 400 of the complete genome
6412	19015	31797	1.32	1.0E-94	AL040518.1	EST_HUMAN	DKFZp434G0314.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G0314 5'
6421	19024	31808	0.79	1.0E-94	H08270.1	EST_HUMAN	y687f02.r1 Soares Infant brain 1N1B Homo sapiens cDNA clone IMAGE:45053 5'
8057	20598	33507	0.56	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
8057	20598	33508	0.56	1.0E-94	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
9180	21757	34703	2.29	1.0E-94	11428710	NT	Homo sapiens paired box gene 5 (B-cell lineage specific activator protein) (PAX5), mRNA

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9702	22201	35173	1.8	1.0E-94	BE780478.1	EST_HUMAN	601468748F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3872099 5'
10845	23461	36483	3.48	1.0E-94	U65590.1	NT	Homo sapiens IL-1 receptor antagonist IL-1Ra (IL-1RN) gene, alternatively spliced forms, complete cds
11197	23702	36753	2.05	1.0E-94	A1272244.1	EST_HUMAN	ap22e02.x1 Schiller oligodendroglioma Homo sapiens cDNA clone IMAGE:1956122 3' similar to TR:Q82845
11592	24035	37104	2.28	1.0E-94	11418871	NT	Q82845 NEURAL CELL ADHESION PROTEIN BIG-2 PRECURSOR ;
12133	12823	25311	1.34	1.0E-94	BE295714.1	EST_HUMAN	Homo sapiens KIAA0164 gene product (KIAA0164), mRNA
1525	14117	26654	2.12	9.0E-95	AF027302.1	NT	601175782F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531038 5'
3191	15803	28275	1.15	9.0E-95	7692027	NT	Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds
3191	15803	28275	1.15	9.0E-95	7692027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
5601	18230	30679	1.59	9.0E-95	X82569.1	NT	M. musculus glyT1 gene (exons 1c and 2)
5601	18230	30680	1.59	9.0E-95	X82569.1	NT	M. musculus glyT1 gene (exons 1c and 2)
8194	20735	33645	1.89	9.0E-95	AF274753.1	NT	Homo sapiens progressive ankylosis-like protein (ANK) mRNA, complete cds
155	12818	25306	10.06	8.0E-95	AF154830.1	NT	Homo sapiens carbamyl phosphate synthetase I mRNA, complete cds
4634	17217	29669	1.92	8.0E-95	AF700998.1	EST_HUMAN	we09e04.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2340608 3' similar to gb:K00558
4634	17217	29670	1.92	8.0E-95	AF700998.1	EST_HUMAN	TUBULIN ALPHA-1 CHAIN (HUMAN);
7028	19562	32389	0.7	8.0E-95	11418378	NT	Homo sapiens KIAA0183 gene product (KIAA0183), mRNA
7290	19818	32677	1.44	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
7290	19818	32678	1.44	8.0E-95	11426529	NT	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 (PSMD11), mRNA
8138	20679	33590	1.93	8.0E-95	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
9287	21867	34832	1.88	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9287	21867	34833	1.88	8.0E-95	11420944	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
9762	22260	35243	3.42	8.0E-95	5174844	NT	Homo sapiens proline dehydrogenase (proline oxidase) (PRODH) mRNA
9793	22291	35243	3.07	8.0E-95	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10134	22628	36617	0.75	8.0E-95	9845523	NT	Homo sapiens early growth response 2 (Krox-20 (Drosophila) homolog) (EGR2), mRNA
10592	23127	36141	1.76	8.0E-95	AF112152.1	NT	Homo sapiens developmental arteries and neural crest EGF-like protein mRNA, complete cds
11357	23811	36871	2.34	8.0E-95	10894024	NT	Homo sapiens HCF-binding transcription factor Zhangfei (ZF), mRNA
12365	24598		25.75	8.0E-95	AA828056.1	EST_HUMAN	zu84b01.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744649 3' similar to contains L1.11 L1 repetitive element ;
267	12953	25441	6.43	7.0E-95	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
287	12953	25442	6.43	7.0E-95	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4456	17042	29486	5.64	7.0E-95	MB5708.1	NT	Homo sapiens Ly-6-like protein (GD55) mRNA, complete cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4505	17089		1.35	7.0E-95	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
8144	21678	34623	0.92	4.0E-95	BE439625.1	EST_HUMAN	HTM1-288F HTM1 Homo sapiens cDNA
11548	23996	37068	1.69	4.0E-95	AW950634.1	EST_HUMAN	EST362704 MAGC ressequences, MAGC Homo sapiens cDNA
11548	23996	37068	1.69	4.0E-95	AW950634.1	EST_HUMAN	EST362704 MAGC ressequences, MAGC Homo sapiens cDNA
224	12885	26370	6.53	3.0E-95	AV648361.1	EST_HUMAN	AV648361 GLC Homo sapiens cDNA clone GLCBIF01 3'
5634	18263	30735	1.75	3.0E-95	BF526041.1	EST_HUMAN	602071146F1 NCL CGAP_Bim64 Homo sapiens cDNA clone IMAGE:4214147 5'
5854	24750	31200	0.72	3.0E-95	4503354	NT	Homo sapiens dedicator of cyclo-kinesis 1 (DOCK1) mRNA
7404	19929	32792	1.38	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGC ressequences, MAGC Homo sapiens cDNA
7404	19929	32793	1.38	3.0E-95	AW958121.1	EST_HUMAN	EST370191 MAGC ressequences, MAGC Homo sapiens cDNA
9277	21803	34753	1.71	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9277	21803	34754	1.71	3.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
9662	22161	35134	0.87	3.0E-95	BF213446.1	EST_HUMAN	601845212F1 NIH_MGC 55 Homo sapiens cDNA clone IMAGE:4070451 5'
10759	23283	36296	2.2	3.0E-95	R83190.1	EST_HUMAN	y87g11.1 Soares fetal liver spleen TNFSL Homo sapiens cDNA clone IMAGE:194468 5'
973	13585	26099	2.57	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
1686	14278	26811	1.55	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1686	14278	26812	1.55	2.0E-95	7662027	NT	Homo sapiens KIAA0255 gene product (KIAA0255), mRNA
1686	14278	26812	1.55	2.0E-95	7662027	NT	Homo sapiens tissue inhibitor of metalloproteinase 3 (Soreby fundus dystrophy, pseudoinflammatory) (TIMP3) mRNA
1984	14566	27127	3.25	2.0E-95	4507512	NT	mRNA
1987	14569	27131	1.57	2.0E-95	BE393873.1	EST_HUMAN	601312161F1 NIH_MGC 44 Homo sapiens cDNA clone IMAGE:3658862 5'
2470	15037	27604	1.23	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2470	15037	27605	1.23	2.0E-95	5453665	NT	Homo sapiens G protein-coupled receptor 19 (GPR19) mRNA
2505	15069	27642	4.2	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2554	15118	27688	1.05	2.0E-95	4758423	NT	Homo sapiens glycine cleavage system protein H (aminomethyl carrier) (GCSH) mRNA
2844	13584	26098	8.08	2.0E-95	4504374	NT	Homo sapiens H factor 1 (complement) (HF1) mRNA
3193	15805	28278	2.54	2.0E-95	AF015452.1	NT	Homo sapiens Usurpin-gamma mRNA, complete cds
3621	18224	28701	2.98	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3621	18224	28702	2.98	2.0E-95	7705900	NT	Homo sapiens unconventional myosin-15 (LOC51168), mRNA
3677	18278	28745	0.72	2.0E-95	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
3813	18413	28877	0.84	2.0E-95	AI290264.1	EST_HUMAN	gm01c02 x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1880546 3' similar to WP:T23G7.4 CE03705
4452	17038	29481	1.42	2.0E-95	7657185	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
5048	17621	30066	3.24	2.0E-95	AF105067.1	NT	Homo sapiens lipopolysaccharide-binding protein (LBP) mRNA, complete cds
5191	17756	30185	3.19	2.0E-95	7661879	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5251	17814	30237	1.69	2.0E-95	AA447831.1	EST_HUMAN	z11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5251	17814	30238	1.69	2.0E-95	AA447831.1	EST_HUMAN	z11d07.r1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786157 5'
5671	18298	30778	5.36	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5671	18298	30779	5.36	2.0E-95	7705764	NT	Homo sapiens CGI-48 protein (LOC51096), mRNA
5876	18498	31223	1.21	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
5876	18498	31224	1.21	2.0E-95	11225608	NT	Homo sapiens angiotensin I converting enzyme (peptidyl-dipeptidase A) 2 (ACE2), mRNA
6281	18899	31670	3.33	2.0E-95	ME9724.1	NT	Human muscle-type phosphofructokinase (PFK-M) gene, exon 7
6577	19175	31974	1.08	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6577	19175	31975	1.08	2.0E-95	11427182	NT	Homo sapiens transcription factor 2, hepatic; LF-B3; variant hepatic nuclear factor (TCF2), mRNA
6885	19281	32084	2.42	2.0E-95	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9), mRNA, complete cds
6885	19281	32426	1.6	2.0E-95	11435773	NT	Homo sapiens huntingtin (Huntington disease) (HD), mRNA
9059	21806	34537	1.85	2.0E-95	11421795	NT	Homo sapiens ribophorin II (RPN2), mRNA
10283	22778	35789	0.49	2.0E-95	11434330	NT	Homo sapiens KIAA1065 protein (KIAA1065), mRNA
10602	23136	36150	2.21	2.0E-95	4757853	NT	Homo sapiens bone morphogenetic protein receptor, type IA (BMPRI1A), mRNA
11546	23994	37065	1.74	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11546	23994	37066	1.74	2.0E-95	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
12103	24365	30871	2.55	2.0E-95	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
12220	24442		1.41	2.0E-95	11417860	NT	Homo sapiens hypothetical protein (HS322B1A), mRNA
12534	24646	30899	8.02	2.0E-95	11418164	NT	Homo sapiens adenylosuccinate lyase (ADSL), mRNA
5799	18424	31140	7.86	1.0E-95	AA284651.1	EST_HUMAN	z123h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6 ;
5799	18424	31141	7.86	1.0E-95	AA284651.1	EST_HUMAN	z123h04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:714007 5' similar to TR:G1067084 G1067084 F55H2.6 ;
7523	20043	32912	4.16	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
7523	20043	32913	4.16	1.0E-95	BF370000.1	EST_HUMAN	RC6-FN0019-290600-011-G11 FN0019 Homo sapiens cDNA
8135	20676	33568	1.51	9.0E-95	BE897259.1	EST_HUMAN	601437232F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3922423 5'
467	15415	25592	1.19	8.0E-95	BE807607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895761 5'
467	15415	25593	1.19	8.0E-95	BE807607.1	EST_HUMAN	601497608F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895761 5'
5702	16328		2.71	8.0E-95	AW836047.1	EST_HUMAN	PMO-LT0019-090300-002-009 L70019 Homo sapiens cDNA
3980	16578	29048	0.99	7.0E-95	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
3360	15968	28445	1.65	6.0E-95	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
3529	16134	28614	11.93	6.0E-95	M26873.1	NT	Human glyceraldehyde-3-phosphate dehydrogenase pseudogene 3'end

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5820	18444	31166	0.85	6.0E-96	11422642	NT	Homo sapiens sialyltransferase 6 (N-acetylglucosaminide alpha 2,3-sialyltransferase) (SIAT6), mRNA
11420	23871	36932	2.52	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11420	23871	36933	2.52	6.0E-96	7662289	NT	Homo sapiens KIAA0763 gene product (KIAA0763), mRNA
11481	23911	36978	1.96	6.0E-96	8923939	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
342	12994	25479	2.95	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
875	13489	26005	3.61	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
875	13489	26006	3.61	5.0E-96	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
2650	15209		0.91	5.0E-96	11416767	NT	Homo sapiens phospholipase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
3081	15677	28151	0.59	5.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
6030	17604		1.6	5.0E-96	X60812.1	NT	H. sapiens DNA for monoamine oxidase type A (7) (partial)
6758	19351	32180	1.1	5.0E-96	AF148773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6878	19612	32445	4.05	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
6878	19612	32446	4.05	5.0E-96	11424399	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
7090	19681	32501	0.78	5.0E-96	AB023177.1	NT	Homo sapiens mRNA for KIAA0960 protein, partial cds
7524	20044	32914	1.7	5.0E-96	AB024334.1	NT	Homo sapiens mRNA for 14-3-3gamma, complete cds
8050	20592	33499	1.62	5.0E-96	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
8050	20592	33500	1.62	5.0E-96	M88347.1	NT	Human type IV collagenase (CLG4B) gene, exon 5
11618	24060	37124	1.66	5.0E-96	7661973	NT	Human type IV collagenase (CLG4B) gene, exon 5
4289	16855		8.01	3.0E-96	H88656.1	EST_HUMAN	Homo sapiens KIAA0175 gene product (KIAA0175), mRNA
440	13073		3.68	2.0E-96	4503098	NT	y87h12.r1 Scores fetal liver spleen 1NLS Homo sapiens cDNA clone IMAGE:212327 5'
777	13396	25897	1.52	2.0E-96	AL163248.2	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4871	17447	29898	1.56	2.0E-96	BE148074.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C048
8911	21449		5.45	2.0E-96	AV689461.1	EST_HUMAN	RC3-H10230-040500-110-g02 HT0230 Homo sapiens cDNA
11795	24176		1.71	2.0E-96	AW249440.1	EST_HUMAN	AV689461 OKC Homo sapiens cDNA clone GKCFMD07 5'
699	13321	25808	2.62	1.0E-96	Y18890.1	NT	2819351: Sprime NIH_MGC 7 Homo sapiens cDNA clone IMAGE:2819351 5'
1817	14407	26951	3.32	1.0E-96	AW955054.1	EST_HUMAN	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
1817	14407	26952	3.32	1.0E-96	AW955054.1	EST_HUMAN	EST367124 MAGC resequences, MAGC Homo sapiens cDNA
2272	14846	27421	1.3	1.0E-96	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
2272	14846	27422	1.3	1.0E-96	M75987.1	NT	Human hepatocyte growth factor gene, exon 1
2306	15398	27455	1.1	1.0E-96	U51472.2	NT	Felis catus superfast myosin heavy chain (sMyHC) mRNA, complete cds
7045	18065	30455	0.98	1.0E-96	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
8154	20695	33608	0.6	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA
8154	20695	33609	0.9	1.0E-96	7661803	NT	Homo sapiens HSPC144 protein (HSPC144), mRNA

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8850	21189	34107	22.03	1.0E-96	11419428	NT	Homo sapiens similar to ectonucleotide pyrophosphatase/phosphodiesterase 3 (H. sapiens) (LOC63214), mRNA
8784	21323	34247	2.21	1.0E-96	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
10064	22559	35553	0.87	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
10064	22559	35554	0.87	1.0E-96	AB033116.1	NT	Homo sapiens mRNA for KIAA1280 protein, partial cds
11781	18023	30404	2.56	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
11781	18023	30405	2.56	1.0E-96	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
3370	19778	28455	0.62	6.0E-97	BF245240.1	EST_HUMAN	601883712F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4081202 5'
7558	20076		2.76	6.0E-97	BE141849.1	EST_HUMAN	IL5-HT0117-011059-004-D07 HT0117 Homo sapiens cDNA
8864	21403	34327	0.74	6.0E-97	BE989012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
8864	21403	34328	0.74	6.0E-97	BE989012.1	EST_HUMAN	601440317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925133 5'
10486	22980	35987	0.52	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
10486	22980	35988	0.52	6.0E-97	AA320332.1	EST_HUMAN	EST22672 Adipose tissue, white II Homo sapiens cDNA 5' end
11284	23737	36793	1.8	6.0E-97	X15804.1	NT	Human mRNA for alpha-actinin
7957	20499	33409	2.45	5.0E-97	AL043314.2	EST_HUMAN	DKFZp434N0323_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434N0323 5'
8085	20626	33540	12.64	5.0E-97	AA18026.1	EST_HUMAN	z97e12.s1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:767758 3' similar to TR:G1304125
9593	22093	35057	2.67	5.0E-97	BF154912.1	EST_HUMAN	G1304125 PMS4 MRNA ;
11421	23872	36934	1.69	5.0E-97	BE148597.1	EST_HUMAN	RCO-BT0812-250900-032-a09 BT0812 Homo sapiens cDNA
11421	23872	36935	1.69	5.0E-97	BE148597.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
975	13587	26102	6.69	4.0E-97	BE004436.1	EST_HUMAN	MRO-HT0241-150500-010-b02 HT0241 Homo sapiens cDNA
1953	14537	27093	0.97	4.0E-97	5453572	NT	GMO-BN0106-170300-283-e06 BN0106 Homo sapiens cDNA
5754	18380	31091	17.27	4.0E-97	4557326	NT	Homo sapiens brefeldin A-inhibited guanine nucleotide-exchange protein 2 (BIG2), mRNA
5912	19571	32399	6.05	4.0E-97	Y11339.2	NT	Homo sapiens apolipoprotein H (beta-2-glycoprotein I) (APOH) mRNA
5912	19571	32400	6.05	4.0E-97	Y11339.2	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7088	19659	32498	1.01	4.0E-97	7710125	NT	Homo sapiens mRNA for GalNAc alpha-2, 6-sialyltransferase 1, long form
7128	19468	32286	1.01	4.0E-97	11422155	NT	Homo sapiens ligase III, DNA, ATP-dependent (LIG3), transcript variant alpha, mRNA
7778	20288	33186	0.74	4.0E-97	10947053	NT	Homo sapiens cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-family C, member 7) (CFTR), mRNA
7778	20288	33187	0.74	4.0E-97	10947053	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8078	20620	33533	0.84	4.0E-97	4557708	NT	Homo sapiens ankyrin 2, neuronal (ANK2), transcript variant 2, mRNA
8289	20840	33761	1.57	4.0E-97	11421783	NT	Homo sapiens laminin, alpha 2 (merosin, congenital muscular dystrophy) (LAMA2) mRNA
8555	21094	34014	0.73	4.0E-97	11423233	NT	Homo sapiens v-src avian sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (SRC), mRNA
							Homo sapiens cytochrome P450, subfamily 1B, polypeptide 1 (CYP4B1), mRNA

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9172	21749	34692	1.23	4.0E-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9172	21749	34693	1.23	4.0E-97	AB011168.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
10333	22827	35822	0.76	4.0E-97	11431060	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
11042	23556	36591	1.85	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11042	23556	36592	1.85	4.0E-97	11863122	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 1, mRNA
11977	24288		4.75	4.0E-97	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
284	12922	25408	2.37	3.0E-97	AB032998.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
907	13521	28039	8.51	3.0E-97	4502186	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
907	13521	28040	8.51	3.0E-97	4502186	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
1490	15443	26623	2.15	3.0E-97	4758813	NT	Homo sapiens N-myc (and STAT) interactor (NMI), mRNA
2483	15400	27618	1.36	3.0E-97	U36255.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 7
3205	15817	28293	37.82	3.0E-97	K02212.1	NT	Human alpha-1-antitrypsin gene (S variant), complete cds
3299	15910	28389	1.48	3.0E-97	5174478	NT	Homo sapiens pericentri (PCNT) mRNA
3893	16492	28952	1.04	3.0E-97	AF136523.1	NT	Homo sapiens bile-salt export pump (BSEP) mRNA, complete cds
4894	17469	29925	28.9	1.0E-97	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
6558	19156	31952	2.38	1.0E-97	BE568466.1	EST_HUMAN	601339520F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681821 5'
9365	20304	33206	0.6	1.0E-97	AW379976.1	EST_HUMAN	RCO-HT0258-211189-011-g05 HT0258 Homo sapiens cDNA
9365	20304	33207	0.6	1.0E-97	AW379976.1	EST_HUMAN	RCO-HT0258-211189-011-g05 HT0258 Homo sapiens cDNA
9679	22178	35153	1.21	1.0E-97	R10887.1	EST_HUMAN	y38c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128134 3'
10584	23119	36134	4.07	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
10584	23119	36135	4.07	1.0E-97	11427757	NT	Homo sapiens KIAA0649 gene product (KIAA0649), mRNA
11189	23694	36743	3.53	1.0E-97	AA563761.1	EST_HUMAN	nk29g02.a1 NCI_CGAP_Cot11 Homo sapiens cDNA clone IMAGE:1014982 3'
11343	23041	36050	18.96	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
11343	23041	36051	18.96	1.0E-97	11426272	NT	Homo sapiens ribosomal protein S15 (RPS15), mRNA
834	13547	28064	5.55	9.0E-98	BE080973.1	EST_HUMAN	PM4-BT0724-010400-008-at12 BT0724 Homo sapiens cDNA
1319	13913	26434	1.41	9.0E-98	8393032	NT	Homo sapiens cal eye syndrome critical region gene 1 (CECR1), mRNA
6445	19047		0.67	9.0E-98	AJ250713.1	NT	Homo sapiens CLDN12 gene for claudin-12
7865	20407	33314	7.35	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
7865	20407	33315	7.35	9.0E-98	4758119	NT	Homo sapiens death-associated protein (DAP), mRNA
9044	21581	34510	2	9.0E-98	X06989.1	NT	Human mRNA for amyloid A4(751) protein
9151	21686	34629	1.94	9.0E-98	11321580	NT	Homo sapiens succinate-CoA ligase, GDP-forming, alpha subunit (SUCLG1), mRNA
9216	21733	34676	1.46	9.0E-98	AB037768.1	NT	Homo sapiens mRNA for KIAA1365 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9282	21788		1.25	9.0E-08	AF057726.1	NT	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 8
9289	21889	34835	1.15	9.0E-08	4507070	NT	Homo sapiens SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
9289	21889	34836	1.15	9.0E-08	4507070	NT	Homo sapiens SW/ISNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 3 (SMARCA3) mRNA
10161	22850	35651	0.54	9.0E-08	AF141325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
10268	22763	35750	0.5	9.0E-08	11431544	NT	Homo sapiens protease-activated receptor 3 (PAR3), mRNA
10883	23404	36422	2.37	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
10883	23404	36423	2.37	9.0E-08	AB023222.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11994	13547	26064	4.29	9.0E-08	BE090973.1	EST_HUMAN	PM4-BT0724-010400-008-a12 BT0724 Homo sapiens cDNA
27	12706		0.82	8.0E-08	AJ251158.1	NT	Homo sapiens partial MICB gene for MHC class I chain-related protein B, exons 2-3 and joined CDS
1607	14199	26732	1.04	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1607	14199	26733	1.04	8.0E-08	5031810	NT	Homo sapiens IL2-inducible T-cell kinase (ITK), mRNA
1764	14354	26900	1.64	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
1764	14354	26901	1.64	8.0E-08	AB017007.1	NT	Homo sapiens PMS2L16 mRNA, partial cds
3863	16461	28925	7.16	8.0E-08	J04469.1	NT	Human mitochondrial creatine kinase (CKMT) gene, complete cds
5276	17838		1.43	8.0E-08	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
6233	18842	31614	1.18	5.0E-08	BE885973.1	EST_HUMAN	601507503F1 NIH_MGC 71 Homo sapiens cDNA clone IMAGE:3909097 5'
12398	24558	30908	1.68	4.0E-08	BE348727.1	EST_HUMAN	H6802.X1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3151899 3'
2222	14797	27370	1.15	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
2639	15198	27772	1.67	3.0E-08	AB014607.1	NT	Homo sapiens mRNA for KIAA0707 protein, partial cds
2777	15330		1.97	3.0E-08	AA07498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
7026	19560	32386	1.66	3.0E-08	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
7026	19560	32387	1.68	3.0E-08	11419210	NT	Homo sapiens activator of S phase kinase (ASK), mRNA
8686	21225	34145	3.05	3.0E-08	H46598.1	EST_HUMAN	yo17g09.r1 Soares adult brain N2b5fHB55Y Homo sapiens cDNA clone IMAGE:178240 5'
9221	21737	34679	0.77	3.0E-08	8922098	NT	Homo sapiens uncharacterized bone marrow protein BM039 (BM039), mRNA
9798	22296	35279	1.8	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
9798	22296	35280	1.8	3.0E-08	AJ403124.1	EST_HUMAN	AJ403124 3.4 (downregulated in larynx carcinoma) Homo sapiens cDNA clone IB
10369	22863	35856	0.86	3.0E-08	BE000454.1	EST_HUMAN	601673686F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956517 5'
10831	23352	36367	3.79	3.0E-08	U59309.1	NT	Human fumarylase precursor (FH) mRNA, nuclear gene encoding mitochondrial protein, complete cds
12598	24685		5.13	3.0E-08	11418177	NT	Homo sapiens Ran GTPase activating protein 1 (RANGAP1), mRNA
765	13384	25883	0.81	2.0E-08	BE261694.1	EST_HUMAN	601149486F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502245 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
	14702	27272	3.36	2.0E-98	BE294281.1	EST_HUMAN	601172658F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528134 5'
2279	14853	27431	1.37	2.0E-98	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
4384	16971	29419	0.74	2.0E-98	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4432	17018	29458	4.65	2.0E-98	4758331	NT	Homo sapiens fatty-acid-Coenzyme A ligase, long-chain 4 (FACL4) mRNA
4953	17528	29868	0.96	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
4953	17528	29868	0.96	2.0E-98	AF218902.1	NT	Homo sapiens attractin precursor (ATRIN) gene, exon 16
5579	18210	30660	4.63	2.0E-98	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6761	18354	32163	1.03	2.0E-98	4505788	NT	Homo sapiens phosphatidylinositol 3-kinase, class 2, alpha polypeptide (PIK3C2A) mRNA
7619	20132	33008	1.13	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
7619	20132	33008	1.13	2.0E-98	11431271	NT	Homo sapiens hypothetical protein FLJ10488 (FLJ10488), mRNA
8544	21083	34004	3.84	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8544	21083	34005	3.84	2.0E-98	11428813	NT	Homo sapiens SH3-domain GRB2-like 2 (SH3GL2), mRNA
8625	21164	34078	0.62	2.0E-98	L76668.1	NT	Homo sapiens NKA14b mRNA, complete cds
8625	21164	34078	0.62	2.0E-98	L76668.1	NT	Homo sapiens NKA14b mRNA, complete cds
9456	21982	34934	3.9	2.0E-98	X12664.1	NT	H. sapiens arginase gene exon 3 (EC 3.5.3.1)
10312	22808	36628	1.31	2.0E-98	7705868	NT	Homo sapiens AIM-1 protein (LOC51151), mRNA
11078	23590	36628	1.6	2.0E-98	U22028.1	NT	Human cytochrome P450 (CYP2A13) gene, complete cds
11999	24305	30989	1.62	2.0E-98	11435947	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
430	13063	25558	57.29	1.0E-98	AB62007.1	EST_HUMAN	tw36b04.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2261743 3' similar to SW:RL28_HUMAN
480	13113	25603	2.16	1.0E-98	AW998611.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A. ;
1832	14420	26970	13.46	1.0E-98	NA9818.1	EST_HUMAN	PMO-BN0065-100300-001-c06 BN0065 Homo sapiens cDNA
							W23705.1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:243585 5' similar to PIR:S54204 S54204 ribosomal protein L29 - human ;
5520	18152	30566	3.14	1.0E-98	AA195694.1	EST_HUMAN	z98c09.r1 Stragene muscle 637209 Homo sapiens cDNA clone IMAGE:628240 5' similar to TR:G806562
5758	18384	31097	1.12	1.0E-98	BE390627.1	EST_HUMAN	G01284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
5758	18384	31098	1.12	1.0E-98	BE390627.1	EST_HUMAN	G01284986F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606692 5'
8928	21466	34383	8.27	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
8928	21466	34384	8.27	1.0E-98	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
5984	18604	31338	0.93	9.0E-99	AB05004.1	EST_HUMAN	QV-B1073-191298-012 BT073 Homo sapiens cDNA
5984	18604	31339	0.93	9.0E-99	AB05004.1	EST_HUMAN	QV-B1073-191298-012 BT073 Homo sapiens cDNA
6191	18801	31571	4.33	9.0E-99	AW988635.1	EST_HUMAN	EST390711 IMAGE:2163421 3' similar to SW:RID_HUMAN
14004	20545	36549	2.39	9.0E-99	AF170926.1	EST_HUMAN	bm69h07.x1 NCI CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:RID_HUMAN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11001	23515	36550	3.39	9.0E-99	A178929.1	EST_HUMAN	tm69h07.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2163421 3' similar to SW:BD_HUMAN
11292	23744	36801	1.97	9.0E-99	AA134604.1	EST_HUMAN	PS5957 BH3 INTERACTING DOMAIN DEATH AGONIST ;
11627	24099	37133	2.11	9.0E-99	AJ271736.1	NT	zn90d02.r1 Stragene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565443 5' similar to
8661	21200	34118	1.59	8.0E-99	9835487	NT	TR:G862994 G862994 GPI-ANCHORED PROTEIN P137. ;
5999	18619	31355	10.3	7.0E-99	AF035808.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
11477	23927	36998	2.52	7.0E-99	AF001886.1	NT	Human endogenous retrovirus, complete genome
497	13129	25618	0.57	6.0E-99	U10991.1	NT	Homo sapiens oscillin (hLn) gene, exon 5
4859	17437	29887	1.3	6.0E-99	4502660	NT	Homo sapiens NK-receptor (KIR-G2) gene, linker region exon
5382	17941	30355	1.01	6.0E-99	8923244	NT	Human G2 protein mRNA, partial cds
6711	19305	32109	1	6.0E-99	7706136	NT	Homo sapiens CD34 antigen (CD34) mRNA
6780	19371	32187	1.39	6.0E-99	L43610.1	NT	Homo sapiens hypothetical protein FLJ20272 (FLJ20272), mRNA
8048	20590	33497	1.11	6.0E-99	X99101.1	NT	Homo sapiens GAP-like protein (LOC51306), mRNA
8700	21239	34182	1.88	6.0E-99	AB036429.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
8797	21336	34261	4.03	6.0E-99	AF080255.1	NT	H. sapiens mRNA for estrogen receptor
8797	21336	34262	4.03	6.0E-99	AF080255.1	NT	Homo sapiens lodestar protein mRNA, complete cds
8854	21393	34315	0.62	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
8854	21393	34316	0.62	6.0E-99	11431994	NT	Homo sapiens inositol 1,4,5-triphosphate receptor, type 1 (ITPR1), mRNA
10598	23132	36146	4.18	6.0E-99	11526299	NT	Homo sapiens BH3 interacting domain death agonist (BID), mRNA
953	13565	26077	9.63	5.0E-99	U35484.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
953	13565	26078	9.63	5.0E-99	U35484.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
2007	14589	27149	1.33	5.0E-99	Y11365.1	NT	H. sapiens IMPA gene, exon 8
4663	17245	29699	1.44	5.0E-99	AF009690.1	NT	Homo sapiens T cell receptor beta locus, TCRBV7S3A2 to TCRBV12S2 region
12009	24311		2.1	5.0E-99	BE900177.1	EST_HUMAN	601513157F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914391 5'
8263	20804		5.49	3.0E-99	M95596.1	NT	Human E2A/HLA fusion protein (E2A/HLF) mRNA, complete cds
1282	13878		15.39	2.0E-99	AW274792.1	EST_HUMAN	4009608.x1 NCI_CGAP_HN9 Homo sapiens cDNA clone IMAGE:2739874 3' similar to gb:M31212 MYOSIN
3297	15908	26388	1.27	2.0E-99	M30938.1	NT	LIGHT CHAIN ALKAL, NON-MUSCLE (ISOFORM (HUMAN);
4641	17223	29677	1.67	2.0E-99	AF095703.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
7687	20179	33066	1.28	2.0E-99	AF257737.1	NT	Homo sapiens short chain L-3-hydroxyacyl-CoA dehydrogenase precursor (HADHSC) gene, nuclear gene encoding mitochondrial protein, complete cds Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8641	21180	34100	9.63	2.0E-99	W23507.1	EST_HUMAN	zb4d406.r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:306635 5' similar to
9079	21615	34550	0.63	2.0E-99	R78254.1	EST_HUMAN	gb:M15182 BETA-GLUCURONIDASE PRECURSOR (HUMAN);
10984	23498	36528	3.8	2.0E-99	AF247457.2	NT	y81b09.r1 Soares placenta NB2HP Homo sapiens cDNA clone IMAGE:145625 5'
11617	24059	37123	1.61	2.0E-99	10863960	NT	Homo sapiens myosin X (MYO10) mRNA, complete cds
337	12989	25476	1.46	1.0E-99	AF114487.1	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
402	13046	25537	1.21	1.0E-99	11528150	NT	Homo sapiens Intersectin long isoform (ITSN) mRNA, complete cds
1468	14058	26592	2.52	1.0E-99	M30838.1	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
1603	14195	26726	2.14	1.0E-99	AF192523.1	NT	Human Ku (p70/p80) subunit mRNA, complete cds
1603	14195	26727	2.14	1.0E-99	AF192523.1	NT	Homo sapiens truncated Niemann-Pick C3 protein (NPC3) mRNA, complete cds
1971	14555	27111	0.91	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
1971	14555	27112	0.91	1.0E-99	4503730	NT	Homo sapiens FK506-binding protein 6 (36kD) (FKBP6) mRNA, and translated products
3121	15735	28204	0.9	1.0E-99	J031171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec) mRNA, complete cds
4469	17055	29499	2.98	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
4469	17055	29500	2.98	1.0E-99	AF098018.1	NT	Homo sapiens fatty acid amide hydrolase (FAAH) gene, exon 14
6898	19630	32467	2.18	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
6898	19630	32468	2.18	1.0E-99	11421007	NT	Homo sapiens glycine receptor, alpha 2 (GLRA2), mRNA
7193	24776	32574	0.6	1.0E-99	X98022.1	NT	H. sapiens EG-AP gene exon 2
9127	21662		1.04	1.0E-99	11419721	NT	Homo sapiens ALEX1 protein (LOC51309), mRNA
9439	21985	34914	1.81	1.0E-99	AW340174.1	EST_HUMAN	hd02h02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2908371 3' similar to TR:O02711
11064	23576	36814	1.82	1.0E-99	5901979	NT	O02711 PRO-POL-DUTPASE POLYPROTEIN ;
11255	23785	36841	2.94	1.0E-99	AB023222.1	NT	Homo sapiens heat shock transcription factor 2 binding protein (HSF2BP), mRNA
11557	24005	37077	1.8	1.0E-99	AF223391.1	NT	Homo sapiens mRNA for KIAA1005 protein, partial cds
11637	24076	37138	1.57	1.0E-99	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11784	24155		9.05	1.0E-99	AF240786.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
1	12682	25138	1.19	1.0E-100	AL163247.2	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2	12682	25138	1.73	1.0E-100	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
72	12750	25227	1.35	1.0E-100	11418230	NT	Homo sapiens chromosome 21 segment HS21C047
72	12750	25228	1.35	1.0E-100	11418230	NT	Homo sapiens Testis-specific XX-related protein on Y (XXRY), mRNA
80	12766	25250	0.79	1.0E-100	AW275237.1	EST_HUMAN	Homo sapiens Testis-specific XX-related protein on Y (XXRY), mRNA
							xv78b11.x1 NCI_OGAP_Bm53 Homo sapiens cDNA clone IMAGE:282480 5 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
180	12842	25326	1.18	1.0E-100	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
339	12991	25478	1.76	1.0E-100	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
365	13014	25497	2.08	1.0E-100	T05087.1	EST_HUMAN	EST02875 Fetal brain, Stratagene (cat#938208) Homo sapiens cDNA clone HFBCR32
462	13096		1.84	1.0E-100	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
515	13148		8.1	1.0E-100	X89631.1	NT	G.gorilla DNA for ZNF80 gene homolog
535	13166	25647	1.78	1.0E-100	BE180609.1	EST_HUMAN	RC3-H10825-040500-022-b09 HT0825 Homo sapiens cDNA
1057	13662	26172	3.18	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1057	13662	26173	3.18	1.0E-100	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA
1483	14076	26614	0.93	1.0E-100	BF530735.1	EST_HUMAN	602072064F1 NCL CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4215039 5'
1594	14187		2.49	1.0E-100	AW207555.1	EST_HUMAN	UI-H-BH-afk-c-07-0-JL.s1 NCL CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2722164 3'
1598	14190	26721	1.32	1.0E-100	AI200857.1	EST_HUMAN	qf6209.x1 Scores_testis_NHT Homo sapiens cDNA clone IMAGE:1754633 3' similar to SW:CYT_COTJA
2284	14858		2.78	1.0E-100	D83349.1	NT	P81061 CYSTATIN 1
2482	15048	27617	0.87	1.0E-100	X62468.1	NT	Ret mRNA for short type PB-cadherin, complete cds
2731	15286	27853	2.8	1.0E-100	11418978	NT	H. sapiens mRNA for IFN-gamma (pKC-4)
3053	15689		3.92	1.0E-100	D11078.1	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
4289	16875	29324	1.83	1.0E-100	AF057354.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
4320	16906	29348	2.66	1.0E-100	4503792	NT	Homo sapiens myotubularin-related protein 1a mRNA, partial cds
5253	17816	30239	3.16	1.0E-100	5032104	NT	Homo sapiens follicle stimulating hormone receptor (FSHR) mRNA
5253	17816	30240	3.16	1.0E-100	5032104	NT	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5493	18127	30535	1.55	1.0E-100	BF244218.1	EST_HUMAN	Homo sapiens small optic lobes (Drosophila) homolog (SOLH) mRNA
5699	18325	30828	0.87	1.0E-100	AW075983.1	EST_HUMAN	601863164F1 NIH_MGC 57 Homo sapiens cDNA clone IMAGE:4080989 5'
5879	18501	31227	1.93	1.0E-100	AU118182.1	EST_HUMAN	x88201.x1 NCL CGAP_CML1 Homo sapiens cDNA clone IMAGE:2573305 3' similar to gb:X12433
5920	18542	31268	1.36	1.0E-100	AF135116.1	NT	PROTEIN PHPS1-2 (HUMAN);
6003	18623	31358	10.01	1.0E-100	X14690.1	NT	AU118182 HEMBA1 Homo sapiens cDNA clone HEMBA1003046 5'
6311	18918	31692	1.06	1.0E-100	4557568	NT	Homo sapiens NF-E2-related factor 3 gene, complete cds
6311	18918	31693	1.06	1.0E-100	4557568	NT	Human mRNA for plasma inter-alpha-trypsin inhibitor heavy chain H(3)
6566	19164		1.29	1.0E-100	5729867	NT	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6623	19220	32025	5.02	1.0E-100	AU140214.1	EST_HUMAN	Homo sapiens ER to nucleus signalling 1 (ERN1) mRNA
6787	19378	32193	1.46	1.0E-100	R10887.1	EST_HUMAN	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
6868	19600	32431	2.42	1.0E-100	7382479	NT	AU140214 PLACE2 Homo sapiens cDNA clone PLACE2000137 5'
							Y38008.s1 Scores fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:129134 3'
							Homo sapiens Rho GTPase activating protein 6 (ARHGAP6), transcript variant 4, mRNA

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6829	19588	32417	1.2	1.0E-100	AA498841.1	EST_HUMAN	es33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6929	19588	32418	1.2	1.0E-100	AA498841.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
6966	19543	32366	1.25	1.0E-100	BF378478.1	EST_HUMAN	es33b06.r1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897587 5' similar to TR:G487418
6966	19543	32367	1.25	1.0E-100	BF378478.1	EST_HUMAN	G487418 ACTIN FILAMENT-ASSOCIATED PROTEIN. ;
6974	19550	32375	8.47	1.0E-100	X04571.1	NT	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8469	21009	33928	12.09	1.0E-100	BF103853.1	EST_HUMAN	MR1-TN0046-060900-004-b05 TN0046 Homo sapiens cDNA
8503	21042		4.61	1.0E-100	AL163203.2	NT	Human mRNA for kidney epidermal growth factor (EGF) precursor
8944	21482	34404	0.67	1.0E-100	AU116951.1	EST_HUMAN	601647357F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:3031310 5'
8944	21482	34405	0.67	1.0E-100	AU116951.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C003
9159	21694	34638	3.35	1.0E-100	AB040918.1	NT	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9234	21956		1.98	1.0E-100	A1972388.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9354	20293	33192	1.65	1.0E-100	AW998611.1	EST_HUMAN	AU116951 HEMBA1 Homo sapiens cDNA clone HEMBA1000343 5'
9407	21916		1.74	1.0E-100	AU127720.1	EST_HUMAN	Homo sapiens mRNA for KIAA1485 protein, partial cds
9504	22004	34961	2.84	1.0E-100	AB046846.1	NT	wr37g09.x1 NCI CGAP_P128 Homo sapiens cDNA clone IMAGE:2499920 3' similar to contains element
9504	22004	34962	2.84	1.0E-100	AB046846.1	NT	MER22 repetitive element ;
9757	22255	35237	1.81	1.0E-100	AW630487.1	EST_HUMAN	PMO-BN0065-100300-001-c08 BN0065 Homo sapiens cDNA
9757	22255	35238	1.81	1.0E-100	AW630487.1	EST_HUMAN	AU127720 NT2RP2 Homo sapiens cDNA clone NT2RP2001918 5'
9817	22413	35388	0.5	1.0E-100	AV732101.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
10366	22860	35853	1.46	1.0E-100	BF347519.1	EST_HUMAN	Homo sapiens mRNA for KIAA1626 protein, partial cds
10452	22945		1.38	1.0E-100	Y10391.1	NT	h83c11.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
10638	23170	36181	7.35	1.0E-100	BF327292.1	EST_HUMAN	h83c11.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969396 5'
11166	23673	36719	2.59	1.0E-100	X94633.1	NT	AV732101 HTF Homo sapiens cDNA clone HTFBIG01 5'
11166	23673	36720	2.59	1.0E-100	X94633.1	NT	602020554F1 NCI CGAP_Bn67 Homo sapiens cDNA clone IMAGE:4156165 5'
11232	23763	36818	4.28	1.0E-100	AF111170.3	NT	Human endogenous retrovirus HERV-K, psi gene
11232	23763	36819	4.28	1.0E-100	AF111170.3	NT	MRO-BN0070-270300-008-h11 BN0070 Homo sapiens cDNA
11261	12682	25138	2.14	1.0E-100	AL163247.2	NT	H. sapiens CD97 gene exon 4
11529	23977		1.65	1.0E-100	AF266285.1	NT	H. sapiens CD97 gene exon 4
11883	24100	37150	9.41	1.0E-100	AF240788.1	NT	H. sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
12000	24306	30990	2.92	1.0E-100	11545732	NT	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
12842	24717	30868	3.53	1.0E-100	11417974	NT	Homo sapiens chromosome 21 segment HS21C047
							Homo sapiens golgin-like protein (GLP) gene, complete cds
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
							Homo sapiens SH3-domain binding protein 1 (SH3BP1), mRNA
							Homo sapiens transcobalamin II; macrocytic anemia (TCN2), mRNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
81	12758	25240	2.04	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
81	12758	25241	2.04	1.0E-101	7110714	NT	Homo sapiens SEC14 (S. cerevisiae)-like 2 (SEC14L2), mRNA
715	13336	25822	1.77	1.0E-101	AB007815.2	NT	Homo sapiens mRNA for KIAA0446 protein, partial cds
733	13353	25848	5.29	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
733	13353	25849	5.29	1.0E-101	7110734	NT	Homo sapiens ventral anterior homeobox 2 (VAX2), mRNA
803	13420	25825	3.37	1.0E-101	7657454	NT	Homo sapiens pascadillo (zabrafish) homolog 1, containing BRCT domain (PES1), mRNA
886	13500	26018	1.96	1.0E-101	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, (GART) mRNA
981	13572	26089	0.88	1.0E-101	Z20656.1	NT	Homo sapiens of cardiac alpha-myosin heavy chain gene
1022	13632	26149	24.99	1.0E-101	BF681218.1	EST_HUMAN	602156474F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4287291 5'
1090	13695	26204	1.58	1.0E-101	A1221878.1	EST_HUMAN	999909.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
1782	14372	26917	0.9	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1782	14372	26918	0.9	1.0E-101	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1988	14570	27132	1.54	1.0E-101	4502896	NT	Homo sapiens carboxypeptidase A1 (pancreatic) (CPA1) mRNA
2101	14890	27248	1.93	1.0E-101	BE843070.1	EST_HUMAN	RC9-ST0281-100600-016-h09 ST0281 Homo sapiens cDNA
2388	15465	27528	1.24	1.0E-101	5728892	NT	Homo sapiens A kinase (PRKA) anchor protein 6 (AKAP6), mRNA
2846	15206	27778	10.93	1.0E-101	X72988.1	NT	H. sapiens EWS gene, exon 5
2771	15324	27891	2.71	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2771	15324	27892	2.71	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
2982	15508		10.39	1.0E-101	AJ252312.1	NT	Homo sapiens genomic downstream Rhesus box
3237	15849	28330	2.92	1.0E-101	4885270	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1) mRNA
3278	15889		2.37	1.0E-101	BF035327.1	EST_HUMAN	601458531F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862086 5'
3427	16036	28515	1.94	1.0E-101	AW965556.1	EST_HUMAN	EST377629 MAGI resequences, MAGI Homo sapiens cDNA
3447	15324	27891	2.93	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3447	15324	27892	2.93	1.0E-101	AJ237744.1	NT	Homo sapiens RIBLIR gene (partial), exon 12
3945	16543	29010	4.29	1.0E-101	AB022785.1	NT	Homo sapiens ASH2L gene, complete cds, similar to Drosophila ash2 gene
5185	17750	30180	1.38	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5185	17750	30181	1.38	1.0E-101	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
5521	18153	30587	1.26	1.0E-101	AW965139.1	EST_HUMAN	EST3777212 MAGI resequences, MAGI Homo sapiens cDNA
6154	18767	31530	3.48	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6154	18767	31531	3.48	1.0E-101	7427512	NT	Homo sapiens cytoplasmic linker 2 (CYLN2), mRNA
6766	19387	32203	1.06	1.0E-101	11430734	NT	Homo sapiens carbonic anhydrase VII (CA7), mRNA
7317	19844		1.18	1.0E-101	11545780	NT	Homo sapiens hypothetical protein FLJ22087 (FLJ22087), mRNA
7361	19887	32749	4.87	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEO3) mRNA, alternative splice form 4, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7361	19887	32750	4.87	1.0E-101	AF208970.1	NT	Homo sapiens Kruppel-type zinc finger protein (PEG3) mRNA, alternative splice form 4, partial cds
7491	20014	32880	11.99	1.0E-101	AW008475.1	EST_HUMAN	w55f12.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2533487 3'
7576	20092		1.86	1.0E-101	BE257384.1	EST_HUMAN	601109217F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349301 5'
7707	20216	33104	7.87	1.0E-101	BF330759.1	EST_HUMAN	RC1-BT0313-220700-018-112 BT0313 Homo sapiens cDNA
7854	20396	33301	0.98	1.0E-101	BE275821.1	EST_HUMAN	601121821F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
7854	20396	33302	0.98	1.0E-101	BE275821.1	EST_HUMAN	601121821F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3345869 5'
7989	20541	33443	6.69	1.0E-101	BF029174.1	EST_HUMAN	601764886F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3998837 5'
8264	20805	33722	0.66	1.0E-101	AW630070.1	EST_HUMAN	h174g10.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8264	20805	33723	0.66	1.0E-101	AW630070.1	EST_HUMAN	h174g10.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2968578 5' similar to gb:J03143 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (HUMAN);
8940	21478	34399	1.55	1.0E-101	AA036800.1	EST_HUMAN	zk29g08.r1 Soares_pregnant_uterus_NHPU Homo sapiens cDNA clone IMAGE:471998 5' similar to PIR:S54840 S54840 YD9335.03c protein - yeast;
9253	21779	34730	0.8	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1951 protein, partial cds
9253	21779	34731	0.8	1.0E-101	AB037772.1	NT	Homo sapiens mRNA for KIAA1951 protein, partial cds
9383	20321	33225	17.2	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9383	20321	33226	17.2	1.0E-101	X60069.1	NT	Human mRNA for pancreatic gamma-glutamyltransferase
9396	21819	34769	16.05	1.0E-101	8845492	NT	Homo sapiens gamma-glutamyltransferase 1 (GGT1), transcript variant 3, mRNA
9672	22171	35146	12.54	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9872	22171	35147	12.54	1.0E-101	BE619687.1	EST_HUMAN	601472808T1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3875953 3'
9808	22306	35280	0.65	1.0E-101	10863960	NT	Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA
10308	22802	35784	1.71	1.0E-101	11428127	NT	Homo sapiens Janus kinase 2 (a protein tyrosine kinase) (JAK2), mRNA
10337	22831	35825	5.16	1.0E-101	AI570293.1	EST_HUMAN	to77d11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326
10337	22831	35826	5.16	1.0E-101	AI570293.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10442	22836	35945	0.85	1.0E-101	BE973648.1	EST_HUMAN	to77d11.x1 NCI CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2184309 3' similar to gb:M26326
10442	22836	35946	0.85	1.0E-101	BE973648.1	EST_HUMAN	KERATIN, TYPE I CYTOSKELETAL 18 (HUMAN);
10757	23281	36295	1.63	1.0E-101	S38327.1	NT	601680825F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950887 5'
10988	23502	36532	1.68	1.0E-101	AB020626.1	NT	branched-chain alpha-keto acid dehydrogenase complex E1 alpha subunit [human, Genomic, 195 nt, segment 8 of 9]
11620	24062	37126	18.03	1.0E-101	AA321316.1	EST_HUMAN	Homo sapiens mRNA for KIAA0818 protein, partial cds
12274	24478		15.99	1.0E-101	AW639051.1	EST_HUMAN	EST23783 Bone marrow Homo sapiens cDNA 5' end similar to defensin 1
43	12722	25183	0.8	1.0E-102	AF012872.1	NT	QV1-DT0088-240200-085-a01 DT0068 Homo sapiens cDNA Homo sapiens phosphatidylinositol 4-kinase 230 (p14K230) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
363	13012	25494	4.36	1.0E-102	AL163303.2	NT	Homo sapiens chromosome 21 segment HS21C103
648	13271	25749	1.2	1.0E-102	BE252470.1	EST_HUMAN	601108282F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3344328 5'
807	13424	25930	1.24	1.0E-102	4557534	NT	Homo sapiens down-regulated in adenoma (DRA) mRNA
1156	13759	26269	5.76	1.0E-102	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
1311	13905	26424	3.09	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1311	13905	26425	3.09	1.0E-102	11437146	NT	Homo sapiens solute carrier family 2 (facilitated glucose transporter), member 9 (SLC2A9), mRNA
1327	13921	26442	1.92	1.0E-102	4826977	NT	Homo sapiens reelin (RELN) mRNA
1404	14056	26569	164.12	1.0E-102	BE408447.1	EST_HUMAN	601289982F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3628901 5'
2348	14919	27493	1.34	1.0E-102	AI124668.1	EST_HUMAN	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to
2348	14919	27494	1.34	1.0E-102	AI124668.1	EST_HUMAN	SW:GG95_HUMAN Q08379 GOLGIN-95 ;
3101	15716	28187	1.56	1.0E-102	7661979	NT	am60c10.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539954 3' similar to
3167	15781	28251	4.07	1.0E-102	AU141005.1	EST_HUMAN	SW:GG95_HUMAN Q08379 GOLGIN-95 ;
3167	15781	28252	4.07	1.0E-102	AU141005.1	EST_HUMAN	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
4316	16802	29346	1.84	1.0E-102	AL163207.2	NT	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
4503	17087	29535	2.55	1.0E-102	BE251310.1	EST_HUMAN	AU141005 PLACE4 Homo sapiens cDNA clone PLACE4000650 5'
5287	17849	30275	1.19	1.0E-102	R68488.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C007
5574	18205	30656	1.66	1.0E-102	AF087133.1	NT	601107843F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3343882 5'
5923	18545	31313	4.52	1.0E-102	AB034951.1	NT	X32c04.f1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140934 5'
5957	18579	31314	2.43	1.0E-102	7705398	NT	Homo sapiens protein phosphatase-1 regulatory subunit 7 (PPP1R7) gene, exon 7
5957	18579	31314	2.43	1.0E-102	7705398	NT	Homo sapiens HSC54 mRNA for heat shock cognate protein 54, complete cds
5962	18584	31318	0.75	1.0E-102	11433046	NT	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
6435	19038	31825	2.89	1.0E-102	AI459825.1	EST_HUMAN	Homo sapiens histone deacetylase 7 (HDAC7), mRNA
7190	19722	32570	0.67	1.0E-102	BE728323.1	EST_HUMAN	Homo sapiens hct domain and RLD 2 (HERC2), mRNA
7217	19748	32604	0.93	1.0E-102	BE386106.1	EST_HUMAN	ar62f09.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2151785 3' similar to TR:Q13137
7392	19917	32781	7.37	1.0E-102	AJ238994.1	NT	Q13137 NDP52 ;
7620	20133	33070	2.75	1.0E-102	AV710738.1	EST_HUMAN	601561505F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3831241 5'
8185	20708	33622	3.41	1.0E-102	BE763051.1	EST_HUMAN	60127215F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618243 5'
8244	20785	33704	1.5	1.0E-102	BE910555.1	EST_HUMAN	Homo sapiens mRNA for Centaurin-alpha2 protein
8431	20971	33883	1.65	1.0E-102	AV694817.1	EST_HUMAN	AV710738 Cu Homo sapiens cDNA clone CuaAKD03 5'
8431	20971	33884	1.65	1.0E-102	AV694817.1	EST_HUMAN	QV3-NT0025-210600-236-108 NT0025 Homo sapiens cDNA
8539	21078	33997	0.52	1.0E-102	AB007923.1	NT	601501107F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903145 5'
							AV694817 GK Homo sapiens cDNA clone GKCEEE11 5'
							AV694817 GK Homo sapiens cDNA clone GKCEEE11 5'
							Homo sapiens mRNA for KIAA0454 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8861	21400	34324	0.75	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
8861	21400	34325	0.75	1.0E-102	BE388063.1	EST_HUMAN	601283770F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3605536 5'
9175	21752	34698	0.57	1.0E-102	AJ762859.1	EST_HUMAN	wf63b06.x1 NCL CGAP_K1c12 Homo sapiens cDNA clone IMAGE:239797.1 3' similar to contains MER4.11
9205	21722	34666	0.76	1.0E-102	AV755842.1	EST_HUMAN	MER4 MER4 repetitive element
9245	21771	34719	2.15	1.0E-102	T70393.1	EST_HUMAN	AV755842 BM Homo sapiens cDNA clone BMFAUD08 5'
9245	21771	34720	2.15	1.0E-102	T70393.1	EST_HUMAN	Yd13407.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
9332	21848	34786	3.3	1.0E-102	AU124629.1	EST_HUMAN	Yd13407.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:67021 5'
10284	22779		0.54	1.0E-102	AF153715.1	NT	AU124629 NT2RM4 Homo sapiens cDNA clone NT2RM4000309 5'
10365	22859	35851	3.54	1.0E-102	AI805037.1	EST_HUMAN	Homo sapiens phospholipid scramblase 1 gene, exon 1 and 5' flanking region
10365	22859	35852	3.54	1.0E-102	AI805037.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10422	22916	35918	1.58	1.0E-102	AA970788.1	EST_HUMAN	RC-BT074-260499-014 BT074 Homo sapiens cDNA
10949	23464	36486	1.83	1.0E-102	BE867468.1	EST_HUMAN	on57h04.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1560823 3' similar to SW:CAV2_HUMAN P51636 CAVEOLIN-2 [11]
10952	23467	36490	6.26	1.0E-102	4507822	NT	601439392F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924166 5'
10952	23467	36491	6.26	1.0E-102	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11200	23705	36756	1.54	1.0E-102	AA868675.1	EST_HUMAN	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11282	23735	36790	3.6	1.0E-102	BF359243.1	EST_HUMAN	ak49h10.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409347 3'
11555	24003	37076	3.66	1.0E-102	U41302.1	NT	RC8-ET0072-150600-011-F01 ET0072 Homo sapiens cDNA
11689	24105		8.01	1.0E-102	AL163280.2	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
12261	24471	30831	6.87	1.0E-102	AW300862.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C080
12588	24681		1.79	1.0E-102	J05235.1	NT	xx07c12.x1 NCL CGAP_Co20 Homo sapiens cDNA clone IMAGE:2668038 3'
73	12751	25229	2.49	1.0E-103	BE908158.1	EST_HUMAN	Human gamma-glutamyl transpeptidase mRNA, complete cds
73	12751	25230	2.49	1.0E-103	BE908158.1	EST_HUMAN	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
104	12780	25262	8.29	1.0E-103	D87078.2	NT	601500405F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902305 5'
222	12883	26368	2.74	1.0E-103	5453793	NT	Homo sapiens mRNA for KIAA0235 protein, partial cds
1017	13627	26140	0.82	1.0E-103	AJ278348.1	NT	Homo sapiens nucleolar protein (KKE/D repeat) (NOP56) mRNA
1286	13681	28406	10.5	1.0E-103	BE877541.1	EST_HUMAN	Homo sapiens mRNA for pregnancy-associated plasma protein-E (PAPPE gene)
1640	14232	28766	2.29	1.0E-103	AF012872.1	NT	601495398F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887876 5'
2018	14600	27163	1.43	1.0E-103	4502428	NT	Homo sapiens phosphatidylinositol 4-kinase 230 (p4K230) mRNA, complete cds
2018	14600	27164	1.43	1.0E-103	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2343	14914	27488	1	1.0E-103	AU134991.1	EST_HUMAN	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2494	15058	27632	1.88	1.0E-103	AF060568.1	NT	AU134991 PLAGE1 Homo sapiens cDNA clone PLACE1000965 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2631	15192	27762	1.54	1.0E-103	BF529378.1	EST_HUMAN	602041882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179429 5'
2631	15192	27763	1.54	1.0E-103	BF529379.1	EST_HUMAN	602041882F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179429 5'
3105	15720		2.9	1.0E-103	BE744722.1	EST_HUMAN	601573113F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3894315 5'
3428	16034	28514	3.71	1.0E-103	AW298245.1	EST_HUMAN	U1-H-BWO-ajh-11-Q-U1 s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2733165 3'
3487	16092	28564	1.19	1.0E-103	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
3818	16418		6.77	1.0E-103	AF023861.1	NT	Macaca mulatta cyclophilin A mRNA, complete cds
3861	16459	28923	1.17	1.0E-103	AA485663.1	EST_HUMAN	ab100112.s1 Stratagene lung (#837210) Homo sapiens cDNA clone IMAGE:840407 3' similar to contains element LTR10 repetitive element:
4075	16671	29132	3.62	1.0E-103	T23683.1	EST_HUMAN	seq3-40 b4HB3MA-Cot109+10-Bio Homo sapiens cDNA clone b4HB3MA-Cot109+10-Bio-7 3'
4946	17521	29683	0.88	1.0E-103	BE000203.1	EST_HUMAN	601873135F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3955953 5'
6091	18707	31455	0.73	1.0E-103	BF569527.1	EST_HUMAN	602186023F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310573 5'
6097	18713	31463	1.8	1.0E-103	AF179995.1	NT	Homo sapiens septin 2 (SEP2) mRNA, partial cds
6413	19016	31788	0.71	1.0E-103	11435033	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6413	19018	31789	0.71	1.0E-103	11435033	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
6587	19184	31885	0.76	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6587	19184	31986	0.78	1.0E-103	AW954566.1	EST_HUMAN	EST366636 MAGC resequences, MAGC Homo sapiens cDNA
6707	24767	32106	1.16	1.0E-103	AA781442.1	EST_HUMAN	aj26e03.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391452 3'
6743	19337	32142	0.86	1.0E-103	AF053490.1	NT	Homo sapiens glycine receptor alpha 2 subunit (GLRA2) gene, exon 4
6819	19409	32227	1.89	1.0E-103	AI590071.1	EST_HUMAN	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6819	19409	32228	1.89	1.0E-103	AI590071.1	EST_HUMAN	Q13769 ANONYMOUS ;
6833	18041	30484	1.67	1.0E-103	5032282	NT	tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
6833	18041	30485	1.67	1.0E-103	5032282	NT	Q13769 ANONYMOUS ;
7047	18067	30457	1.07	1.0E-103	11431100	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7101	19871	32510	1.13	1.0E-103	AJ289880.1	NT	Homo sapiens dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272 (DMD), transcript variant Dp427m, mRNA
7278	18806	32665	1.34	1.0E-103	AW965776.1	EST_HUMAN	Homo sapiens ribosomal protein L3-like (RPL3L), mRNA
7372	19898	32759	3.36	1.0E-103	BE748158.1	EST_HUMAN	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
7749	20257	33152	4.44	1.0E-103	AI590071.1	EST_HUMAN	EST377849 MAGC resequences, MAGC Homo sapiens cDNA
							601571537F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3838545 5'
							tm58b05.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
							Q13769 ANONYMOUS ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7749	20257	33153	4.44	1.0E-103	AI590071.1	EST_HUMAN	Im58b05.x1 NCI CGAP_Brm25 Homo sapiens cDNA clone IMAGE:2162289 3' similar to TR:Q13769
8556	21095	34015	1.14	1.0E-103	AU140344.1	EST_HUMAN	Q13769 ANONYMOUS. ;
8556	21095	34016	1.14	1.0E-103	AU140344.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
8637	21176	34095	1.13	1.0E-103	BF109244.1	EST_HUMAN	AU140344 PLACE2 Homo sapiens cDNA clone PLACE2000374 5'
9036	21573	34502	2.82	1.0E-103	6005921	NT	7160e03.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3525964 3' similar to SW:PTNF_HUMAN Q16825 PROTEIN-TYROSINE PHOSPHATASE D1 ;
9036	21573	34503	2.82	1.0E-103	6005921	NT	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9075	21612	34544	1.08	1.0E-103	AA581086.1	EST_HUMAN	Homo sapiens triple functional domain (PTPRF interacting) (TRIO), mRNA
9117	21653	34584	1.29	1.0E-103	AA774980.1	EST_HUMAN	nd13c02.s1 NCI CGAP_Ov1 Homo sapiens cDNA clone IMAGE:800162 3' similar to gb:L02426 26S
9870	22465	35449	1.55	1.0E-103	Z37876.1	NT	PROTEASE SUBUNIT 4 (HUMAN);
10011	22506	35497	1.64	1.0E-103	AW963678.1	EST_HUMAN	ae94412.s1 Stralagene schizo brain S11 Homo sapiens cDNA clone IMAGE:970871 3' similar to gb:X03747_cds1 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 (HUMAN);
10137	22632	35621	9.08	1.0E-103	AI878956.1	EST_HUMAN	H sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2)
10521	23059	36089	2.78	1.0E-103	BE549706.1	EST_HUMAN	EST1375749 MAGe resequences, MAGH Homo sapiens cDNA
10612	23145	36156	3.46	1.0E-103	AI792759.1	EST_HUMAN	au51g04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518326 5' similar to TR:O15046 O15048 KIAA0338 ;
10713	23241	36257	2.21	1.0E-103	11424061	NT	7b41f03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3230813 3' similar to gb:M69043 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN (HUMAN);
10713	23241	36258	2.21	1.0E-103	11424061	NT	d02d06.y6 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1522283 5' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING ;
10724	23251	36266	3.66	1.0E-103	AF149773.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
10724	23251	36267	3.66	1.0E-103	AF149773.1	NT	Homo sapiens AXL receptor tyrosine kinase (AXL), mRNA
11253	23783	36639	2.51	1.0E-103	AU136283.1	EST_HUMAN	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11320	23018	36027	5.36	1.0E-103	L43610.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
11590	24033	37103	4.36	1.0E-103	BE644611.1	EST_HUMAN	AU136283 PLACE1 Homo sapiens cDNA clone PLACE1003923 5'
11684	24101		2.23	1.0E-103	AF224669.1	NT	Homo sapiens polycystic kidney disease (PKD1) gene, exons 27-30
11717	24126		1.91	1.0E-103	11526291	NT	7e68a10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3287610 3' similar to contains MER29.13 MER29 repetitive element ;
11916	24254	31010	2.99	1.0E-103	AB011399.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
254	12914	25398	4.81	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens hypothetical protein FLJ20454 (FLJ20454), mRNA
254	12914	25399	4.81	1.0E-104	AL037549.3	EST_HUMAN	Homo sapiens gene for AF-6, complete cds
254	12914	25399	4.81	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564H1072 5'
254	12914	25399	4.81	1.0E-104	AL037549.3	EST_HUMAN	DKFZp564H1072_r1 564 (synonym: hfb2) Homo sapiens cDNA clone DKFZp564H1072 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1932	14516	27072	2.06	1.0E-104	4502428	NT	Homo sapiens bone morphogenetic protein 8 (osteogenic protein 2) (BMP8) mRNA
2235	14810	27382	2.22	1.0E-104	AA132975.1	EST_HUMAN	z022c06.s1 Strategene colon (#837204) Homo sapiens cDNA clone IMAGE:587626 3' similar to gb:Z14116.ma1 CD59 GLYCOPROTEIN PRECURSOR (HUMAN);
2245	14819	27394	1.47	1.0E-104	BE744628.1	EST_HUMAN	601577480F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926438 5'
2407	14875	27548	0.89	1.0E-104	BF334422.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2407	14875	27549	0.89	1.0E-104	BF334422.1	EST_HUMAN	RC1-CT0249-110900-214-112 CT0249 Homo sapiens cDNA
2481	15047	27816	1.28	1.0E-104	5031670	NT	Homo sapiens ARP2 (actin-related protein 2, yeast) homolog (AC:TR2), mRNA
2896	15513	27883	8.17	1.0E-104	M34071.1	NT	Human lymphocytic antigen CD59/MEM43 mRNA, complete cds
2941	15557		3.21	1.0E-104	Y11151.1	NT	H. sapiens gene encoding phenylpyruvate tautomerase II
3438	16046		1.77	1.0E-104	AA319436.1	EST_HUMAN	EST21658 Adrenal gland tumor Homo sapiens cDNA 5' end
3661	16263	28735	0.63	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3661	16263	28736	0.63	1.0E-104	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
4015	16613	29086	1.2	1.0E-104	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
4210	16799	29248	0.62	1.0E-104	F11745.1	EST_HUMAN	HSC3A071 normalized infant brain cDNA Homo sapiens cDNA clone c-31a07
4466	17052	29496	6.67	1.0E-104	X02761.1	NT	Human mRNA for fibronectin (FN precursor)
4715	17296	29740	1.28	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
4715	17296	29741	1.28	1.0E-104	AF231920.1	NT	Homo sapiens chromosome 21 unknown mRNA
5330	17891	30305	1.84	1.0E-104	4502152	NT	Homo sapiens apolipoprotein B (including Ag(x) antigen) (APOB) mRNA
6095	18711	31459	1.18	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6095	18711	31460	1.18	1.0E-104	U43379.1	NT	Human Down Syndrome region of chromosome 21 DNA
6139	18753	31511	0.98	1.0E-104	AB017332.1	NT	Homo sapiens alk3 mRNA for Aurora/pl1-related kinase 3, complete cds
6593	19180	31963	8.25	1.0E-104	AI768797.1	EST_HUMAN	w03b12.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2401727 3' similar to TR:Q14145 Q14145 KIAA0132 PROTEIN; contains element LTR7 repetitive element;
6593	19180	31964	8.25	1.0E-104	AI768797.1	EST_HUMAN	KIAA0132 PROTEIN; contains element LTR7 repetitive element;
6756	19349	32158	1.07	1.0E-104	7706512	NT	Homo sapiens PDZ domain-containing guanine nucleotide exchange factor 1 (LOC51735), mRNA
6895	19629	32465	1.48	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
6895	19629	32466	1.48	1.0E-104	BE314182.1	EST_HUMAN	601150451F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503220 5'
7276	19804	32863	2.22	1.0E-104	11425572	NT	Homo sapiens adaptor-related protein complex 2, beta 1 subunit (AP2B1), mRNA
8533	21072	33992	0.71	1.0E-104	BF509244.1	EST_HUMAN	UI-H-B14-aaw-b-09-0-U1.s1 NCI_CGAP_Sub08 Homo sapiens cDNA clone IMAGE:3086176 3'
9094	21630	34568	2.59	1.0E-104	BF448230.1	EST_HUMAN	mad16g11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365948 3'
9187	21704	34646	0.6	1.0E-104	AA882308.1	EST_HUMAN	z988008.s1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:462897 3'
9208	21725		1.62	1.0E-104	T74219.1	EST_HUMAN	yc83f02.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:22440 5'
9238	21784	34710	4.74	1.0E-104	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9238	21764	34711	4.74	1.0E-104	AF091395.1	NT	Homo sapiens Tiro isoform mRNA, complete cds
9362	20301	33201	4.6	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9362	20301	33202	4.6	1.0E-104	BF352841.1	EST_HUMAN	IL3-HT0619-080900-249-F07 HT0619 Homo sapiens cDNA
9668	22167	35142	0.69	1.0E-104	AW103848.1	EST_HUMAN	xd78d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9668	22167	35143	0.69	1.0E-104	AW103848.1	EST_HUMAN	xd78d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2603523 3' similar to TR:Q24116
9858	22355	35338	0.84	1.0E-104	AF113514.1	NT	Q24116 HYPOTHETICAL 29.4 KD PROTEIN ;
10005	22500	35490	3.86	1.0E-104	BE791713.1	EST_HUMAN	Homo sapiens histone acetyltransferase MORF mRNA, complete cds
10005	22500	35491	3.86	1.0E-104	BE791713.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10299	22793	35783	1.05	1.0E-104	AV728070.1	EST_HUMAN	601581503F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3935977 5'
10338	22832	35827	4.98	1.0E-104	AU130765.1	EST_HUMAN	AV728070 HTC Homo sapiens cDNA clone HTCBYA07 5'
10445	22839	35949	3.04	1.0E-104	U66535.1	NT	AU130765 NT2RP3 Homo sapiens cDNA clone NT2RP3001398 5'
10457	22951		1.04	1.0E-104	11427757	NT	Human beta4-integrin (ITGB4) gene, exons 19, 20, 21, 22, 23, 24 and 25
11176	23683	36728	2.44	1.0E-104	BE720191.1	EST_HUMAN	Homo sapiens KIAA0849 gene product (KIAA0849), mRNA
11176	23683	36728	2.44	1.0E-104	BE720191.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
11208	23712	36766	5.34	1.0E-104	BF694288.1	EST_HUMAN	RC0-HT0885-310700-021-b09 HT0885 Homo sapiens cDNA
12538	24848		2.96	1.0E-104	BE393892.1	EST_HUMAN	602141215F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302507 5'
300	15384	25445	2.78	1.0E-105	4502168	NT	601312181F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3658676 5'
450	12679	25135	15.84	1.0E-105	4505150	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
620	13247	25720	5.78	1.0E-105	AF032897.1	NT	Homo sapiens Meis1 (mouse) homolog (MEIS1) mRNA
620	13247	25721	5.78	1.0E-105	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1719	14311		1.84	1.0E-105	AB020981.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
1859	14447	27004	1.35	1.0E-105	AL163280.2	NT	Homo sapiens mRNA for cyclin B2, complete cds
1970	14554	27110	1.24	1.0E-105	D50918.1	NT	Homo sapiens chromosome 21 segment HS21C080
2231	14806	27379	1.36	1.0E-105	AA318369.1	EST_HUMAN	Human mRNA for KIAA0128 gene, partial cds
2747	15302		1.43	1.0E-105	AA584808.1	EST_HUMAN	EST20609 Spleen I Homo sapiens cDNA 5' end similar to autimmune antigen Ku, p70/p80 subunit
3039	15655		3.35	1.0E-105	AJ228041.1	NT	no10d05.s1 NCL CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100265 3'
3394	16002	28482	0.72	1.0E-105	7304922	NT	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
3394	16002	28483	0.72	1.0E-105	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4173	16764	29212	2.65	1.0E-105	AW961688.1	EST_HUMAN	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4853	17431	29891	0.65	1.0E-105	BE868981.1	EST_HUMAN	EST373761 MAGE resequences, MAGG Homo sapiens cDNA
4853	17431	29892	0.65	1.0E-105	BE868981.1	EST_HUMAN	EST373761 MAGE resequences, MAGG Homo sapiens cDNA
4853	17431	29892	0.65	1.0E-105	BE868981.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'
4853	17431	29892	0.65	1.0E-105	BE868981.1	EST_HUMAN	601445823F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850156 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4874	17449	29900	1.06	1.0E-105	AA699335.1	EST_HUMAN	z44g02.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:433682 3'
5073	17648		4.94	1.0E-105	AL163208.2	NT	Homo sapiens chromosome 21 segment HS21C008
5533	18165	30579	0.97	1.0E-105	AF016704.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 2
5594	18224		1.12	1.0E-105	11420134	NT	Homo sapiens Retine-derived POU-domain factor-1 (RPF-1), mRNA
6985	19483	32303	1.68	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
6985	19483	32304	1.68	1.0E-105	BF314302.1	EST_HUMAN	601901028F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130334 5'
7058	18077	30430	3.65	1.0E-105	11418198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7058	18077	30431	3.65	1.0E-105	11418198	NT	Homo sapiens GTPase activating protein-like (GAPL), mRNA
7328	19655	32718	1.09	1.0E-105	BE902616.1	EST_HUMAN	601677279F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960019 5'
7800	20343	33252	0.87	1.0E-105	X12566.1	NT	Human mRNA for dcl proto-oncogene
7971	20513	33420	5.86	1.0E-105	T05087.1	EST_HUMAN	EST02975 Fetal brain, Strategene (cat#936206) Homo sapiens cDNA clone HFBGR32
8337	20878	33789	1.43	1.0E-105	AW007194.1	EST_HUMAN	ws50c10.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2500628 3' similar to SW:ACSA_PENCH P36333 ACETYL-COENZYME A SYNTHETASE ;
8858	21397	34320	0.75	1.0E-105	AW840817.1	EST_HUMAN	RC1-CN0008-070100-011-005 CN0008 Homo sapiens cDNA
8980	21518	34444	2.92	1.0E-105	AW016878.1	EST_HUMAN	UI-H-B10p-abt-b-12-0-U1.s1 NCI_CGAP_Sub2 Homo sapiens cDNA clone IMAGE:2711782 3'
9131	21668	34606	0.87	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-409 OT0062 Homo sapiens cDNA
9131	21668	34607	0.87	1.0E-105	AW882372.1	EST_HUMAN	QV2-OT0062-140300-083-409 OT0062 Homo sapiens cDNA
9487	21944	34891	1.07	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
9487	21944	34892	1.07	1.0E-105	BE867793.1	EST_HUMAN	601443755F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847884 5'
10812	23334	36347	6.07	1.0E-105	AF254822.1	NT	Homo sapiens SMARCA4 isoform (SMARCA4) gene, complete cds, alternatively spliced
11109	23619	36660	2.15	1.0E-105	D63548.1	NT	Homo sapiens COL4A6 gene for a6(IV) collagen, exon 31
11161	23668	36713	2.07	1.0E-105	7705936	NT	Homo sapiens Ran binding protein 11 (LOC51194), mRNA
11457	23907	36974	2.56	1.0E-105	AW027554.1	EST_HUMAN	p87892 PROTEASE ;
11524	23972	37042	1.82	1.0E-105	BF430921.1	EST_HUMAN	7018c10.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3574291 3' similar to TR:P97680 P97680
13	12692	25148	2.28	1.0E-106	AI804463.1	EST_HUMAN	RIN1 ;
162	12825		1.55	1.0E-106	AW503208.1	EST_HUMAN	IL-BT057-281198-001 BT057 Homo sapiens cDNA
219	12880	25366	1.75	1.0E-106	AI865065.1	EST_HUMAN	UI-HF-BNO-akt-g-07-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078348 5'
567	13188	25678	1.82	1.0E-106	AW965556.1	EST_HUMAN	tg78c01.x1 NCI_CGAP_U1r1 Homo sapiens cDNA clone IMAGE:2215008 3'
633	13258	25733	2.3	1.0E-106	J00146.1	NT	EST377629 MAGE resequences, MAGE Homo sapiens cDNA
634	13258	25733	3.03	1.0E-106	J00146.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1572	14166	26698	1.57	1.0E-106	AF145712.1	NT	Human dihydrofolate reductase pseudogene (psi-hd1)
1739	14329	26873	4.72	1.0E-106	U48724.1	NT	Homo sapiens soluble neuropilin-1 mRNA, complete cds
							Human epidermal growth factor receptor (EGFR) precursor-mRNA, exon 4, partial cds

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1757	14347	26892	0.89	1.0E-106	U04510.1	NT	Homo sapiens type IV collagen alpha 5 chain (COL4A5) gene, exon 41
1839	14427	26978	5.32	1.0E-106	AA527446.1	EST_HUMAN	ng41c05.s1 NC1_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element
1839	14427	26979	5.32	1.0E-106	AA527446.1	EST_HUMAN	LTR3 repetitive element
2167	14744	27313	2.48	1.0E-106	BE144286.1	EST_HUMAN	ng41c05.s1 NC1_CGAP_Co3 Homo sapiens cDNA clone IMAGE:937352 3' similar to contains element
2358	14927	27501	3.35	1.0E-106	4504184	NT	LTR3 repetitive element
2636	15198	27769	1.49	1.0E-106	BE260201.1	EST_HUMAN	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
2788	15339	27910	0.69	1.0E-106	AI276526.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2852	14071	26609	1.52	1.0E-106	4504184	NT	q76h10.x1 Soares_NihMIPu_S1 Homo sapiens cDNA clone IMAGE:1878307 3'
2852	14071	26610	1.52	1.0E-106	4504184	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2859	15516	27985	0.98	1.0E-106	BE384296.1	EST_HUMAN	Homo sapiens glutathione S-transferase theta 1 (GSTT1), mRNA
2868	15583	28063	6.37	1.0E-106	AB037747.1	NT	601272875F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3613818 5'
2868	15583	28064	6.37	1.0E-106	AB037747.1	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3214	15826	28303	2.04	1.0E-106	8922965	NT	Homo sapiens mRNA for KIAA1326 protein, partial cds
3214	15826	28304	2.04	1.0E-106	8922965	NT	Homo sapiens hypothetical protein FLJ11273 (FLJ11273), mRNA
3420	16028	28509	0.72	1.0E-106	AB008681.1	NT	Homo sapiens gene for activin receptor type IIB, complete cds
3488	16093	28565	1.14	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
3488	16093	28566	1.14	1.0E-106	AB033104.1	NT	Homo sapiens mRNA for KIAA1278 protein, partial cds
4111	16705	29158	9.08	1.0E-106	AW974650.1	EST_HUMAN	Homo sapiens mRNA for KIAA1278 protein, partial cds
4111	16705	29159	9.08	1.0E-106	AW974650.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
4706	17288	29732	1.47	1.0E-106	BE144286.1	EST_HUMAN	EST386875 MAGE resequences, MAGN Homo sapiens cDNA
5438	17993	30399	8.5	1.0E-106	S67479.1	NT	MR0-HT0165-140200-008-d10 HT0165 Homo sapiens cDNA
5572	18203	30853	2.76	1.0E-106	AA781155.1	EST_HUMAN	(GC)IS-vitamin D-binding protein/group specific component [human, peripheral blood leukocytes, Genomic, 2128 nt, segment 5 of 9]
6017	18338	31375	0.87	1.0E-106	AU130113.1	EST_HUMAN	q24b09.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391225 3' similar to gb:X12433 PROTEIN
6017	18338	31376	0.87	1.0E-106	AU130113.1	EST_HUMAN	PHPS1-2 (HUMAN);
6145	18759	31517	0.82	1.0E-106	AU143428.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6145	18759	31518	0.82	1.0E-106	AU143428.1	EST_HUMAN	AU130113 NT2RP3 Homo sapiens cDNA clone NT2RP3000274 5'
6250	18859	31631	13.05	1.0E-106	BF878574.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6355	18960	31738	0.69	1.0E-106	BE897112.1	EST_HUMAN	AU143428 Y79AA1 Homo sapiens cDNA clone Y79AA1001912 5'
6551	19149	31945	19.14	1.0E-106	11545913	NT	602154012F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295087 5'
6551	19149	31946	19.14	1.0E-106	11545913	NT	601439670F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924841 5'
6551	19149	31946	19.14	1.0E-106	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA

Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit, BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7406	19931	32795	5.83	1.0E-106	AA663778.1	EST_HUMAN	sae72e07.s1 Sirelagene schain brain S11 Homo sapiens cDNA clone IMAGE:969732 3' similar to gb:X65873
7453	19977	32842	4.92	1.0E-106	11429817 NT	NT	KINESIN HEAVY CHAIN (HUMAN); Homo sapiens XPMC2 protein (LOC57109), mRNA
7514	20035	32901	1.23	1.0E-106	BE292722.1	EST_HUMAN	601105736F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988345 5'
7606	20119	32995	8.75	1.0E-106	11425503 NT	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7608	20119	32996	8.75	1.0E-106	11425503 NT	NT	Homo sapiens sorting nexin 11 (SNX11), mRNA
7769	20277	33176	0.72	1.0E-106	AW163047.1	EST_HUMAN	euf105.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783649 5' similar to TR:O75834
7926	20468	33376	5.97	1.0E-106	BE741408.1	EST_HUMAN	O75834 CULLIN-4A;
7926	20468	33377	5.97	1.0E-106	BE741408.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8115	20856	33565	13.85	1.0E-106	A1523068.1	EST_HUMAN	601594331F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948463 5'
8564	21103	34022	0.74	1.0E-106	BE387950.1	EST_HUMAN	aif88a07.x1 Barstead aorta HPLR86 Homo sapiens cDNA clone IMAGE:2127732 3' similar to gb:X068233
8564	21103	34023	0.74	1.0E-106	BE387950.1	EST_HUMAN	CALGRANULIN B (HUMAN);
8640	21179	34099	3.9	1.0E-106	A1654123.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8645	21184	34103	0.54	1.0E-106	A1654123.1	EST_HUMAN	601282717F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604493 5'
8982	21520	34448	0.56	1.0E-106	AW839831.1	EST_HUMAN	yvz2a05.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2283632 3' similar to SW:ICAB6_HUMAN
9074	21611	34542	2	1.0E-106	AA825307.1	EST_HUMAN	CO5084 69 KD ISLET CELL AUTOANTIGEN;
9074	21611	34543	2	1.0E-106	AA825307.1	EST_HUMAN	wu38c03.x1 Soares_Dieckgraefe_cdon_NHCD Homo sapiens cDNA clone IMAGE:2522308 3' similar to TR:O70273 O70273 ETS HOMOLOGOUS FACTOR ; QM4-LT0059-150200-098-c08 LT0059 Homo sapiens cDNA cc67ea08.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1354790 3' cc67ea08.s1 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1354790 3'
9210	21727	34670	2.03	1.0E-106	A1750447.1	EST_HUMAN	cn03a04.y1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NH7BC_cn03a04 random
9350	21864	34914	1.46	1.0E-106	A1479589.1	EST_HUMAN	tm41f02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13 TAR1 PTR5 repetitive element ; tm41f02.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2160699 3' similar to contains MSR1.13 TAR1 PTR5 repetitive element ; TAR1 PTR5 repetitive element ;
9350	21864	34915	1.48	1.0E-106	A1479589.1	EST_HUMAN	TAR1 PTR5 repetitive element ;
9913	22409	35385	1.35	1.0E-106	BF389234.1	EST_HUMAN	601282367F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604217 5'
9996	22481	35479	1.47	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
9996	22481	35480	1.47	1.0E-106	BF027310.1	EST_HUMAN	601671674F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954403 5'
10139	22634	35624	8.16	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10139	22634	35625	8.16	1.0E-106	AA604417.1	EST_HUMAN	np57b10.s1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1130395 3'
10185	22680	35672	1.56	1.0E-106	AW363299.1	EST_HUMAN	RCC-GT0318-201169-031-e11 G10318 Homo sapiens cDNA RCO-GT0318-201169-031-e11 G10318 Homo sapiens cDNA
10190	22865	35677	0.77	1.0E-106	11439432 NT	NT	Homo sapiens multimarin (MMRN), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10100	22885	35678	0.77	1.0E-106	11436432	NT	Homo sapiens multimerin (MMRN), mRNA
10358	22852	35846	0.45	1.0E-106	AL039886.1	EST_HUMAN	DKFZ434F0712_r1 434 (synonym: hts3) Homo sapiens cDNA clone DKFZ434F0712 5'
10472	22866	35976	3.31	1.0E-106	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
10775	23289	36304	6.85	1.0E-106	BF032755.1	EST_HUMAN	801453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
10775	23289	36305	6.85	1.0E-106	BF032755.1	EST_HUMAN	801453461F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857366 5'
10941	23457	36480	2.93	1.0E-106	JO5200.1	NT	Human ryanodine receptor mRNA, complete cds
10941	23457	36481	2.93	1.0E-106	JO5200.1	NT	Human ryanodine receptor mRNA, complete cds
11286	23739	36795	1.67	1.0E-106	BE257385.1	EST_HUMAN	601109219F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3349997 5'
11418	23869	36928	1.83	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11418	23869	36930	1.83	1.0E-106	BE010882.1	EST_HUMAN	RC5-BN0192-100500-021-B02 BN0192 Homo sapiens cDNA
11762	24867	30986	5.89	1.0E-106	AW410405.1	EST_HUMAN	fh05h11.x1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2861644 5'
11991	24301	30987	4.03	1.0E-106	BE69498.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
11991	24301	30987	4.03	1.0E-106	BE69498.1	EST_HUMAN	601433087F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918524 5'
12216	24439		3.44	1.0E-106	BE695905.1	EST_HUMAN	RC1-CT0249-090800-024-d05 CT0249 Homo sapiens cDNA
255	12915		2.78	1.0E-107	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
286	12942		1.25	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
658	13281	25761	1.82	1.0E-107	AF155103.1	NT	Homo sapiens NY-REN-25 antigen mRNA, partial cds
846	13462	25970	1.45	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
919	13532	26050	2.27	1.0E-107	X60459.1	NT	Human IFNAR gene for interferon alpha/beta receptor
1004	13615	26129	8.14	1.0E-107	AF154121.1	NT	Homo sapiens sodium-dependent high-affinity dicarboxylate transporter (NADC3) mRNA, complete cds
1321	13915	26437	1.33	1.0E-107	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1615	14208	26741	2.61	1.0E-107	BF087405.1	EST_HUMAN	QV2-HT0540-120900-358-a05 HT0540 Homo sapiens cDNA
1788	14378	26922	2.7	1.0E-107	AF136275.1	NT	Homo sapiens cathepsin Z precursor (CTS2) gene, exon 3
1880	14466	27023	0.89	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
1880	14466	27024	0.89	1.0E-107	AB007922.2	NT	Homo sapiens mRNA for KIAA0453 protein, partial cds
2249	14823	27399	1.17	1.0E-107	U13729.1	NT	Human dipeptidyl peptidase IV (CD26) gene, exon 20
2400	14968	27541	0.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CH0031-190100-001-d03 CH0031 Homo sapiens cDNA
2400	14968	27542	0.94	1.0E-107	AW842451.1	EST_HUMAN	PM1-CH0031-190100-001-d03 CH0031 Homo sapiens cDNA
2572	15135	27708	5.5	1.0E-107	BE732460.1	EST_HUMAN	601567819F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
2572	15135	27707	5.5	1.0E-107	BE732460.1	EST_HUMAN	601567819F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842309 5'
3040	15656	28135	3.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CH0031-190100-001-d03 CH0031 Homo sapiens cDNA
3040	15656	28136	3.03	1.0E-107	AW842451.1	EST_HUMAN	PM1-CH0031-190100-001-d03 CH0031 Homo sapiens cDNA
3134	15748	28217	3.02	1.0E-107	5902097	NT	Homo sapiens SMT3 (suppressor of mit two 3, yeast) homolog 2 (SMT3H2), mRNA

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3898	18497	28959	4.68	1.0E-107	AF020671.1	NT	Homo sapiens myotubularin (MTM1) gene, exon 9
3972	18570	29039	1.69	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
3972	18570	29040	1.69	1.0E-107	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
6025	18644	31386	4.74	1.0E-107	BE5867468.1	EST_HUMAN	601442558F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846484 5'
7369	19824	32789	1.4	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BN0-aif-c-08-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078310 5'
7369	19824	32789	1.4	1.0E-107	AW503913.1	EST_HUMAN	UI-HF-BN0-aif-c-08-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078310 5'
7536	20056	32930	1.28	1.0E-107	AI765078.1	EST_HUMAN	wh56F04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2384797 3'
8309	21909	34858	0.88	1.0E-107	AU122469.1	EST_HUMAN	AU122469 MAMMA1 Homo sapiens cDNA clone MAMMA1002433 5'
10533	23070	36083	2.05	1.0E-107	BE168726.1	EST_HUMAN	QV1-HT0516-140300-107-c10 HT0516 Homo sapiens cDNA
10583	23118	36133	3.35	1.0E-107	AJ392850.1	EST_HUMAN	ig10d06.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2108363 3' similar to SW:AACT_DICD1 P05095 ALPHA-ACTININ 3, NON MUSCULAR ;
10825	23348	36382	2.16	1.0E-107	L49141.1	NT	Homo sapiens neuroendocrine-specific protein (NSP) gene, exon 4
10839	23360	36375	2.39	1.0E-107	BF7666511.1	EST_HUMAN	602123963F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281039 5'
11203	23708	36780	4.35	1.0E-107	BE540550.1	EST_HUMAN	601066881F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3452829 5'
11203	23709	36016	4.67	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11271	23009	36017	4.67	1.0E-107	11419701	NT	Homo sapiens HSPC049 protein (HSPC049), mRNA
11577	24023	37092	3.77	1.0E-107	4507822	NT	Homo sapiens UDP glycosyltransferase 2 family, polypeptide B11 (UGT2B11) mRNA
11830	25014		7.41	1.0E-107	AA001415.1	EST_HUMAN	z45e01.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:381944 3' similar to contains THR.b1 THR repetitive element ;
189	12850		1.3	1.0E-108	AA341934.1	EST_HUMAN	EST147363 Fetal muscle Homo sapiens cDNA 5' end
990	13602	28116	1.64	1.0E-108	BE286042.1	EST_HUMAN	601177018F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532348 5'
1308	13902	26421	4.66	1.0E-108	Y18000.1	NT	Homo sapiens NF2 gene
2123	14701	27271	0.95	1.0E-108	BF028728.1	EST_HUMAN	601671914F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954939 5'
2368	14939	27511	1.91	1.0E-108	AI886040.1	EST_HUMAN	h81e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
2368	14939	27512	1.91	1.0E-108	AI886040.1	EST_HUMAN	h81e10.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2248938 3' similar to gb:M14219 BONE
							PROTEOGLYCAN II PRECURSOR (HUMAN);
							PROTEOGLYCAN II PRECURSOR (HUMAN);
2472	15039	27607	7.53	1.0E-108	BE206694.1	EST_HUMAN	bb25b10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963899 3' similar to gb:X53777 60S
3392	16000	28478	0.73	1.0E-108	AF032897.1	NT	RIBOSOMAL PROTEIN L23 (HUMAN); gb:J05277 Mouse hexokinase mRNA, complete cds (MOUSE);
3392	16000	28479	0.73	1.0E-108	AF032897.1	NT	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
							Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
4237	16825	29275	1.43	1.0E-108	AW664438.1	EST_HUMAN	h121a11.x1 NCI_CGAP_GUT1 Homo sapiens cDNA clone IMAGE:2972060 3' similar to SW:3BP1_MOUSE P55194 SH3-BINDING PROTEIN 3BP-1 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4624	17207	29856	1.92	1.0E-108	U72981.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4624	17207	29857	1.92	1.0E-108	U72981.1	NT	Human hepatocyte nuclear factor 4-alpha gene, exon 2
4926	17501	29949	2.86	1.0E-108	7661979	NT	Homo sapiens KIAA0187 gene product (KIAA0187), mRNA
5044	17617	30062	0.93	1.0E-108	AW504799.1	EST_HUMAN	UI-HF-BNO-ah-e-04-Q-UI.1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3080166 5'
5084	17657	30098	2.16	1.0E-108	AJ008005.1	NT	Homo sapiens PSN1 gene, alternative transcript
5318	17880	30299	0.81	1.0E-108	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA
5670	18287	30777	1.2	1.0E-108	AW384094.1	EST_HUMAN	RC0-HT0372:241199-031-403 HT0372 Homo sapiens cDNA
5718	18344	30851	2.96	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
5718	18344	30852	2.96	1.0E-108	BE869016.1	EST_HUMAN	601444922F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3848980 5'
6084	18701		0.83	1.0E-108	AF012823.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 20
6153	18768	31529	0.88	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403:240700-001-c10 CT0403 Homo sapiens cDNA
6288	18896	31666	5.83	1.0E-108	AF264717.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FVE-DSP2 mRNA, complete cds
6288	18896	31667	5.83	1.0E-108	AF264717.1	NT	Homo sapiens FVE domain-containing dual specificity protein phosphatase FVE-DSP2 mRNA, complete cds
6409	19012	31795	1.16	1.0E-108	AJ133269.1	NT	Homo sapiens caveolin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
6499	18768	31529	1.01	1.0E-108	BF334851.1	EST_HUMAN	PM4-CT0403:240700-001-c10 CT0403 Homo sapiens cDNA
6732	19328	32130	0.85	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
6732	19328	32131	0.85	1.0E-108	AF016706.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 4
7211	19742	32596	5.04	1.0E-108	11431857	NT	Homo sapiens G protein-coupled receptor, family C, group 5, member B (GPCR5B), mRNA
7465	19987	32852	3.44	1.0E-108	4758333	NT	Homo sapiens delta-6 fatty acid desaturase (FADS6) mRNA
7492	20015	32881	1.67	1.0E-108	BE252607.1	EST_HUMAN	601113471F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354064 5'
7516	20036	32903	1.06	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4181037 5'
7516	20036	32904	1.06	1.0E-108	BF528912.1	EST_HUMAN	602043384F1 NCI_CGAP_Brn87 Homo sapiens cDNA clone IMAGE:4181037 5'
8008	20350		1.77	1.0E-108	AF083500.1	NT	Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
8058	20800	33509	1.47	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-Q-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8058	20800	33510	1.47	1.0E-108	AW408694.1	EST_HUMAN	UI-HF-BMO-ads-e-12-Q-UI.1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3062878 5'
8977	21315	34439	1.08	1.0E-108	AF203977.1	NT	Homo sapiens ETS-family transcription factor EHF (EHF) mRNA, complete cds
9016	21552	34480	0.52	1.0E-108	N44974.1	EST_HUMAN	y95h10.1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:273283 5' similar to PIR:A45773
10501	22995	36004	0.49	1.0E-108	11428155	NT	A45773 ketch protein, long form - fruit fly
10547	20279	33176	1.87	1.0E-108	BE556227.1	EST_HUMAN	Homo sapiens similar to high-mobility group (nonhistone chromosomal) protein 4 (H. sapiens) (LOC63446), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10707	18037	30497	2.06	1.0E-108	Y12490.1	NT	Homo sapiens mRNA for Golgi-associated microtubule-binding protein (GMAP-210)
11151	23659	36703	4.23	1.0E-108	AW966185.1	EST_HUMAN	EST378258 MAGE resequences, MAGI Homo sapiens cDNA
11204	23709	36761	1.81	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11204	23709	36762	1.81	1.0E-108	AV708790.1	EST_HUMAN	AV708790 ADC Homo sapiens cDNA clone ADCAEE03 5'
11249	23778		2.91	1.0E-108	11441465	NT	Homo sapiens G protein-coupled receptor 48 (GPR48), mRNA
11305	23798	36857	1.72	1.0E-108	D63539.1	NT	Homo sapiens COL4A9 gene for $\alpha 1(V)$ collagen, exon 23
12005	24308	30991	5.17	1.0E-108	AK024447.1	NT	Homo sapiens mRNA for FLJ00037 protein, partial cds
12414	24667		7.56	1.0E-108	BF346356.1	EST_HUMAN	602018571F1 NCJ CGAP Bm67 Homo sapiens cDNA clone IMAGE:4164297 5'
46	12725	25186	2.13	1.0E-109	AW803116.1	EST_HUMAN	IL2-UM0077-280400-079-D08 UM0077 Homo sapiens cDNA
69	12747	25225	3.04	1.0E-109	D86974.1	NT	Human mRNA for KIAA0220 gene, partial cds
235	12895	25378	4.41	1.0E-109	11422486	NT	Homo sapiens hypothetical protein FLJ11316 (FLJ11316), mRNA
246	12805	25366	2.89	1.0E-109	11438391	NT	Homo sapiens reticulocalbin 1, EF-hand calcium binding domain (RCN1), mRNA
492	13125	25610	4.89	1.0E-109	4507712	NT	Homo sapiens tetrahydropteridine repeat domain 2 (TTC2) mRNA
624	13251	25725	19.67	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0998 protein, partial cds
624	13251	25726	19.67	1.0E-109	AB023216.1	NT	Homo sapiens mRNA for KIAA0998 protein, partial cds
1050	13657	26168	0.72	1.0E-109	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1244	13842	26359	24.19	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1245	13842	26359	15.92	1.0E-109	M28699.1	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
1589	14182	26714	0.98	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959836 5'
1589	14182	26715	0.98	1.0E-109	BE293673.1	EST_HUMAN	601186922F2 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959836 5'
1915	14500	27055	3.28	1.0E-109	DT3643.2	NT	Homo sapiens mRNA for KIAA0018 protein, partial cds
2263	14857	27434	1.19	1.0E-109	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
2292	14866	27441	2.08	1.0E-109	Y17123.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
2652	15211	27763	2.89	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2652	15211	27764	2.86	1.0E-109	AI022328.1	EST_HUMAN	ow95a01.x1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1654536 3' similar to TR:002197 002197 CIRCULATING CATHODIC ANTIGEN. ;
2653	15212	27765	2.01	1.0E-109	4504206	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
3094	15709	28180	1.68	1.0E-109	N85190.1	EST_HUMAN	J2816F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA clone J2816 5' similar to ZINC FINGER PROTEIN ZNF43
3435	16043	28524	1.34	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3435	16043	28525	1.34	1.0E-109	AW893192.1	EST_HUMAN	CM3-NN0009-190400-150-f10 NN0009 Homo sapiens cDNA
3589	16173	28655	0.9	1.0E-109	AF240698.1	NT	Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds
3909	16508		0.93	1.0E-109	BE146144.1	EST_HUMAN	MRO-HT0209-110400-108-a04 HIT0209 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4228	16816	29264	4.43	1.0E-109	AB55417.1	EST_HUMAN	ts9e08.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:2289330 3' similar to WP.F53A2.8
4493	17078	29528	2.7	1.0E-109	4504206	NT	CE16100;
4705	17287	29731	1.18	1.0E-109	7682083	NT	Homo sapiens guanylate cyclase activator 1A (retina) (GUCA1A) mRNA
5051	17624	30069	1.14	1.0E-109	R15400.1	EST_HUMAN	Homo sapiens KIAA0377 gene product (KIAA0377), mRNA
5465	18100	30418	0.78	1.0E-109	BF67318.1	EST_HUMAN	ya48e08.r1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:53057 5'
5516	18148	30560	2.6	1.0E-109	5174822	NT	602136446F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4272922 5'
5792	18417		1.24	1.0E-109	BE179358.1	EST_HUMAN	Homo sapiens placental protein 11 (serine proteinase) (P11) mRNA
6085	24758	31448	1.02	1.0E-109	BF379888.1	EST_HUMAN	RC1-HT0615-200400-022-404 HT0615 Homo sapiens cDNA
6147	18417		1.3	1.0E-109	BE179358.1	EST_HUMAN	RC1-HT0615-200400-022-404 HT0615 Homo sapiens cDNA
6491	19092	31875	0.8	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
6491	19092	31876	0.8	1.0E-109	M23442.1	NT	Human interleukin 4 (IL-4) gene, complete cds
7289	19817	32676	0.95	1.0E-109	AB046811.1	NT	Homo sapiens mRNA for KIAA1591 protein, partial cds
7566	20083	32959	4.08	1.0E-109	BF182707.1	EST_HUMAN	Homo sapiens AT-binding transcription factor 1 (ATBF1), mRNA
7568	20085	32961	5.94	1.0E-109	BF182707.1	EST_HUMAN	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
7568	20085	32962	5.94	1.0E-109	AL049784.1	NT	601809495F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4040279 5'
8114	20655	33564	1.17	1.0E-109	AA077498.1	EST_HUMAN	Novel human gene mapping to chromosome 13
8227	20768	33687	1.27	1.0E-109	AW748130.1	EST_HUMAN	PM0-BT0340-091298-002-e05 BT0340 Homo sapiens cDNA
8581	21130		2.85	1.0E-109	AA077498.1	EST_HUMAN	7B18H01 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B18H01
8669	21208	34125	14.1	1.0E-109	BE787540.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8669	21208	34126	14.1	1.0E-109	BE787540.1	EST_HUMAN	601478417F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3882124 5'
8808	21446	34368	0.57	1.0E-109	BE145672.1	EST_HUMAN	IL0-HT0205-071199-142-q01 HT0205 Homo sapiens cDNA
9163	21698	34642	1.82	1.0E-109	H94860.1	EST_HUMAN	ye80g08.r1 Soares retina N255HR Homo sapiens cDNA clone IMAGE:222110 5' similar to SP.A53491
9272	21798	34747	0.54	1.0E-109	BE397088.1	EST_HUMAN	A53491 BUMETANIDE-SENSITIVE NA-K-Cl COTRANSPORTER - SPINY
9272	21798	34748	0.54	1.0E-109	BE397088.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
9405	21914	34863	3.55	1.0E-109	F06804.1	EST_HUMAN	601289760F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3620030 5'
10653	23185	36200	2.73	1.0E-109	BE540909.1	EST_HUMAN	HSC1EC121 normalized infant brain cDNA Homo sapiens cDNA clone e-1ec12
10653	23185	36201	2.73	1.0E-109	BE540909.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449598 5'
10687	23217	36229	35.59	1.0E-109	BF694831.1	EST_HUMAN	601063030F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3449598 5'
10847	23368	36386	2	1.0E-109	7682279	NT	602080724F2 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4245341 5'
10847	23368	36387	2	1.0E-109	7682279	NT	Homo sapiens KIAA0744 gene product: histone deacetylase 7 (KIAA0744), mRNA
11004	23518	36553	1.95	1.0E-109	AU121370.1	EST_HUMAN	Homo sapiens KIAA0744 gene product: histone deacetylase 7 (KIAA0744), mRNA
11248	23778	36835	2.84	1.0E-109	4502838	NT	AU121370 HEMBB1 Homo sapiens cDNA clone HEMBB1002690 5'
							Homo sapiens Chediak-Higashi syndrome 1 (CHST1) mRNA

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11285	23738	36794	6.81	1.0E-109	W16510.1	EST_HUMAN	zb08b12.1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:301439 5' similar to
12131	14866	27441	1.6	1.0E-108	Y17123.1	NT	PIR:S43969 S43969 p54-beta stress-activated protein kinases - rat;
12252	24463	30961	15.45	1.0E-109	AB011399.1	NT	Homo sapiens SNF5/INI1 gene, exon 6
3	12683	25139	1.19	1.0E-110	7549804	NT	Homo sapiens gene for AF-3, complete cds
40	12719	25179	4.51	1.0E-110	5803073	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
40	12719	25180	4.61	1.0E-110	5803073	NT	Homo sapiens leucine-zipper-like transcriptional regulator, 1 (LZTR1), mRNA
114	12683	25139	0.83	1.0E-110	7549804	NT	Homo sapiens deiodinase, iodothyronine, type II (DIO2), transcript variant 2, mRNA
316	12970	25459	1	1.0E-110	D87281.1	NT	Human mRNA for inward rectifier potassium channel, complete cds
553	13184	25662	0.93	1.0E-110	U84550.1	NT	Human dystrobrevin (DTN) gene, exon 20
1222	13822	26337	0.97	1.0E-110	5031620	NT	Homo sapiens calcitonin receptor-like (CALCRL) mRNA
1322	13916	26438	1.28	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
1965	14549	27105	1.48	1.0E-110	BE379477.1	EST_HUMAN	601237545F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609683 5'
2103	14682		1.65	1.0E-110	BF508898.1	EST_HUMAN	U1H-BJ4-aes-b-05-0-U1.s1 NCJ_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
2868	15484		0.95	1.0E-110	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
3065	13916	26438	0.85	1.0E-110	AB032253.1	NT	Homo sapiens BAZ1B mRNA for bromodomain adjacent to zinc finger domain 1B, complete cds
3123	15737		1.2	1.0E-110	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein
3228	15840	28319	6.37	1.0E-110	11436041	NT	(L44L) and FTP3 (FTP3) genes, complete cds
3228	15840	28320	6.37	1.0E-110	11436041	NT	Homo sapiens pregnancy-zone protein (PZP), mRNA
4128	16720	29175	0.92	1.0E-110	BE018556.1	EST_HUMAN	Homo sapiens pregnancy-zone protein (PZP), mRNA
4281	16867	29314	1.06	1.0E-110	M15918.1	NT	bb92a05.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048848 5' similar to TR:O60312 O60312
4740	17321	29761	2.32	1.0E-110	A017213.1	EST_HUMAN	KIAA0566 PROTEIN ;
4758	17339	29785	3.28	1.0E-110	AU117812.1	EST_HUMAN	Human autoimmune antigen small nuclear ribonucleoprotein E pseudogene
5109	17681		1.8	1.0E-110	7692441	NT	cu32b10.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:1627963 3' similar to
5498	18132	30540	2.16	1.0E-110	BE299408.1	EST_HUMAN	SW/N121_RAT_P02591 NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 ;
5900	18522	31247	0.7	1.0E-110	BE621069.1	EST_HUMAN	AU117812 HEMBA1 Homo sapiens cDNA clone HEMBA1002241 5'
5917	18539	31264	6.81	1.0E-110	11419323	NT	Homo sapiens KIAA1002 protein (KIAA1002), mRNA
5917	18539	31265	6.81	1.0E-110	M55112.1	NT	601118710F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3028538 5'
6818	24771	32226	3.2	1.0E-110	U08888.1	NT	601493677F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3893795 5'
7159	19691	32536	0.83	1.0E-110	U08888.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
7159	19691	32537	0.83	1.0E-110	U08888.1	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
							Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 7
							Human GS2 gene, exon 2
							Human GS2 gene, exon 2

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7364	19890	32753	0.74	1.0E-110	AI560289.1	EST_HUMAN	U12008.x1 NCL_CGAP_Brr25 Homo sapiens cDNA clone IMAGE:2167407 3' similar to SW.ETV1_HUMAN P50549 ETS TRANSLOCATION VARIANT 1
7454	19878	32843	11.26	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB8 Homo sapiens cDNA clone DCBCGE01 5'
7454	19878	32844	11.26	1.0E-110	AV714276.1	EST_HUMAN	AV714276 DCB8 Homo sapiens cDNA clone DCBCGE01 5'
7478	20000	32865	2.84	1.0E-110	AB020875.1	NT	Homo sapiens mRNA for KIAA0868 protein, partial cds
7571	20088	32864	1.05	1.0E-110	AU137923.1	EST_HUMAN	AU137923 PLACE1 Homo sapiens cDNA clone PLACE1007511 5'
9258	21784	34737	0.54	1.0E-110	BE302594.1	EST_HUMAN	be88701.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2805561 5' similar to TR:O77258 O77258 EG:114D9.2 PROTEIN.
9497	21997	34953	2.91	1.0E-110	AW838394.1	EST_HUMAN	QV2-L T0053-020400-119-e04 L T0053 Homo sapiens cDNA
10226	22721	35712	3.91	1.0E-110	11432732	NT	Homo sapiens galactokinase 2 (GALK2), mRNA
10826	23158	36171	3.89	1.0E-110	Y12337.1	NT	H. sapiens mRNA for myotonic dystrophy protein kinase like protein
10846	23367	36384	3.87	1.0E-110	BE734357.1	EST_HUMAN	G01565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
10846	23367	36385	3.87	1.0E-110	BE734357.1	EST_HUMAN	G01565604F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3840433 5'
11317	23015	36024	3.28	1.0E-110	AA446529.1	EST_HUMAN	zw67g02.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781298 5' similar to TR:G1145816 G1145816 FKBP54
11719	24128		2.86	1.0E-110	BE897218.1	EST_HUMAN	G01439784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924548 5'
11849	24209		11.86	1.0E-110	AW082258.1	EST_HUMAN	IL0-BT0163-040889-094-g10 BT0163 Homo sapiens cDNA
12092	24360		2.73	1.0E-110	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12239	25027		8.39	1.0E-110	BF364546.1	EST_HUMAN	PM3-NN1082-140900-008-f12 NN1082 Homo sapiens cDNA
12537	14682		1.43	1.0E-110	BF508896.1	EST_HUMAN	UJ-H-B14-aos-b-05-O-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085784 3'
186	12847		28.49	1.0E-111	U43701.1	NT	Human ribosomal protein L23a mRNA, complete cds
210	12871	25357	0.94	1.0E-111	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
764	13363		1.84	1.0E-111	BF035327.1	EST_HUMAN	G01458531F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3862086 5'
773	13392	25892	5.48	1.0E-111	8383092	NT	Homo sapiens cat eye syndrome critical region gene 1 (OECR1), mRNA
962	13573	26089	2.34	1.0E-111	M25142.1	NT	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 32 to 34
1670	14263	26797	2.34	1.0E-111	7662177	NT	Homo sapiens KIAA0555 gene product (KIAA0555), mRNA
4250	16838	26288	1.25	1.0E-111	7661669	NT	Homo sapiens DKFZP434D156 protein (DKFZP434D156), mRNA
4423	17008	29451	4.84	1.0E-111	K02268.1	NT	Human enkephalin B (enKB) gene, exon 4 and 3' flank and complete cds
5814	18438	31160	0.91	1.0E-111	BE867809.1	EST_HUMAN	G01443690F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847655 5'
6183	18793	31562	1.58	1.0E-111	A1344879.1	EST_HUMAN	gp08g12.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917574 3' similar to gb:M29893 RAS- RELATED PROTEIN RAL-A (HUMAN);
6781	19372	32188	1	1.0E-111	AL040762.1	EST_HUMAN	DKFZP434C1815.1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZP434C1815 5'
6898	19632	32470	1.3	1.0E-111	AW284948.1	EST_HUMAN	UJ-H-BW0-ail-d-03-O-U1.s1 NCL_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729525 3'
7471	19993	32856	2.68	1.0E-111	BF366228.1	EST_HUMAN	IL2-NT0101-280700-114-E03 NT0101 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7540	20060	32934	3.47	1.0E-111	AI761228.1	EST_HUMAN	wf68401.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398465 3' similar to gb:J04813 CYTOCHROME P450 IIAs (HUMAN);
7610	20123	33000	1.1	1.0E-111	U80017.1	NT	Homo sapiens basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal apoptosis inhibitory protein (nailp) and survival motor neuron protein (smn) genes, complete cds
8038	20580	33486	0.77	1.0E-111	AA278868.1	EST_HUMAN	zs79g03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8038	20580	33487	0.77	1.0E-111	AA278868.1	EST_HUMAN	zs79g03.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:703732 5' similar to TR:G1256410 G1256410 11-ZINC-FINGER TRANSCRIPTION FACTOR. ;
8128	20870	33580	0.89	1.0E-111	11431898	NT	Homo sapiens protein x0001 (LOC51185), mRNA
8183	20724	33638	5.9	1.0E-111	U66533.1	NT	Human beta4-integrin (ITGB4) gene, exon 13
8613	21152	34066	0.82	1.0E-111	11420516	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic 2 (NFATC2), mRNA
8710	21249	34172	0.89	1.0E-111	AK024453.1	NT	Homo sapiens mRNA for FLJ00045 protein, partial cds
8743	21282	34280	23.24	1.0E-111	BF214802.1	EST_HUMAN	601847132F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4078303 5'
8817	21356	34281	12.59	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
8817	21356	34281	12.59	1.0E-111	X17033.1	NT	Human mRNA for integrin alpha-2 subunit
9017	21554	34482	3.03	1.0E-111	AF091395.1	NT	Homo sapiens Trio isoform mRNA, complete cds
9241	21767	34716	0.58	1.0E-111	BF333210.1	EST_HUMAN	QV2-BT0817-270900-398-406 BT0817 Homo sapiens cDNA aa58g02.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:825170 3' similar to gb:L09235 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10056	22551	35546	2.03	1.0E-111	AA504160.1	EST_HUMAN	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS (HUMAN);
10082	22577		1.53	1.0E-111	DT0083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10173	22868	35663	5.78	1.0E-111	AA131248.1	EST_HUMAN	231101.r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10922	23441	36462	4.93	1.0E-111	U68159.1	NT	Human thrombopoietin receptor (MPL) gene, exons 1,2,3,4,5 and 6
11674	24093	37146	4.3	1.0E-111	11417801	NT	Homo sapiens meningoeloma (disrupted in balanced translocation) 1 (MN1), mRNA
12234	24450	30954	2.23	1.0E-111	AV708482.1	EST_HUMAN	AV708482 ADC Homo sapiens cDNA clone ADCAO808 5'
12360	24816	30791	6.35	1.0E-111	W22562.1	EST_HUMAN	72C9 Human retina cDNA Tsp5091-cleaved sublibrary Homo sapiens cDNA not directional
12507	18039	30498	1.31	1.0E-111	AB033356.1	NT	Homo sapiens mRNA for neuroxin 1-alpha protein, complete cds
636	13259	25734	1.69	1.0E-112	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
638	13261	25736	5.94	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
638	13261	25737	5.94	1.0E-112	U29103.1	NT	Human steroidogenic acute regulatory protein (STAR) gene, exon 5
660	13283	25763	1.42	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-ect-g-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
660	13283	25764	1.42	1.0E-112	BF509039.1	EST_HUMAN	UI-H-B14-ect-g-04-0-U1.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086023 3'
1039	13649	26161	3.88	1.0E-112	AF157623.1	NT	Homo sapiens HTRA serine protease (PRSS11) gene, complete cds
1100	13705	26213	2	1.0E-112	P52742	SWISSPROT	ZINC FINGER PROTEIN 135
1722	14313	26853	4.44	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1722	14313	26854	4.44	1.0E-112	7682125	NT	Homo sapiens KIAA0440 protein (KIAA0440), mRNA
1856	14444	27000	1.56	1.0E-112	AF248540.1	NT	Homo sapiens Intersectin 2 (SH3D1B), mRNA, complete cds
2550	15114	27684	1.81	1.0E-112	BE868859.1	EST_HUMAN	601442874F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846858 5'
3114	15729		0.59	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
3953	16551	28020	0.74	1.0E-112	BE076073.1	EST_HUMAN	MR2-BT0590-090300-113-09 BT0590 Homo sapiens cDNA
4709	17291	29735	0.65	1.0E-112	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1), mRNA
4884	17441	29891	5.1	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
4884	17441	29892	5.1	1.0E-112	AB037832.1	NT	Homo sapiens mRNA for KIAA1411 protein, partial cds
5848	18472	31198	38.42	1.0E-112	NA6046.1	EST_HUMAN	y95d07.r1 Soares melanocyte 2N6HM Homo sapiens cDNA clone IMAGE:273229 5'
6227	18836	31609	1.36	1.0E-112	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
6294	18902	31672	0.85	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-08-Q-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6294	18902	31673	0.85	1.0E-112	AW502437.1	EST_HUMAN	UI-HF-BR0p-ajs-g-08-Q-UJ.r1 NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075658 5'
6397	18000	31778	1.2	1.0E-112	BE747686.1	EST_HUMAN	60159471F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948557 5'
6747	19340	32146	0.68	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6747	19340	32147	0.68	1.0E-112	BE273103.1	EST_HUMAN	601142755F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3506508 5'
6928	19587	32416	1.36	1.0E-112	BF574235.1	EST_HUMAN	602131405F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4270921 5'
7375	19901	32764	1.57	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
7375	19901	32765	1.57	1.0E-112	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8134	20675	33587	1.93	1.0E-112	AU18051.1	EST_HUMAN	AU18051 HEMBA1 Homo sapiens cDNA clone HEMBA1002773 5'
8887	21425	34350	2.49	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
8887	21425	34351	2.49	1.0E-112	BE867635.1	EST_HUMAN	601443151F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847285 5'
9807	22305	35289	2.06	1.0E-112	BF111413.1	EST_HUMAN	7130g07.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523020 3' similar to
10657	23189	36205	3.51	1.0E-112	AW863327.1	EST_HUMAN	TR:Q9VW35 Q9VW35 CG8743 PROTEIN. ;
10743	23267	36283	1.85	1.0E-112	T93967.1	EST_HUMAN	MR3-SN0009-100400-106-b12 SN0009 Homo sapiens cDNA
10743	23267	36284	1.85	1.0E-112	T93967.1	EST_HUMAN	y456d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
10827	23348	36384	4.28	1.0E-112	AJ249900.1	NT	SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
10976	23491	36521	1.76	1.0E-112	BE280479.1	EST_HUMAN	y456d10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112243 3' similar to
11051	23584	36599	2.08	1.0E-112	AJ904584.1	EST_HUMAN	SP:C40H1.1 CE00109 OVARIAN PROTEIN ;
11062	23574	36611	4.71	1.0E-112	AW377870.1	EST_HUMAN	Homo sapiens mRNA for secreted modular calcium-binding protein (smoc1 gene)
							601155323F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138989 5'
							IL-BT061-311298-009 BT061 Homo sapiens cDNA
							PMO-CT0237-141099-001-002 CT0237 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
772	13391	25890	5.13	1.0E-113	A1365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
772	13391	25891	5.13	1.0E-113	A1365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
978	13590	26105	6.33	1.0E-113	M11965.1	NT	Human X-linked phosphoglycerate kinase gene, exon 8
1588	14181	26713	2.48	1.0E-113	A1365586.1	EST_HUMAN	ac95f01.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1953625 3'
1983	15395	27128	0.92	1.0E-113	AF240775.1	NT	Homo sapiens eIF4E-transporter mRNA, complete cds
2142	14720	27291	1.02	1.0E-113	BF515218.1	EST_HUMAN	UI-HBW1-ant-f-03-Q-U1.s1 NCI CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3082876 3'
3164	15778	28249	2.08	1.0E-113	AJ223948.1	NT	Homo sapiens mRNA for putative RNA helicase, 3' end
5454	24852		3.07	1.0E-113	BE780858.1	EST_HUMAN	601469465F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872536 5'
5684	18311	30806	6	1.0E-113	AJ127214.1	EST_HUMAN	AU127214 NT2RP2 Homo sapiens cDNA clone NT2RP2000807 5'
6080	18697	31444	3.89	1.0E-113	AU140291.1	EST_HUMAN	AU140291 PLACE2 Homo sapiens cDNA clone PLACE2000274 5'
6106	18722	31475	1	1.0E-113	AF016535.1	NT	Homo sapiens P-glycoprotein (mdr1) mRNA, complete cds
6220	18830	31604	2.43	1.0E-113	11525737	NT	Homo sapiens UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 8 (GalNAc-T8) (GALNT8), mRNA
6304	18911	31684	0.88	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
6304	18911	31685	0.88	1.0E-113	9961249	NT	Homo sapiens ATP-binding cassette, sub-family B (MDR/TAP), member 4 (ABCB4), transcript variant B, mRNA
8458	19059	31844	0.71	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
6458	19059	31845	0.71	1.0E-113	6006002	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
7362	19888	32751	0.77	1.0E-113	BE282161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
7362	19888	32752	0.77	1.0E-113	BE282161.1	EST_HUMAN	601152078F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3508362 5'
9024	21561	34488	3	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9024	21561	34489	3	1.0E-113	BE382842.1	EST_HUMAN	601297709F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3627554 5'
9322	21838		0.72	1.0E-113	BE772987.1	EST_HUMAN	RC1-FT0134-280600-021-402 FT0134 Homo sapiens cDNA
9745	22243	35224	1.2	1.0E-113	11428367	NT	Homo sapiens transmembrane protein 2 (TMEM2), mRNA
9843	22341	35323	0.55	1.0E-113	M21535.1	NT	Human erg protein (ets-related gene) mRNA, complete cds
9863	22458	35441	0.81	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
9863	22458	35442	0.81	1.0E-113	5453997	NT	Homo sapiens RAN binding protein 7 (RANBP7), mRNA
11002	23516	36551	1.71	1.0E-113	AW500519.1	EST_HUMAN	UI-HF-BNO-aq-b-12-Q-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077326 5'
11011	23525	36559	2.11	1.0E-113	AW630291.1	EST_HUMAN	hh81a09.y1 NCI CGAP_GU1 Homo sapiens cDNA clone IMAGE:2969176 5' similar to TR:O60327 O60327
11011	23525	36560	2.11	1.0E-113	AW630291.1	EST_HUMAN	KIAA0584 PROTEIN ;
11097	19059	31844	1.58	1.0E-113	6006002	NT	KIAA0584 PROTEIN ;
							Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11097	19059	31845	1.58	1.0E-113	600602	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
11141	23649	36691	3.51	1.0E-113	BE29288.1	EST_HUMAN	601105529F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988368 5'
11370	23822	36884	2.53	1.0E-113	AA580720.1	EST_HUMAN	nc80803.1 NCI CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN
11370	23822	36885	2.53	1.0E-113	AA580720.1	EST_HUMAN	nc80803.1 NCI CGAP_GC1 Homo sapiens cDNA clone IMAGE:797069 5' similar to SW:FEN1_HUMAN
62	12741	25213	1.2	1.0E-114	Y17151.2	NT	P39748 FLAP ENDONUCLEASE-1;
62	12741	25214	1.2	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
62	12741	25215	1.2	1.0E-114	Y17151.2	NT	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
673	13297	25779	22.22	1.0E-114	T70551.1	EST_HUMAN	Yd15c01.s1 Soares fetal liver spleen 1NFS Homo sapiens cDNA clone IMAGE:108288 3' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN); contains Alu repetitive element;
1109	13713	28223	2.83	1.0E-114	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1356	13950	26476	3.57	1.0E-114	7657529	NT	Homo sapiens thalidomide tumor deletion region protein 1 (RTDR1), mRNA
1684	14276	26809	1.26	1.0E-114	6631094	NT	Homo sapiens minichromosome maintenance deficient (S. cerevisiae) 3 (MCM3), mRNA
1711	14304	26841	7.13	1.0E-114	6678073	NT	Homo sapiens nucleoporin-like protein 1 (NLP_1), mRNA
2830	12727	25189	2.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
2830	12727	25190	2.13	1.0E-114	AB033102.1	NT	Homo sapiens mRNA for KIAA1276 protein, partial cds
3165	15779	28250	2.36	1.0E-114	X04086.1	NT	Human gene for catalase (EC 1.11.1.6) exon 2 mapping to chromosome 11, band p13
3207	15819	28295	1.02	1.0E-114	BF206374.1	EST_HUMAN	601869932F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100214 5'
4088	16684	29142	1.81	1.0E-114	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
4480	17065	29515	0.92	1.0E-114	J03171.1	NT	Human interferon-alpha receptor (HuIFN-alpha-Rec), complete cds
5324	17888	30302	0.89	1.0E-114	BE275324.1	EST_HUMAN	601122173F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346099 5'
5380	17920	30334	0.93	1.0E-114	AA194468.1	EST_HUMAN	zq05e05.1 Stralagene muscle 837209 Homo sapiens cDNA clone IMAGE:528832 5' similar to contains MER22.3 MER22 repetitive element;
5597	18227	30674	1.36	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5597	18227	30675	1.36	1.0E-114	4506880	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A) mRNA
5781	18406	31122	1.35	1.0E-114	9257201	NT	Homo sapiens clathrin, heavy polypeptide-like 1 (CLTCL1), transcript variant 2, mRNA
7137	19476	32674	1.13	1.0E-114	AB041533.1	NT	Homo sapiens HCMOGT-1 mRNA for sperm antigen, complete cds
7288	19816	32675	1.2	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7288	19816	32675	1.2	1.0E-114	AU134187.1	EST_HUMAN	AU134187 OVARC1 Homo sapiens cDNA clone OVARC1001444 5'
7326	19853	32715	7.05	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7326	19853	32716	7.05	1.0E-114	Y18000.1	NT	Homo sapiens NF2 gene
7832	20374	33280	1.88	1.0E-114	4557600	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2) mRNA
8108	20849	33557	1.81	1.0E-114	A1363139.1	EST_HUMAN	qy68d06.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2017163 3'
8108	20849	33558	1.81	1.0E-114	A1363139.1	EST_HUMAN	qy68d06.x1 NCI_CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2017163 3'
8635	21174	34093	4.12	1.0E-114	U63041.1	NT	Human neural cell adhesion molecule CD55 mRNA, complete cds
8702	21241	34195	5.52	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
8702	21241	34166	5.52	1.0E-114	AB011133.1	NT	Homo sapiens mRNA for KIAA0561 protein, partial cds
9110	21646	34586	0.92	1.0E-114	BF109832.1	EST_HUMAN	789g12.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3526847 3' similar to TR:Q9UJH6 Q9UJH6 TRANSMEMBRANE PROTEIN 2 ;
9335	21849		18.44	1.0E-114	AW327455.1	EST_HUMAN	iq3f05.x1 NIH_MGC_2 Homo sapiens cDNA clone IMAGE:2846744 5'
9384	20322	33227	3.14	1.0E-114	AF077754.1	NT	Homo sapiens tyrosine kinase pp60c-src (SRC) gene, exon 12 and partial cds
9497	21992		6.13	1.0E-114	MT13636.1	NT	Human ceruloplasmin mRNA
10045	22540	35537	0.94	1.0E-114	BE870004.1	EST_HUMAN	601449752F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3853500 5'
10066	22561	35556	1.32	1.0E-114	AL163227.2	NT	Homo sapiens chromosome 21 segment HS21C027
10434	22928	35935	0.71	1.0E-114	BE171984.1	EST_HUMAN	MFO-HT0559-250200-002-007 HT0559 Homo sapiens cDNA
10666	23198		13.62	1.0E-114	BE302686.1	EST_HUMAN	ba73g12.y1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2906086 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4 (HUMAN); gb:M20632 Mouse LLRep3 protein mRNA from a repetitive element, complete (MOUSE);
11070	23582	36622	3.31	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
11070	23582	36623	3.31	1.0E-114	AV733454.1	EST_HUMAN	AV733454 cda Homo sapiens cDNA clone cdABA08 5'
12137	25093		3.79	1.0E-114	11418041	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
12410	24565	30609	2.85	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
12410	24565	30910	2.85	1.0E-114	11034850	NT	Homo sapiens hypothetical protein (DJ1042K10.2), mRNA
25	12704	25162	6.12	1.0E-115	47581111	NT	Homo sapiens HLA-B associated transcript-1 (D6S81E) mRNA
135	12800	25288	2.34	1.0E-115	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kd) (POLR2A) mRNA
139	12804		8.73	1.0E-115	4537887	NT	Homo sapiens keratin 18 (KRT18) mRNA
314	12868	25456	3.77	1.0E-115	AW804759.1	EST_HUMAN	QV4-UM0094-300300-156-b08 UM0094 Homo sapiens cDNA
561	13192	25670	0.85	1.0E-115	A1339206.1	EST_HUMAN	q06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5 ;
561	13192	25671	0.95	1.0E-115	A1339206.1	EST_HUMAN	q06f01.x1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1946809 3' similar to TR:O00536 O00536 TTF-I INTERACTING PEPTIDE 5 ;
819	13436	25942	1.29	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
819	13436	25943	1.29	1.0E-115	5174702	NT	Homo sapiens transforming growth factor beta-activated kinase-binding protein 1 (TAB1), mRNA
821	13438	25945	190.74	1.0E-115	4503794	NT	Homo sapiens ferritin, heavy polypeptide 1 (FTH1) mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1606	14198	26730	1.2	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1606	14198	26731	1.2	1.0E-115	AF228180.1	NT	Homo sapiens alpha-aminoadipate semialdehyde synthase mRNA, complete cds
1881	14487	27025	1.19	1.0E-115	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2125	14703	27273	1.11	1.0E-115	BE745489.1	EST_HUMAN	601578838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
2125	14703	27274	1.11	1.0E-115	BE745489.1	EST_HUMAN	601578838F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928832 5'
3149	15763	28230	2.81	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3149	15763	28231	2.81	1.0E-115	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
3519	16124	28604	2.12	1.0E-115	AJ277892.1	NT	Homo sapiens partial TTN gene for titin
4115	16709	29164	4.23	1.0E-115	AB002348.2	NT	Homo sapiens mRNA for KIAA0350 protein, partial cds
4353	16940	29382	1.31	1.0E-115	AL137163.1	NT	Novel human gene mapping to chromosome X
4490	17075	29525	2.98	1.0E-115	6812858	NT	Homo sapiens sir2-like 3 (SIRT3), mRNA
4529	17113	29557	4.4	1.0E-115	4759279	NT	Homo sapiens EphA4 (EPHA4) mRNA
4783	17363	29813	2.89	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4783	17363	29814	2.89	1.0E-115	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
5032	17606	30050	3.79	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5032	17606	30051	3.79	1.0E-115	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
5550	18182	30597	2.42	1.0E-115	AW970335.1	EST_HUMAN	EST382416 MAGE rescues, MAGK Homo sapiens cDNA
5617	18246	30697	1.07	1.0E-115	BF665387.1	EST_HUMAN	602119346F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276738 5'
5732	18358	31063	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5732	18358	31064	1.79	1.0E-115	11425128	NT	Homo sapiens similar to ER to nucleus signalling 1 (H. sapiens) (LOC63433), mRNA
5869	18491	31217	1.1	1.0E-115	A1928799.1	EST_HUMAN	au64q01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518558 3' similar to gb:U07807
5869	18491	31218	1.1	1.0E-115	A1928799.1	EST_HUMAN	au64q01.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518558 3' similar to gb:U07807
6408	19011	31793	0.89	1.0E-115	11428785	NT	DYNAMIN-1 (HUMAN);
6408	19011	31794	0.89	1.0E-115	11428785	NT	Homo sapiens sperm surface protein (HSS), mRNA
6529	19129	31923	20.52	1.0E-115	11428038	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63436), mRNA
6649	19245	32047	1.74	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
6649	19245	32048	1.74	1.0E-115	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
7014	19512	32333	0.69	1.0E-115	T86774.1	EST_HUMAN	yd88608.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:115095 5' similar to SP-DPOG YEAST P15801 DNA POLYMERASE GAMMA;
7322	19849	32709	1.16	1.0E-115	A1076598.1	EST_HUMAN	oz31a06.x1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'
7322	19849	32710	1.16	1.0E-115	A1076598.1	EST_HUMAN	oz31a06.x1 Soares, total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1676914 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7438	19862	32828	6.85	1.0E-115	AB023212.1	NT	Homo sapiens mRNA for KIAA0965 protein, partial cds
8101	20842	33553	12.93	1.0E-115	BE930187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8101	20842	33554	12.93	1.0E-115	BE930187.1	EST_HUMAN	RC8-ET0081-130700-011-G01 ET0081 Homo sapiens cDNA
8747	21286	34207	4.14	1.0E-115	11434772	NT	Homo sapiens eukaryotic translation initiation factor 4B (EIF4B), mRNA
9690	22189	35162	0.58	1.0E-115	BF382029.1	EST_HUMAN	601816362F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050108 5'
9910	22407	35382	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
9910	22407	35383	2.13	1.0E-115	AB002336.1	NT	Human mRNA for KIAA0338 gene, partial cds
10414	22908	35906	1.08	1.0E-115	A1221878.1	EST_HUMAN	q999609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10414	22908	35907	1.08	1.0E-115	A1221878.1	EST_HUMAN	q999609.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1843336 3'
10420	22914	35914	0.88	1.0E-115	A1524687.1	EST_HUMAN	PHENYLALANINE TRNA SYNTHETASE
10448	22942	35952	0.79	1.0E-115	BE868285.1	EST_HUMAN	th12a07.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2118038 3' similar to TR:O16129 O16129
10596	23130	36144	3.79	1.0E-115	AW571544.1	EST_HUMAN	601509879F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911610 5'
11140	23648	36689	1.94	1.0E-115	BE045890.1	EST_HUMAN	X32208.x1 NCL CGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to SW:CAYP_CANFA
11140	23648	36690	1.94	1.0E-115	BE045890.1	EST_HUMAN	h954c10.x1 NCL CGAP_Pan3 Homo sapiens cDNA clone IMAGE:3123186 3' similar to TR:O88378 O88378
11276	23729	36784	2.64	1.0E-115	BE045890.1	EST_HUMAN	PRP4 PROTEIN KINASE HOMOLOG
11698	24111		1.46	1.0E-115	AF240786.1	NT	PRP4 PROTEIN KINASE HOMOLOG
598	13227	25701	2.19	1.0E-116	BE275502.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1E subunit (CACNA1E) mRNA
833	13450	25957	1.23	1.0E-116	4507334	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
892	13506		0.9	1.0E-116	4507334	NT	601121347F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2888875 5'
2040	14622	27190	3.39	1.0E-116	5174478	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2040	14622	27191	3.39	1.0E-116	5174478	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
2072	14652	27224	1.95	1.0E-116	AL133080.1	EST_HUMAN	Homo sapiens pericentriolar (PONT) mRNA
2145	15458	27293	2.87	1.0E-116	MT19824.1	NT	Homo sapiens pericentriolar (PONT) mRNA
2145	15458	27294	2.87	1.0E-116	MT19824.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2346	14917	27491	1.87	1.0E-116	5453941	NT	Human apolipoprotein B-100 (apoB) gene, exons 17 and 18
2380	14949		0.97	1.0E-116	U78308.1	NT	Homo sapiens protein phosphatase, EF hand calcium-binding domain 1 (PPEF1) mRNA
2497	15061	27635	2.84	1.0E-116	AB018333.1	NT	Human olfactory receptor olfr17-201-1 (OR17-201-1) gene, olfactory receptor olfr17-32 (OR17-32) gene and olfactory receptor pseudo_olfr17-01 (OR17-01) pseudogene, complete cds
2792	15404	27893	2.18	1.0E-116	BE889256.1	EST_HUMAN	Homo sapiens mRNA for KIAA0790 protein, partial cds
							601513337F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914600 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3209	15821	28296	4.18	1.0E-116	L77570.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
3209	15821	28297	4.18	1.0E-116	L77570.1	NT	Homo sapiens DGeorge syndrome critical region, centromeric end
4467	17053	29497	2.11	1.0E-116	5031954	NT	Homo sapiens sodium phosphate transporter 3 (NPT3) mRNA
4981	17555	29987	1.86	1.0E-116	A1907098.1	EST_HUMAN	PM-BT135-070499-016 BT135 Homo sapiens cDNA
5363	17923	30337	0.88	1.0E-116	AJ243213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5
5483	18117	30525	0.82	1.0E-116	AJ302082.1	EST_HUMAN	q118d04.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898695 3' similar to contains element MER25 repetitive element;
6132	18748	31502	2.1	1.0E-116	W42822.1	EST_HUMAN	zc24407.r1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone IMAGE:323245 5' similar to SW:MDHM_MOUSE P08249 MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR ;
6359	18963	31740	1.81	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6359	18963	31741	1.81	1.0E-116	AB046856.1	NT	Homo sapiens mRNA for KIAA1636 protein, partial cds
6423	19026	31809	1.14	1.0E-116	BE408097.1	EST_HUMAN	601302281F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3636764 5'
6530	19130	31924	1.96	1.0E-116	BF877910.1	EST_HUMAN	602084730F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249087 5'
6637	19233	32382	1.82	1.0E-116	BE158133.1	EST_HUMAN	MR2-HT0378-210203-102-b04 HT0379 Homo sapiens cDNA
7023	19557	32382	2.08	1.0E-116	C02844.1	EST_HUMAN	C02844 Human heart cDNA (YNakamura) Homo sapiens cDNA clone 3NHC0367
7254	19782	32638	7.16	1.0E-116	AV716314.1	EST_HUMAN	AV716314 DCB Homo sapiens cDNA clone DCB8CG08 5'
8310	20851	33775	1.4	1.0E-116	AA354258.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
8310	20851	33776	1.4	1.0E-116	AA354258.1	EST_HUMAN	EST62685 Jurkat T-cells V Homo sapiens cDNA 5' end similar to similar to keratin 2
8416	20956	33873	1.49	1.0E-116	A1904151.1	EST_HUMAN	CM-BT043-090289-075 BT043 Homo sapiens cDNA
8668	21407	34331	1.15	1.0E-116	BE565507.1	EST_HUMAN	601338288F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3680880 5'
9028	21565	34494	2.75	1.0E-116	AJ216352.1	EST_HUMAN	q109c05.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1844168 3' similar to gb:X53741_ma1 FIBULIN-1, ISOFORM A PRECURSOR (HUMAN);
9592	22092	35056	1.36	1.0E-116	11418946	NT	Homo sapiens laminin, alpha 2 (merotin, congenital muscular dystrophy) (LAMA2), mRNA
10171	22666	35661	0.87	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10171	22666	35662	0.87	1.0E-116	AJ277441.1	NT	Homo sapiens partial mRNA for xylosyltransferase I (XT-I) gene
10250	22745	35733	0.82	1.0E-116	BE158913.1	EST_HUMAN	QV4-HT0401-281268-063-c09 HT0401 Homo sapiens cDNA
10597	23103	36117	3.89	1.0E-116	BF335849.1	EST_HUMAN	CM2-CT0482-300800-349-e08 CT0482 Homo sapiens cDNA
11015	23529	36565	3.63	1.0E-116	AJ367140.1	EST_HUMAN	qq41e04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1935102 3' similar to WP:B0495.7 CE01766 ;
12456	24948	25691	3.62	1.0E-116	AL134889.1	EST_HUMAN	DKFZp782L110.1_1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp782L110 5'
594	13214	25691	1.88	1.0E-117	4826636	NT	Homo sapiens acetyl-Coenzyme A carboxylase alpha (ACACA), mRNA
1116	15433	26231	1.46	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxrth) gene, exons 13a through 15
1288	13865	26382	0.81	1.0E-117	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1789	14379	26923	1.28	1.0E-117	AF123320.1	NT	Homo sapiens lymphocyte activation-associated protein mRNA, complete cds
1871	14457	27014	5.27	1.0E-117	M19816.1	NT	Human apolipoprotein B-100 (apoB) gene, exon 10
2252	14826	27402	1.15	1.0E-117	AY957699.1	EST_HUMAN	EST1369769 MAGE sequences, MAGE Homo sapiens cDNA
3306	15917	28394	1.53	1.0E-117	AA978114.1	EST_HUMAN	op32c11.s1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1578548 3'
4062	16659	29122	8.83	1.0E-117	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
4436	17022	29482	2.27	1.0E-117	8659564	NT	Homo sapiens collagen, type IV, alpha 5 (Alport syndrome) (COL4A5), mRNA
4677	17259	29710	2.1	1.0E-117	AL042120.1	EST_HUMAN	DKFZp434C1120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434C1120 5'
4933	17508	29955	10.14	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
4933	17508	29956	10.14	1.0E-117	AF134304.2	NT	Homo sapiens Scar2 (SCAR2) gene, partial cds
5074	17847	30088	3.29	1.0E-117	AB020673.1	NT	Homo sapiens mRNA for KIAA0866 protein, complete cds
5551	18183	30598	3.8	1.0E-117	BE730508.1	EST_HUMAN	601562657F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832214 5'
7473	19995	32858	5.22	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7473	19995	32860	5.22	1.0E-117	L76571.1	NT	Homo sapiens nuclear hormone receptor (shp) gene, 3' end of cds
7550	20069	32944	4.48	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7550	20069	32945	4.48	1.0E-117	AV717788.1	EST_HUMAN	AV717788 DCB Homo sapiens cDNA clone DCBBAE01 5'
7919	20481	33387	3.77	1.0E-117	AI950145.1	EST_HUMAN	wp86b07.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2468629 3' similar to TR:O75065
8253	20794	33711	1.07	1.0E-117	10834989	NT	O75065 KIAA0477 PROTEIN ;
8253	20794	33712	1.07	1.0E-117	10834989	NT	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8350	20891	33811	1.32	1.0E-117	AI904151.1	EST_HUMAN	Homo sapiens neural cell adhesion molecule 1 (NCAM1), mRNA
8350	20891	33812	1.32	1.0E-117	AI904151.1	EST_HUMAN	CN-BT043-090299-075 BT043 Homo sapiens cDNA
9223	21739	34682	1.73	1.0E-117	D16524.1	NT	CN-BT043-090299-075 BT043 Homo sapiens cDNA
9701	22200	35172	1.71	1.0E-117	BE733922.1	EST_HUMAN	Human gene for very low density lipoprotein receptor, exon 11
9857	24786	35335	0.63	1.0E-117	AF099033.1	NT	601569317F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3843748 5'
10482	22956	35967	1.98	1.0E-117	11420222	NT	Homo sapiens gamma-aminobutyric acid type B receptor 2 (GABABR2) mRNA, complete cds
10737	23262	36277	1.89	1.0E-117	D83776.1	NT	Homo sapiens Drosophila Kelch like protein (DKELCHL), mRNA
10901	23421	36439	1.81	1.0E-117	W80605.1	EST_HUMAN	Human mRNA for KIAA0191 gene, partial cds
10917	23436	36456	1.65	1.0E-117	11424835	NT	zfb3b11.r1 Soares_fetal heart Nbr-H19W Homo sapiens cDNA clone IMAGE:347229 5' similar to gb.M14219 BONE PROTEOGLYCAN II PRECURSOR (HUMAN);
10917	23436	36457	1.65	1.0E-117	11424835	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11153	23660	36704	3.46	1.0E-117	AB011541.1	NT	Homo sapiens protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1 (PIN1), mRNA
11153	23660	36705	3.46	1.0E-117	AB011541.1	NT	Homo sapiens mRNA for MEGF8, partial cds
11272	23725		31.65	1.0E-117	BE269856.1	EST_HUMAN	Homo sapiens mRNA for MEGF8, partial cds
							601186203F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3544286 5'

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Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11464	23914	36981	2.04	1.0E-117	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11464	23914	36982	2.04	1.0E-117	4501843	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
11936	25026		1.7	1.0E-117	AF224669.1	NT	Homo sapiens mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating enzyme E2D 3 (UBE2D3) genes, complete cds
12662	15433	28231	1.81	1.0E-117	AF124393.1	NT	Mus musculus fragile-X-related protein 1 (Fxr1h) gene, exons 13a through 15
74	12752	25231	8.91	1.0E-118	AF161500.1	NT	Homo sapiens HSPC151 mRNA, complete cds
99	12775	25257	0.88	1.0E-118	AL045854.1	EST_HUMAN	DKFZp4341056_t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4341056 5'
543	13174	25654	5.79	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (DJ328E19.C1.1), mRNA
947	15429	26073	1.3	1.0E-118	5174680	NT	Homo sapiens sine oculis homeobox (Drosophila) homolog 1 (SIX1) mRNA
2275	14849	27425	1.93	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2275	14849	27426	1.93	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2275	14849	27427	1.93	1.0E-118	BE389705.1	EST_HUMAN	601281947F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3604019 5'
2367	14938		0.98	1.0E-118	AW951729.1	EST_HUMAN	EST363799 IMAGE:3604019 5'
2768	15322	27888	2.82	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
2768	15322	27889	2.82	1.0E-118	U07000.1	NT	Human breakpoint cluster region (BCR) gene, complete cds
3138	15752		4.01	1.0E-118	Y13932.1	NT	Homo sapiens PRKY exon 7
3229	15841	28321	6.49	1.0E-118	A1347694.1	EST_HUMAN	qp01105.x1 NC1_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
3229	15841	28322	6.49	1.0E-118	A1347694.1	EST_HUMAN	qp01105.x1 NC1_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1916769 3'
4162	16753	29204	9.69	1.0E-118	D23660.1	NT	Human mRNA for ribosomal protein, complete cds
4817	17395	28848	1.45	1.0E-118	11425793	NT	Homo sapiens KIAA0478 gene product (KIAA0478), mRNA
5616	18245	30695	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5616	18245	30696	1.89	1.0E-118	AF142624.1	NT	Homo sapiens calcium channel gamma 4 subunit (CACNG4) gene, exon 3
5813	18437	31158	1.01	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5813	18437	31159	1.01	1.0E-118	11422054	NT	Homo sapiens reelin (RELN), mRNA
5890	18513	31239	0.77	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5890	18513	31240	0.77	1.0E-118	U08892.1	NT	Human GS2 gene, exon 6
5944	18564	31294	0.92	1.0E-118	M55109.1	NT	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 4
6023	18642	31363	1.2	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6023	18642	31364	1.2	1.0E-118	11425900	NT	Homo sapiens T-box 4 (TBX4), mRNA
6098	18714	31464	1.4	1.0E-118	11420764	NT	Homo sapiens T-box 4 (TBX4), mRNA
6793	19384	32169	1.58	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
6793	19384	32200	1.58	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
7154	19866	32528	1.03	1.0E-118	AL043761.1	EST_HUMAN	DKFZp43400127_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43400127 5'
7154	19866	32528	1.03	1.0E-118	AL043761.1	EST_HUMAN	DKFZp43400127_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp43400127 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7597	20111	32988	4.89	1.0E-118	11431050	NT	Homo sapiens chromosome 2 open reading frame 3 (C2ORF3), mRNA
7609	20122	32989	0.7	1.0E-118	L46590.1	NT	Homo sapiens very long chain acyl-CoA dehydrogenase gene, exons 1-20, complete cds
7913	20455	33361	2.75	1.0E-118	BE781223.1	EST_HUMAN	601469139F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872247 5'
8323	20864	33788	6.06	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8323	20864	33789	6.06	1.0E-118	BE062855.1	EST_HUMAN	QV0-BT0263-090200-097-h03 BT0263 Homo sapiens cDNA
8328	20869	33792	1.44	1.0E-118	AA443024.1	EST_HUMAN	z688407.1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8328	20869	33793	1.44	1.0E-118	AA443024.1	EST_HUMAN	z688407.1 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:811789 5'
8607	21146	34061	0.89	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8607	21146	34062	0.89	1.0E-118	AB002381.1	NT	Human mRNA for KIAA0383 gene, partial cds
8955	21194	34112	1.61	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8955	21194	34113	1.61	1.0E-118	4557732	NT	Homo sapiens latent transforming growth factor beta binding protein 2 (LTBP2) mRNA
8955	21903	34425	5.31	1.0E-118	BE263134.1	EST_HUMAN	601144863F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160502 5'
8956	21534	34464	0.52	1.0E-118	AL048474.2	EST_HUMAN	DKF2p586K1824_r1 586 (synonym: huta1) Homo sapiens cDNA clone DKF2p586K1824
9512	22012	34971	1.62	1.0E-118	7657016	NT	Homo sapiens hypothetical protein (D3328E19.C1.1), mRNA
9897	22394	35370	0.62	1.0E-118	AL138321.1	EST_HUMAN	DKF2p547O017_r1 547 (synonym: hibr1) Homo sapiens cDNA clone DKF2p547O017 5'
10237	22732	35723	0.98	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10237	22732	35724	0.98	1.0E-118	BE736213.1	EST_HUMAN	601307146F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3641603 5'
10277	22772	35761	1.6	1.0E-118	BF195407.1	EST_HUMAN	7n17e09.x1 NCI_CGAP_Bn23 Homo sapiens cDNA clone IMAGE:3564785.3 similar to SW:ZP3A_HUMAN
10425	22919	35921	0.52	1.0E-118	AW286351.1	EST_HUMAN	P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR
11157	23684	36710	4.87	1.0E-118	AA315007.1	EST_HUMAN	U1H-BW0-alo-a-07-0-J1 st NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729772 3'
11433	23883	36949	1.94	1.0E-118	BE908676.1	EST_HUMAN	EST186814 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' and similar to dynein, light chain 1, cytoplasmic
11433	23883	36950	1.94	1.0E-118	BE908676.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11436	23886	36953	1.69	1.0E-118	BF093687.1	EST_HUMAN	601499514F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3901563 5'
11436	23886	36954	1.69	1.0E-118	BF093687.1	EST_HUMAN	QV0-JM00091-120900-385-b12 UM0091 Homo sapiens cDNA
11806	24049	37115	1.58	1.0E-118	BE218235.1	EST_HUMAN	QV0-JM00091-120900-385-b12 UM0091 Homo sapiens cDNA
788	13406	25911	2.89	1.0E-119	AF170492.1	NT	h96a06.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175474 3' similar to TR:Q9Z2H4
1075	15432	28169	1.82	1.0E-119	7705607	NT	Q9Z2H4 G PROTEIN-COUPLED RECEPTOR LGRA4
1977	14560	27118	2.24	1.0E-119	AB023147.1	NT	Homo sapiens chloride channel CLC4 (CLC4) mRNA, complete cds
3136	15750	28218	1.04	1.0E-119	8922205	NT	Homo sapiens CGI-105 protein (LOC51011), mRNA
3277	15888		0.79	1.0E-119	AA916760.1	EST_HUMAN	Homo sapiens mRNA for KIAA0930 protein, partial cds
							Homo sapiens hypothetical protein FLJ10052 (FLJ10052), mRNA
							on10b05.st NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556241 3' similar to WP:E04F6.2
							CE01214

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
4026	16624	29096	1.09	1.0E-119	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
5540	18172	30587	3.45	1.0E-119	EST_HUMAN	AU133389 NT2RP4 Homo sapiens cDNA clone NT2RP4001991 5'
5553	18185	30600	15.55	1.0E-119	NT	Human neurofibromin (NF1) gene, complete cds
5557	18189	30605	3.01	1.0E-119	EST_HUMAN	RC1-NN0073-250800-018-g06 NN0073 Homo sapiens cDNA
5625	18254	30723	1.52	1.0E-119	EST_HUMAN	AV693731 GKC Homo sapiens cDNA clone GKCDH03 5'
6276	18884	31652	5.76	1.0E-119	EST_HUMAN	qb77c09.x1 Soares_fetal_hear1_NbHH19W Homo sapiens cDNA clone IMAGE:1706128 3' similar to SW:K1CJ_MOUSE P02535 KERATIN, TYPE I CYTOSKELETAL 10 ;
6429	19032	31815	0.68	1.0E-119	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6429	19032	31816	0.68	1.0E-119	NT	Homo sapiens matrix metalloproteinase 28 (MMP28) mRNA, complete cds
6473	19074	31857	1.06	1.0E-119	EST_HUMAN	tm23f10.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2157451 3'
6588	19185	31987	2.82	1.0E-119	NT	Human c-fes/fos proto-oncogene
6598	19195	32000	4.9	1.0E-119	EST_HUMAN	EST386296 MAGE resequences, MAGM Homo sapiens cDNA
7440	19964	32830	1.27	1.0E-119	EST_HUMAN	601592005F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3946081 5'
8596	21135	34050	0.94	1.0E-119	EST_HUMAN	601280584F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3622528 5'
9670	22169	35145	0.55	1.0E-119	NT	Homo sapiens melanoma differentiation associated protein-5 (MDA5), mRNA
9821	22319	35303	1.04	1.0E-119	NT	Homo sapiens KIAA0477 gene product (KIAA0477), mRNA
10145	22640	35630	2.78	1.0E-119	EST_HUMAN	aa32f05.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814977 5'
10398	22892	35896	0.92	1.0E-119	NT	Homo sapiens partial IL-12RB1 gene for IL-12 receptor beta1 chain, exons 16-17
10438	22932	35940	0.66	1.0E-119	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
10502	22966	36005	3.99	1.0E-119	NT	Homo sapiens hypothetical protein FLJ10206 (FLJ10206), mRNA
11092	23594		10.54	1.0E-119	EST_HUMAN	Homo sapiens Scd mRNA for stearyl-CoA desaturase, complete cds
11997	25012		3.05	1.0E-119	EST_HUMAN	602186072F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310633 5'
258	12917	25404	0.65	1.0E-120	NT	RC3-C10212-240899-011-103 GT0212 Homo sapiens cDNA
323	12977	25495	0.77	1.0E-120	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
1079	13694	26195	2.62	1.0E-120	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1079	13694	26196	2.62	1.0E-120	NT	Homo sapiens intersectin 2 (SH3D1B) mRNA, complete cds
1471	14063	26599	3.24	1.0E-120	EST_HUMAN	yy40g12.r1 Soares melanocyte 2NBHM Homo sapiens cDNA clone IMAGE:273768 5'
1645	14237	26772	2.49	1.0E-120	NT	Homo sapiens cysteine-rich repeat-containing protein S62 precursor, mRNA, complete cds
1842	14430	26983	1.64	1.0E-120	NT	Homo sapiens disintegrin and metalloprotease domain 10 (ADAM10) mRNA
3348	12977	25495	1.04	1.0E-120	NT	Homo sapiens synaptotagmin 1 (SYNJ1), mRNA
4449	17035	29478	1.68	1.0E-120	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4449	17035	29479	1.68	1.0E-120	NT	Homo sapiens cAMP-specific phosphodiesterase 8A (PDE8A) mRNA, partial cds
4769	17350	29801	2.82	1.0E-120	NT	Homo sapiens stanniocalcin (STC) gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4769	17350	29802	2.82	1.0E-120	AF098463.1	NT	Homo sapiens stanniocalcin (STC) gene, partial cds
5150	17720	30151	1.11	1.0E-120	AF054821.1	NT	Homo sapiens cytochrome P-450 mRNA, complete cds
5442	17997		0.95	1.0E-120	AL163213.2	NT	Homo sapiens chromosome 21 segment HS21C013
5911	18533	31258	13.5	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
5911	18533	31259	13.5	1.0E-120	BF568222.1	EST_HUMAN	602183994F1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300174 5'
7573	20089	32965	1.78	1.0E-120	D34619.1	NT	Human TBXAS1 gene for thromboxane synthase, exon 7
7835	20377	33282	1.81	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
7835	20377	33283	1.81	1.0E-120	Y00067.1	NT	Human gene for neurofilament subunit M (NF-M)
8274	20815	33737	2.9	1.0E-120	BF337599.1	EST_HUMAN	602035352F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4183333 5'
8343	20884	33805	0.8	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8343	20884	33806	0.8	1.0E-120	AB033057.1	NT	Homo sapiens mRNA for KIAA1231 protein, partial cds
8347	20888	33808	2.83	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8347	20888	33809	2.83	1.0E-120	AB007964.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0495
8390	20930	33850	1.13	1.0E-120	AB007934.1	NT	Homo sapiens mRNA for KIAA0495 protein, partial cds
9421	21930	34877	4.6	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9421	21930	34878	4.6	1.0E-120	BE392102.1	EST_HUMAN	601307739F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3625544 5'
9660	22169	35131	3.07	1.0E-120	BF306541.1	EST_HUMAN	601888956F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4122876 5'
9675	22174	35150	8.09	1.0E-120	AU133205.1	EST_HUMAN	AU133205 NT2RP4 Homo sapiens cDNA clone NT2RP4001541 5'
9692	22191	35165	0.89	1.0E-120	AL049801.1	NT	Novel human gene mapping to chromosome 13, similar to rat RhoGAP
9698	22483	35469	2.88	1.0E-120	AB029000.1	NT	Homo sapiens mRNA for KIAA1077 protein, partial cds
11008	23520	36555	14.73	1.0E-120	BE266387.1	EST_HUMAN	601176727F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532015 5'
11222	23753	36810	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11222	23753	36811	2.12	1.0E-120	BE867619.1	EST_HUMAN	601443135F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847281 5'
11504	23953	37021	1.55	1.0E-120	U94774.1	NT	Human muscle glycogen phosphorylase (PYGM) gene, 5'UTR and exon 1
12153	24395	30975	1.31	1.0E-120		NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
77	12754	25236	0.92	1.0E-121	Y18000.1	NT	Homo sapiens NF2 gene
401	13045	25536	1.68	1.0E-121	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLACE1000899 5'
753	15423	25967	1.19	1.0E-121	5032192	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
2008	14590	27150	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2008	14590	27151	0.98	1.0E-121	4755139	NT	Homo sapiens inositol polyphosphate-4-phosphatase, type I, 107kD (INPP4A), splice variant a, mRNA
2150	14727	27300	1.74	1.0E-121	L70631.1	NT	Homo sapiens metabotropic glutamate receptor 1 beta (mGluR1beta) mRNA, complete cds
2966	15612	28092	1.03	1.0E-121	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes

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Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3117	15731	28201	3.63	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3117	15731	28202	3.63	1.0E-121	Y19208.1	NT	Homo sapiens hHb3 gene for hair keratin, exons 1 to 9
3589	16193	28677	0.94	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3589	16193	28678	0.94	1.0E-121	AB037758.1	NT	Homo sapiens mRNA for KIAA1337 protein, partial cds
3741	16342	28810	8.78	1.0E-121	AF155158.2	NT	Homo sapiens adaptor-related protein complex AP-4 epsilon subunit mRNA, complete cds
4424	17009	29452	1.42	1.0E-121	AI263294.1	EST_HUMAN	qx57b01.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2005417.3
5112	17684	30120	3.54	1.0E-121	X91937.1	NT	H. sapiens ECE-1 gene (exon 17)
5472	18106	30425	1.02	1.0E-121	BE222250.1	EST_HUMAN	hu0808.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166119.3
5750	18376	31086	0.69	1.0E-121	BE271424.1	EST_HUMAN	601140485F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3049820.5
6968	19545		1.06	1.0E-121	AJ271736.1	NT	Homo sapiens Xq pseudautosomal region, segment 2/2
7042	18062	30451	0.75	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA
7042	18062	30452	0.75	1.0E-121	AW898086.1	EST_HUMAN	RC3-NN0066-270400-011-f02 NN0066 Homo sapiens cDNA
7878	20420	33328	1.86	1.0E-121	11436217	NT	Homo sapiens gamma-aminobutyric acid (GABA) A receptor, alpha 2 (GABRA2), mRNA
7882	20424	33332	2.19	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
7882	20424	33333	2.18	1.0E-121	D84122.1	NT	Homo sapiens DNA for prostacyclin synthase, exon 8
9772	22270	35254	0.9	1.0E-121	AW583858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.1
9772	22270	35255	0.9	1.0E-121	AW583858.1	EST_HUMAN	la05g05.y1 Human Pancreatic Islets Homo sapiens cDNA 5' similar to TR:075457 075457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA.1
10655	23187	36203	3.45	1.0E-121	11427768	NT	Homo sapiens COX11 (yeast) homolog, cytochrome c oxidase assembly protein (COX11), mRNA
10662	23194	36209	4.2	1.0E-121	AF064200.1	NT	Homo sapiens UDP-glucuronosyltransferase 2B4 precursor (UGT2B4) mRNA, UGT2B4*E458 allele, complete cds
10948	23369	36388	3.51	1.0E-121	7330334	NT	Homo sapiens chloride intracellular channel 4 like (CLIC4L), mRNA
10975	23396	36412	2.11	1.0E-121	N59624.1	EST_HUMAN	w74c01.a1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:248448.3
289	12845	25430	1.68	1.0E-122	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
358	13007	25490	3.01	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
380	13027	25515	1.61	1.0E-122	11528176	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1), mRNA
915	13528	26047	5.29	1.0E-122	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
1262	13859	26378	4.63	1.0E-122	M20707.1	NT	Human kappa-immunoglobulin germline pseudogene (Chr22.4) variable region (subgroup V kappa II)
1731	14322	26864	1.08	1.0E-122	AF167706.1	NT	Homo sapiens cysteine-rich repeat-containing protein S52 precursor, mRNA, complete cds
1750	14340	26887	1.8	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1750	14340	26888	1.8	1.0E-122	11418424	NT	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
1850	14438	26895	6.15	1.0E-122	BE606024.1	EST_HUMAN	601497032F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3899558.5

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2533	15097	27669	5.48	1.0E-122	BF316170.1	EST_HUMAN	601886173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2533	15097	27670	5.48	1.0E-122	BF316170.1	EST_HUMAN	601886173F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125234 5'
2864	15483	27657	1.11	1.0E-122	AF264717.1	NT	Homo sapiens FYVE domain-containing dual specificity protein phosphatase FYVE-DSP2 mRNA, complete cds
4972	17546	29888	1.23	1.0E-122	4502166	NT	Homo sapiens amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease) (APP), mRNA
5127	17699		1.26	1.0E-122	AW504645.1	EST_HUMAN	UI-HF-BND-ali-a-03-0-UI-r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3079948 5'
5752	18378	31089	1.36	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
6853	18378	31089	6.96	1.0E-122	BE256039.1	EST_HUMAN	601113567F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354232 5'
7266	19794	32650	0.68	1.0E-122	AA868671.1	EST_HUMAN	ak49108 s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1409339 3'
8731	21270	34189	0.55	1.0E-122	AJ276801.1	NT	Homo sapiens mRNA for doublesex and mab-3 related transcription factor 1 (DMRT1)
8958	21498	34419	1.37	1.0E-122	11424216	NT	Homo sapiens retinal giant larvae (Drosophila) homolog 2 (LLGL2), mRNA
9247	21773	34723	0.9	1.0E-122	A359618.1	EST_HUMAN	qy42h07 x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW/MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
9247	21773	34724	0.9	1.0E-122	A359618.1	EST_HUMAN	qy42h07 x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013757 3' similar to SW/MTA1_HUMAN Q13330 METASTASIS-ASSOCIATED PROTEIN MTA1.1
10040	22535	35531	0.71	1.0E-122	AL117234.1	NT	Novel human gene mapping to chromosome X, isoform of dbi (proto-oncogene)
10866	23387	36402	1.55	1.0E-122	AW955834.1	EST_HUMAN	EST367804 MAGE resequences, MAGD Homo sapiens cDNA
11738	24141		3.99	1.0E-122	11418187	NT	Homo sapiens phosphonamniolase 1 (PMM1), mRNA
202	12863	25347	19.89	1.0E-123	U31519.1	NT	Human phosphoenolpyruvate carboxykinase (PCK1) gene, promoter region and partial cds
800	13417	25921	2.06	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
800	13417	25922	2.06	1.0E-123	BF345274.1	EST_HUMAN	602018058F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153670 5'
1051	13658	26169	5.07	1.0E-123	AL163249.2	NT	Homo sapiens chromosome 21 segment HS21C049
1060	13665	26176	5.53	1.0E-123	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1281	13876	26397	4.2	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
1281	13876	26398	4.2	1.0E-123	4505818	NT	Homo sapiens phosphatidylinositol-4-phosphate 5-kinase, type II, beta (PIP5K2B) mRNA, and translated products
2147	14724	27296	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2147	14724	27297	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2147	14724	27298	3.41	1.0E-123	M55419.1	NT	Human amelogenin (AMELY) gene, 3' end of cds
2354	14925		5.59	1.0E-123	7705962	NT	Homo sapiens RAB9-like protein (LOC51209), mRNA
3288	15899	26378	0.67	1.0E-123	6912817	NT	Homo sapiens glutamyl-peptide cyclotransferase (glutamyl cyclase) (QPCT), mRNA
5638	18267	30739	1.6	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5638	18267	30740	1.6	1.0E-123	L34219.1	NT	Homo sapiens retinaldehyde-binding protein (ORALBP) gene, complete cds
5769	18395	31109	1.33	1.0E-123	BE769746.1	EST_HUMAN	601591108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945433 5'
6595	19192	31997	2.14	1.0E-123	AU118435.1	EST_HUMAN	AU118435 HEMBA1 Homo sapiens cDNA clone HEMBA1003591 5'
7076	19648	32486	0.71	1.0E-123	H53198.1	EST_HUMAN	yq84a03.1 Soares fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:202444 5' similar to SP:YAK1_YEAST P14680 PROTEIN KINASE YAK1;
7084	19655	32494	1.22	1.0E-123	U42224.1	NT	Human growth hormone releasing hormone gene, exon 7
7245	19774	32631	0.68	1.0E-123	U55258.1	NT	Human hBRAVONI-CAM precursor (hBRAVONI-CAM) gene, complete cds
7433	19967	32922	0.73	1.0E-123	11525833	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 2 (HS3ST2), mRNA
7638	20150	33034	1.31	1.0E-123	11438439	NT	Homo sapiens 2'-5'-oligoadenylate synthetase 2 (OAS2), mRNA
7647	20159	33046	1.79	1.0E-123	BE263001.1	EST_HUMAN	601152815F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509162 5'
7764	20272	33170	0.8	1.0E-123	N35841.1	EST_HUMAN	yx89d11.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkpA - Phycomyces blakesleeanus;
7764	20272	33171	0.8	1.0E-123	N35841.1	EST_HUMAN	yx89d11.1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:268917 5' similar to PIR:S49611 S49611 protein kinase PkpA - Phycomyces blakesleeanus;
8472	21012		2.25	1.0E-123	AW371924.1	EST_HUMAN	RC4-BT0311-251198-012-e07 BT0311 Homo sapiens cDNA
9291	21991	34838	2.04	1.0E-123	AB007923.1	NT	Homo sapiens mRNA for KIAA0454 protein, partial cds
9424	21933	34882	39.79	1.0E-123	U09823.1	NT	Oryctolagus cuniculus New Zealand white elongation factor 1 alpha (Rabefla2) mRNA, complete cds
11567	24014	37083	5.42	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
11567	24014	37084	5.42	1.0E-123	BF677292.1	EST_HUMAN	602086791F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250879 5'
280	12946	25431	0.93	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
290	12946	25432	0.93	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
298	12952		1.2	1.0E-124	DB7675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
511	13144	26630	2.28	1.0E-124	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
720	13340	25828	4	1.0E-124	AA397551.1	EST_HUMAN	z81b04.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
720	13340	25830	4	1.0E-124	AA397551.1	EST_HUMAN	z81b04.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL=REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT);
789	13407	25912	4.86	1.0E-124	AF155654.1	NT	Human putative ribosomal protein S1 mRNA
841	13457	25966	1.18	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
937	13550	26066	5.09	1.0E-124	7705446	NT	Homo sapiens hypothetical protein (HSPC068), mRNA
1358	13952	26479	0.62	1.0E-124	11419092	NT	Homo sapiens ring finger protein (RNF), mRNA
1391	13985	26511	6.15	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds
1391	13985	26512	6.15	1.0E-124	AF274892.1	NT	Homo sapiens glucose transporter 3 gene, exons 9, 10, and complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1851	14439	26998	3.15	1.0E-124	AJ131712.1	NT	Homo sapiens mRNA for nucleolar RNA-helicase (nol61 gene)
2107	14685	27253	1.73	1.0E-124	BE79524.1	EST_HUMAN	601491715F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3893954 5'
3537	16142	28624	0.72	1.0E-124	S79684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/IR1) gene, exon
3537	16142	28625	0.72	1.0E-124	S79684.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJ6/IR1) gene, exon
3967	16565	29034	0.66	1.0E-124	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
4150	16742	29196	0.8	1.0E-124	4504116	NT	Homo sapiens glutamate receptor, ionotropic, kainate 1 (GRIK1) mRNA
4855	17433	29884	2.18	1.0E-124	AB024069.1	NT	Homo sapiens gene for B120, exon 11
5068	17641		1.29	1.0E-124	M18178.1	NT	Human fibronectin gene extra type III repeat (EDII), exon x+1
5258	17819	30244	0.87	1.0E-124	AW963390.1	EST_HUMAN	EST375463 MAGE resequences, MAGE Homo sapiens cDNA
5501	18135	30545	10.59	1.0E-124	8922337	NT	Homo sapiens hypothetical protein FLJ10300 (FLJ10300), mRNA
5852	18476	31199	1.05	1.0E-124	4506786	NT	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6048	18687	31406	6.57	1.0E-124	BF696135.1	EST_HUMAN	Homo sapiens IQ motif containing GTPase activating protein 1 (IQGAP1) mRNA
6317	18924	31701	0.88	1.0E-124	AV711263.1	EST_HUMAN	AV711263 Cu Homo sapiens cDNA clone CuADF07 5'
6563	19161	31959	0.9	1.0E-124	11420654	NT	Homo sapiens ubiquitin specific protease 9, X chromosome (Drosophila fat facets related) (USP9X), mRNA
7083	19654	32493	3.45	1.0E-124	Y11717.1	NT	M. musculus mRNA for hoxa3 gene
7191	19723	32571	1.23	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2866585 5'
7191	19723	32572	1.23	1.0E-124	BE271295.1	EST_HUMAN	600943771F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:2866585 5'
7555	20074	32950	1.15	1.0E-124	AA630331.1	EST_HUMAN	ec08h05.s1 Strategene HeLa cell c3 937218 Homo sapiens cDNA clone IMAGE:855897 3'
8201	20742	33655	18.99	1.0E-124	4506854	NT	Homo sapiens ribosomal protein L5 (RPL5) mRNA
8399	20939	33881	1.45	1.0E-124	AW612106.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
8399	20939	33882	1.45	1.0E-124	AW612106.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9089	21625	34580	1.42	1.0E-124	AI798964.1	EST_HUMAN	hg94a09.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2953240 3' similar to TR:O95162
9089	21625	34581	1.42	1.0E-124	AI798964.1	EST_HUMAN	O95162 PEROXISOMAL SHORT-CHAIN ALCOHOL DEHYDROGENASE. ;
9411	21920	34868	2.52	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9411	21920	34869	2.52	1.0E-124	AV645633.1	EST_HUMAN	wc43g03.x1 NCI_CGAP_P128 Homo sapiens cDNA clone IMAGE:2321428 3'
9498	21998	34954	1.14	1.0E-124	AF022655.1	NT	AV645633 GLC Homo sapiens cDNA clone GLCAGE04 3'
9498	21998	34955	1.14	1.0E-124	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9526	22026	34984	8.22	1.0E-124	AI767133.1	EST_HUMAN	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
9526	22026	34985	8.22	1.0E-124	AI767133.1	EST_HUMAN	w193f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
9785	22283	35269	1.66	1.0E-124	AW503755.1	EST_HUMAN	w193f02.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2400891 3'
11213	23716	36770	3.81	1.0E-124	AW685683.1	EST_HUMAN	UI-HF-BNO-akz-b-04-0-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078946 5'
							h105c06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2980906 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11347	23045	36056	2.26	1.0E-124	AI446455.1	EST_HUMAN	t19e03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN ;
11347	23045	36057	2.26	1.0E-124	AI446455.1	EST_HUMAN	t19e03.x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2141980 3' similar to TR:O31662 O31662 YKRS PROTEIN ;
11818	13340	25829	6.1	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
11818	13340	25830	6.1	1.0E-124	AA397551.1	EST_HUMAN	z81b04.r1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G300482 G300482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ;
12264	24474	30934	1.28	1.0E-124	AB029016.1	NT	Homo sapiens mRNA for KIAA1093 protein, partial cds
12542	24960	30632	2.42	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12542	24960	30633	2.42	1.0E-124	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
341	12953		8.05	1.0E-125	AB032988.1	NT	Homo sapiens mRNA for KIAA1172 protein, partial cds
451	12680	25136	3.95	1.0E-125	BE743922.1	EST_HUMAN	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
672	13296	25777	23.21	1.0E-125	AI110856.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
672	13296	25778	23.21	1.0E-125	AI110856.1	EST_HUMAN	HA0088 Human fetal liver cDNA library Homo sapiens cDNA
757	13376	25871	1.7	1.0E-125	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
893	13507	26025	2.68	1.0E-125	AA042813.1	EST_HUMAN	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
1036	13646	26158	2.18	1.0E-125	AL183210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1193	13794	26303	1.9	1.0E-125	7662279	NT	Homo sapiens KIAA0744 gene product; histone deacetylase 7 (KIAA0744), mRNA
1712	15448	26842	1.85	1.0E-125	7661867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
1836	14424	26975	0.96	1.0E-125	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1847	14435	26981	2.28	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
1847	14435	26982	2.28	1.0E-125	AF015450.1	NT	Homo sapiens Usurpin-alpha mRNA, complete cds
2397	14965	27536	1.03	1.0E-125	AA011278.1	EST_HUMAN	z01g09.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:429568 5'
2632	15193	27764	1.06	1.0E-125	4504686	NT	Homo sapiens inhibin, alpha (INH4) mRNA
2632	15193	27765	1.06	1.0E-125	4504686	NT	Homo sapiens inhibin, alpha (INH4) mRNA
3925	16523	28991	1.59	1.0E-125	AA042813.1	EST_HUMAN	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65857_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
4648	17230	28686	2.78	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4648	17230	28687	2.78	1.0E-125	11425114	NT	Homo sapiens zinc finger protein ZNF287 (ZNF287), mRNA
4724	17305	28749	1.54	1.0E-125	BE315412.1	EST_HUMAN	601141152F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3140796 5'
5932	18554	31281	0.69	1.0E-125	BF683845.1	EST_HUMAN	602139874F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4300770 5'

Table 4

Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6033	18652	31394	1.55	1.0E-125	11438448	NT	Homo sapiens KIAA0985 protein (KIAA0985), mRNA
6052	18670	31409	1.18	1.0E-125	BE175189.1	EST_HUMAN	QV2-HT0577-010500-165-506 HT0577 Homo sapiens cDNA
6089	18705	31453	3.2	1.0E-125	BE822680.1	EST_HUMAN	601433472F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918952 5'
6129	18744	31497	0.75	1.0E-125	AI679904.1	EST_HUMAN	tu67c07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2256108 3' similar to WP:C45G9.2
6695	19291	32094	1.55	1.0E-125	BE562526.1	EST_HUMAN	CE01854 ;
6695	19291	32095	1.55	1.0E-125	BE562526.1	EST_HUMAN	601338826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688790 5'
7121	19461	32277	65.83	1.0E-125	X03427.1	NT	601335826F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3688790 5'
7121	19461	32278	65.83	1.0E-125	X03427.1	NT	Homo sapiens IGF-II gene, exon 5
7538	20058	32932	0.75	1.0E-125	BE278823.1	EST_HUMAN	Homo sapiens IGF-II gene, exon 5
8483	21022	33938	1	1.0E-125	U60288.1	NT	601159076F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505603 5'
8483	21022	33939	1	1.0E-125	U60288.1	NT	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9046	21563	34512	9.65	1.0E-125	BE181640.1	EST_HUMAN	Human chromosome 10 duplicated adrenoleukodystrophy (ALD) gene segment containing exons 8-10
9046	21563	34513	9.65	1.0E-125	BE181640.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
9303	21903	34852	1.05	1.0E-125	AI565998.1	EST_HUMAN	QV1-HT0638-070500-191-d12 HT0638 Homo sapiens cDNA
10350	22844	35839	0.53	1.0E-125	BE794576.1	EST_HUMAN	tn52p03.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2171081 3' similar to TR:Q14089 Q14089
10388	22892	35876	0.73	1.0E-125	AB002298.1	NT	HYPOTHETICAL PROTEIN ;
10562	23098	36112	3.76	1.0E-125	AF043458.1	NT	Human mRNA for KIAA0300 gene, partial cds
11016	23530	36596	4.05	1.0E-125	AB014597.1	NT	Homo sapiens LREL gene, exon 5
11169	23676	36722	1.56	1.0E-125	AF026029.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
11174	23681	36727	6.41	1.0E-125	AF026029.1	NT	Homo sapiens myosin, heavy polypeptide 1, skeletal muscle, adult (MYH1), mRNA
11279	23732	36787	2.99	1.0E-125	AW812899.1	EST_HUMAN	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds
11375	23827	36888	6.08	1.0E-125	BE074287.1	EST_HUMAN	RC3-ST0186-250200-018-c11 ST0186 Homo sapiens cDNA
11375	23827	36889	6.08	1.0E-125	BE074287.1	EST_HUMAN	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
806	13423	25929	3.44	1.0E-126	4758007	NT	QV3-BT0569-020200-075-g09 BT0569 Homo sapiens cDNA
809	13426	25932	1.92	1.0E-126	M61836.1	NT	Homo sapiens CDC-like kinase (CLK) mRNA
952	13564	26076	295	1.0E-126	X68735.1	NT	Human laminin B1 chain gene, exon 20
3108	15723	28194	9.08	1.0E-126	AA160709.1	EST_HUMAN	H. sapiens gene for alpha1-antichymotrypsin, exon 3
3108	15723	28195	9.08	1.0E-126	AA160709.1	EST_HUMAN	zo72c03.r1 Stralagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592420 5'
3691	16292	28761	0.98	1.0E-126	X53941.1	NT	zo72c03.r1 Stralagene pancreas (#637208) Homo sapiens cDNA clone IMAGE:592420 5'
3716	16317	28785	2.02	1.0E-126	7657038	NT	H. sapiens DNA for liver cytochrome b5 pseudogene
							Homo sapiens death receptor 6 (DR6), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4902	17477	29933	1.03	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4902	17477	29934	1.03	1.0E-126	AF101108.1	NT	Homo sapiens collagen type XI alpha-1 (COL11A1) gene, exon 63
4961	17536	29978	1.31	1.0E-126	N34078.1	EST_HUMAN	yk78c08.r1 Soares melanocyte 2NbrHM Homo sapiens cDNA clone IMAGE:267850 5'
6380	18984	31764	3.46	1.0E-126	AA460075.1	EST_HUMAN	z66603.r1 Soares fetal Nb2HF8_9w Homo sapiens cDNA clone IMAGE:786444 5' similar to
6432	19035	31820	4.2	1.0E-126	AB040958.1	NT	TR:G1145880 G1145880 TITIN;
6432	19035	31821	4.2	1.0E-126	AB040958.1	NT	Homo sapiens mRNA for KIAA1525 protein, partial cds
7511	20032	32897	0.85	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7511	20032	32898	0.85	1.0E-126	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
7819	20361	33267	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1204 protein, partial cds
7819	20361	33268	0.92	1.0E-126	AB037715.1	NT	Homo sapiens mRNA for KIAA1294 protein, partial cds
7929	20471	33380	5.78	1.0E-126	X16609.1	NT	Human mRNA for arkylin (variant 2.1)
8124	20865	33575	0.85	1.0E-126	AA483368.1	EST_HUMAN	ne74b12.s1 NCL OGAP_Ew1 Homo sapiens cDNA clone IMAGE:909983 similar to SW:TSG6_HUMAN
9711	22209	35181	0.52	1.0E-126	4505424	NT	P89066 TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PRECURSOR ;
10672	23204	36217	1.73	1.0E-126	M63196.1	NT	Homo sapiens neuro-oncological ventral antigen 1 (NOVAT), splice variant 1, mRNA
10738	23263	36278	3.69	1.0E-126	BF883175.1	EST_HUMAN	Human macrophage mannose receptor (MRC1) gene, exon 5
11392	23844	36908	2.32	1.0E-126	BE261660.1	EST_HUMAN	602139138F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4298240 5'
11638	16292	28761	2.52	1.0E-126	X53941.1	NT	601149404F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502128 5'
12304	18036	30496	6.76	1.0E-126	BE743922.1	EST_HUMAN	H. sapiens DNA for liver cytochrome b5 pseudogene
183	12845	25330	4.5	1.0E-127	AB024597.1	NT	601577981F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926685 5'
183	12845	25331	4.5	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
184	12845	25330	2.76	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
184	12845	25331	2.76	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
295	12951	25439	1.3	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
295	12951	25440	1.3	1.0E-127	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
914	13527	28046	2.22	1.0E-127	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
949	13561	26075	1.37	1.0E-127	U72621.2	NT	Homo sapiens lost on transformation LOT1 mRNA, complete cds
1729	14320	26862	1.33	1.0E-127	4827053	NT	Homo sapiens ubiquitin specific protease 8 (USP8) mRNA
2111	14689	27256	2.81	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA
2111	14689	27257	2.81	1.0E-127	5803065	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 (LILRA1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2241	14816	27389	5.62	1.0E-127	4506620	NT	Homo sapiens ribosomal protein L26 (RPL26) mRNA
2381	14950	27523	3.29	1.0E-127	AF245505.1	NT	Homo sapiens adiccan mRNA, complete cds
2640	15199	27773	5.29	1.0E-127	X12881.1	NT	Human mRNA for cyokeratin 18
3753	16354	28822	1.02	1.0E-127	AF114488.1	NT	Homo sapiens Intersectin short isoform (ITSN) mRNA, complete cds
3884	16482	28944	0.75	1.0E-127	AW161207.1	EST_HUMAN	au80e06.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2782594 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN ; contains element MER22 repetitive element;
4194	16783	29232	0.66	1.0E-127	AF135186.1	NT	Homo sapiens delayed rectifier potassium channel subunit Isk mRNA, complete cds
4303	16889	29332	0.61	1.0E-127	AL163247.2	NT	Homo sapiens chromosome 21 segment HS21C047
4340	16927	29367	21.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4340	16927	29368	21.24	1.0E-127	7706239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
4595	17178	29625	0.66	1.0E-127	AF252297.1	NT	Homo sapiens cytochrome P450 retinoid metabolizing protein P450RAI-2 mRNA, complete cds
4708	17280	29734	5.02	1.0E-127	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
4738	17319		2.84	1.0E-127	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
4780	17361	29811	1.04	1.0E-127	6912639	NT	Homo sapiens Ring1 and YY1 binding protein (RYBP), mRNA
5884	18506	31232	2.37	1.0E-127	W03547.1	EST_HUMAN	za01a10.r1 Soares melanocyte 2NblHM Homo sapiens cDNA clone IMAGE:281258 5' similar to SW:PIPB_RAT P10688 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1;
5912	18534	31260	0.86	1.0E-127	4826863	NT	Homo sapiens neuronal cell adhesion molecule (NRCAM) mRNA
5970	18591	31326	4.81	1.0E-127	X85784.1	NT	Homo sapiens NOS2 gene, exon 6
6310	18917	31691	2.21	1.0E-127	X84060.1	NT	H. sapiens TCF11 gene, exon 3-6
6463	19064	31849	5.89	1.0E-127	4904778	NT	Homo sapiens Integrin, beta 8 (ITGB8) mRNA
6764	19357	32166	0.93	1.0E-127	11421595	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3), mRNA
7122	19462	32279	0.85	1.0E-127	4826977	NT	Homo sapiens reelin (RELN) mRNA
7760	20268	33165	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7760	20268	33166	1.31	1.0E-127	11421914	NT	Homo sapiens Pendred syndrome (PDS), mRNA
7763	20271	33169	0.87	1.0E-127	BF871355.1	EST_HUMAN	602151232F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4292575 5'
8820	21359	34265	0.7	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8820	21359	34266	0.7	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9558	22058	35019	4.96	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9558	22058	35020	4.96	1.0E-127	AF274863.1	NT	Homo sapiens secretory pathway component Sec31B-1 mRNA, alternatively spliced, complete cds
9787	22285	35270	0.66	1.0E-127	AI288932.1	EST_HUMAN	qm84h09.x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1896449 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10245	22740	35730	2.25	1.0E-127	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
11037	23551	36585	6.54	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA
11037	23551	36586	6.54	1.0E-127	11417339	NT	Homo sapiens similar to heat shock 70kD protein 98 (mortalin-2) (H. sapiens) (LOC63184), mRNA
11490	23939	37009	1.9	1.0E-127	BE985415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919817 5'
11490	23939	37010	1.9	1.0E-127	BE985415.1	EST_HUMAN	601434784F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919817 5'
12046	12845	25330	1.43	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12046	12845	25331	1.43	1.0E-127	AB024597.1	NT	Homo sapiens mRNA for casein kinase I epsilon, complete cds
12253	24464	30862	1.7	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
12620	24967		2.23	1.0E-127	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
485	13118	25605	2.44	1.0E-128	BE385817.1	EST_HUMAN	601278127F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618822 5'
1195	13766	26305	1	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1195	13766	26306	1	1.0E-128	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
2115	14693	27260	4.14	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, intron/exon repeat regions
2115	14693	27261	4.14	1.0E-128	U02523.1	NT	Human FAU1P pseudogene, intron/exon repeat regions
2250	14824	27400	18.53	1.0E-128	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
3441	16049	28527	1.14	1.0E-128	AB033073.1	NT	Homo sapiens mRNA for KIAA1247 protein, partial cds
4771	17352	29804	5.43	1.0E-128	11426673	NT	Homo sapiens prospero-related homeobox 1 (PROX1), mRNA
5734	18360	31068	6.97	1.0E-128	X69539.1	NT	H sapiens gene for inter-alpha-trypsin inhibitor heavy chain H1, exon 12
6550	19148	31944	2.08	1.0E-128	11420965	NT	Homo sapiens phosphodiesterase 1C, calmodulin-dependent (70kD) (PDE1C), mRNA
7010	19508	32328	8.01	1.0E-128	BF224345.1	EST_HUMAN	7q86b10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE: 3'
8206	20747	33659	0.75	1.0E-128	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
8206	20747	33660	0.75	1.0E-128	AB037816.1	NT	Homo sapiens mRNA for KIAA1395 protein, partial cds
10043	22538	35535	1.62	1.0E-128	AA639198.1	EST_HUMAN	ns04a11.1 NCI_CGAP_Ew1 Homo sapiens cDNA clone IMAGE:1182620 similar to TR:G951338 G951338
10598	23123	36137	5.48	1.0E-128	11425254	NT	CHROMOSOME SEGREGATION GENE HOMOLOG CAS ;
10597	23131	36145	5.15	1.0E-128	AA926959.1	EST_HUMAN	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2D (GRIN2D), mRNA
11905	24244		4.37	1.0E-128	AW956260.1	EST_HUMAN	om68h08.s1 NCI_CGAP_GCC4 Homo sapiens cDNA clone IMAGE:1552383 3' similar to gb:X54941 CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 1 (HUMAN);
127	13071	25568	12.06	1.0E-128	S37722.1	NT	EST367360 IMAGE resequences, MAGG Homo sapiens cDNA
438	13071	25568	14.64	1.0E-128	S37722.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1756	14346	26891	2.48	1.0E-128	AL096690.1	NT	insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1019 nt, segment 2 of 4]
1761	14351	26896	1.62	1.0E-128	AF240786.1	NT	Novel human mRNA containing Zinc finger C2H2 type domains
							Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1761	14351	26897	1.62	1.0E-128	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1886	14471	27029	2.2	1.0E-128	11418522	NT	Homo sapiens zinc finger protein 76 (expressed in testis) (ZNF76), mRNA
3162	15776	28244	1.41	1.0E-128	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3162	15776	28245	1.41	1.0E-128	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
3162	15776	28246	1.41	1.0E-128	Q14585	SWISSPROT	ZINC FINGER PROTEIN HZF10
4244	16832	29283	1.95	1.0E-128	AB040892.1	NT	Homo sapiens mRNA for KIAA1459 protein, partial cds
4367	16954	29394	2.57	1.0E-128	AW755254.1	EST_HUMAN	GMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
4367	16954	29395	2.57	1.0E-128	AW755254.1	EST_HUMAN	Cardiomyopathy associated gene 5
8241	18850	31620	4.78	1.0E-128	AJ006345.1	NT	GMYA5 Human cardiac muscle expression library Homo sapiens cDNA clone 4151935 similar to CMYA5
7181	19713	32561	4.38	1.0E-128	AJ006345.1	NT	Cardiomyopathy associated gene 5
7241	19770	32626	14.44	1.0E-128	11420850	NT	Homo sapiens KVLQT1 gene
7535	20055	32928	0.78	1.0E-128	AF041056.1	NT	Homo sapiens similar to ribosomal protein S26 (H. sapiens) (LOC63694), mRNA
8260	20801	32929	0.78	1.0E-128	AF041056.1	NT	Homo sapiens WSCR4 gene, exons 3 and 4
9991	22486	35473	1.16	1.0E-128	11437282	NT	Homo sapiens WSCR4 gene, exons 3 and 4
9991	22486	35474	1.16	1.0E-128	11437282	NT	Homo sapiens mRNA for KIAA0634 protein, partial cds
11102	23612	36652	3.34	1.0E-128	AA625526.1	EST_HUMAN	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11177	19770	32626	11.7	1.0E-128	11420850	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
11892	24235		2.32	1.0E-128	H83155.1	EST_HUMAN	af7207.r1 Soares_NhHMPu_ST Homo sapiens cDNA clone IMAGE:1047589 5'
12297	24494		2.07	1.0E-128	AL120739.1	EST_HUMAN	Homo sapiens similar to ribosomal protein S28 (H. sapiens) (LOC63694), mRNA
80	12757	25239	1.85	1.0E-130	7708530	NT	Y49C05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:198112 5' similar to
1212	13812	26326	1.23	1.0E-130	AB037835.1	NT	SP-B48150 B48150 HP-25-HIBERNATION-RELATED PROTEIN - TAMIAS ASIATICUS=ASIAN ;
1706	14299	26836	8.52	1.0E-130	BE275192.1	EST_HUMAN	DKFZp762K171_r1 762 (synonym: hmel2) Homo sapiens cDNA clone DKFZp762K171 5'
1706	14299	26837	8.52	1.0E-130	BE275192.1	EST_HUMAN	Homo sapiens hypothetical protein (HSPC242), mRNA
2027	14609		4.6	1.0E-130	X04092.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
2127	14705		1.69	1.0E-130	8394394	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2799	15351		7.47	1.0E-130	AJ010230.1	NT	601121995F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3346366 5'
2903	15520	27989	1.17	1.0E-130	BE564219.1	EST_HUMAN	Human gene for catalase (EC 1.11.1.6) exon 9 mapping to chromosome 11, band p13
2903	15520	27990	1.17	1.0E-130	BE564219.1	EST_HUMAN	Homo sapiens candidate taste receptor T2R16 (T2R16), mRNA
3637	16240	28716	0.96	1.0E-130	AF240898.1	NT	Homo sapiens RET finger protein-like 1 antisense transcript, partial
							601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
							601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
							Homo sapiens retinol dehydrogenase homolog isoform-1 (RDH) mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3831	15520	27989	5.82	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
3831	15520	27990	5.82	1.0E-130	BE564219.1	EST_HUMAN	601343016F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685466 5'
4010	16608	29081	1.56	1.0E-130	AW503580.1	EST_HUMAN	UI-HF-BNO-aky-g-08-Q-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3078731 5'
4147	16739	29192	1.18	1.0E-130	M67710.1	NT	Human T-cell receptor (V alpha 22.1, J alpha RPM14265-variant, C alpha 1) mRNA
4638	17219	29672	9	1.0E-130	AW843983.1	EST_HUMAN	CM4-CN0045-180200-511-f02 CN0045 Homo sapiens cDNA
5258	17821	30246	1.11	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-e11 CT0318 Homo sapiens cDNA
5258	17821	30247	1.11	1.0E-130	AW363299.1	EST_HUMAN	RC0-CT0318-201199-031-e11 CT0318 Homo sapiens cDNA
6910	19569	32396	0.74	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6910	19569	32397	0.74	1.0E-130	AW843875.1	EST_HUMAN	CM0-CN0045-170200-225-g03 CN0045 Homo sapiens cDNA
6923	19582	32411	0.7	1.0E-130	11425446	NT	Homo sapiens estrogen-responsive B box protein (EBBP), mRNA
7301	19829	32687	2.1	1.0E-130	11416777	NT	Homo sapiens solute carrier family 6 (neurotransmitter transporter, L-proline), member 7 (SLC6A7), mRNA
8616	21155		0.98	1.0E-130	AF008551.1	NT	Homo sapiens aurora-related kinase 1 (ARK1) mRNA, complete cds
8753	21292	34212	4.06	1.0E-130	AW956242.1	EST_HUMAN	EST368312 IMAGE resequences, MAGD Homo sapiens cDNA
9141	21678	34619	1.97	1.0E-130	AB037756.1	NT	Homo sapiens mRNA for KIAA1335 protein, partial cds
9846	22344		0.78	1.0E-130	AW103454.1	EST_HUMAN	xd36e06.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2595874 3'
4	12684	25140	2.27	0.0E+00	AA228126.1	EST_HUMAN	zr58c04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811
4	12684	25141	2.27	0.0E+00	AA228126.1	EST_HUMAN	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.
8	12687	25145	1.56	0.0E+00	4885136	NT	G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.
17	12696	25152	2.85	0.0E+00	8923349	NT	Homo sapiens checkpoint suppressor 1 (CHES1), mRNA
17	12696	25153	2.85	0.0E+00	8923349	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
24	12703	25160	4.29	0.0E+00	D83327.1	NT	Homo sapiens hypothetical protein FLJ20371 (FLJ20371), mRNA
24	12703	25161	4.29	0.0E+00	D83327.1	NT	Homo sapiens DCRR1 mRNA, partial cds
29	12708	25165	30.44	0.0E+00	AF141349.1	NT	Homo sapiens DCRR1 mRNA, partial cds
37	12716	25175	38.88	0.0E+00	AF141349.1	NT	Homo sapiens beta-tubulin mRNA, complete cds
39	12718	25178	23.21	0.0E+00	M58600.1	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
42	12721	25182	7.78	0.0E+00	M58600.1	NT	Homo sapiens Cdc42 effector protein 2 (CEP2), mRNA
44	12723	25184	4.41	0.0E+00	M58600.1	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
61	12740	25211	8.23	0.0E+00	Y17151.2	NT	Human heparin cofactor II (HCF2) gene, exons 1 through 5
61	12740	25212	8.23	0.0E+00	Y17151.2	NT	Homo sapiens RNA-binding protein S1, serine-rich domain (RNPS1), mRNA
63	12742	25216	1	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
63	12742	25217	1	0.0E+00	D78804.1	EST_HUMAN	Homo sapiens mRNA for multidrug resistance protein 3 (ABCC3)
							Homo sapiens cDNA clone GEN-516108 5'
							HUM516108B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516108 5'
							HUM516108B Human placenta polyA+ (TFujiwara) Homo sapiens cDNA clone GEN-516108 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
64	12743	25218	28.22	0.0E+00	L16568.1	NT	Human ribosomal protein L7 (RPL7) mRNA, complete cds
66	12745	25222	11.83	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07.3'
66	12745	25222	11.83	0.0E+00	AW069534.1	EST_HUMAN	cr48e07.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr48e07.3'
70	12748	25226	0.8	0.0E+00	M60976.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
71	12749		0.85	0.0E+00	M60976.1	NT	Human von Willebrand factor pseudogene corresponding to exons 23 through 34
79	12756	25237	3.66	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
79	12756	25238	3.66	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
82	12756	25237	1.9	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
82	12756	25238	1.9	0.0E+00	4758977	NT	Homo sapiens protein tyrosine phosphatase, non-receptor type substrate 1 (PTPNS1) mRNA
85	12761	25244	0.85	0.0E+00	4501850	NT	Homo sapiens amiloride binding protein 1 (amilinodase (copper-containing)) (ABP1), nuclear gene encoding mitochondrial protein, mRNA
86	12762		38.11	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
95	12771	25253	37.46	0.0E+00	5016088	NT	Homo sapiens actin, beta (ACTB) mRNA
98	12774	25256	28.23	0.0E+00	U89277.1	NT	Human polyhomeotic 1 homolog (HPH1) mRNA, partial cds
105	12781	25263	2.28	0.0E+00	A1114743.1	EST_HUMAN	HA1347 Human fetal liver cDNA library Homo sapiens cDNA
106	12782	25264	2.19	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
112	12785	25268	0.64	0.0E+00	X91213.1	NT	H. sapiens next1 gene (exon 2)
121	12792	25274	1.98	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833.3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
122	12792	25274	2.44	0.0E+00	A1623701.1	EST_HUMAN	ts38b05.x1 NCI CGAP_U14 Homo sapiens cDNA clone IMAGE:2230833.3' similar to TR:Q99551 Q99551 MITOCHONDRIAL TRANSCRIPTION TERMINATION FACTOR PRECURSOR. ;
123	15383	25275	2.64	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270017.5'
123	15383	25276	2.64	0.0E+00	N36040.1	EST_HUMAN	yy01h09.r1 Soares melanocyte 2NbhM Homo sapiens cDNA clone IMAGE:270017.5'
128	12795	25281	1.12	0.0E+00	4505458	NT	Homo sapiens neuropilin 2 (NRP2) mRNA
136	12801	25289	3.85	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
136	12801	25290	3.85	0.0E+00	4505938	NT	Homo sapiens polymerase (RNA) II (DNA directed) polypeptide A (220kD) (POLR2A) mRNA
144	13059	25562	0.8	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
146	12809	25297	0.85	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310.5'
146	12809	25298	0.85	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Stratagene fetal spleen (#937205) Homo sapiens cDNA clone IMAGE:68310.5'
164	12827		35.47	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
168	12831	25317	2.84	0.0E+00	BF036881.1	EST_HUMAN	601460375F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3663803.5'
170	12833		92.51	0.0E+00	4504444	NT	Homo sapiens heterogeneous nuclear ribonucleoprotein A1 (HNRPA1) mRNA
173	12836	25320	0.75	0.0E+00	AF111168.2	NT	Homo sapiens canine palmitoyl transferase, subunit II gene, complete cds, and unknown genes
175	12838	25321	1.22	0.0E+00	BE295973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864.5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
176	12838	25321	0.84	0.0E+00	BE205973.1	EST_HUMAN	601174270F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3529864 5'
177	12839	25322	2.37	0.0E+00	W73973.1	EST_HUMAN	zdf2b05.r1 Soares_fetal_hair1_NH19W Homo sapiens cDNA clone IMAGE:345201 5' similar to
178	12840	25323	0.77	0.0E+00	BE162832.1	EST_HUMAN	gb:X16282_cds1 ZINC FINGER PROTEIN CLONE 847 (HUMAN);
178	12840	25324	0.77	0.0E+00	BE162832.1	EST_HUMAN	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
178	12841	25325	1.97	0.0E+00	AF244088.1	NT	QV3-HT0457-140200-088-004 HT0457 Homo sapiens cDNA
182	12844	25328	24.45	0.0E+00	AL163202.2	NT	Homo sapiens zinc finger protein mRNA, complete cds
182	12844	25329	24.45	0.0E+00	AL163202.2	NT	Homo sapiens chromosome 21 segment HS21C002
193	12853	25336	4.25	0.0E+00	BE018970.1	EST_HUMAN	b624a12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
193	12853	25337	4.25	0.0E+00	BE018970.1	EST_HUMAN	CE22631 ;
198	12858	25340	2.9	0.0E+00	AB018327.1	NT	b624a12.y1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2963854 5' similar to WP:Y57A10A.Z
198	12858	25341	2.9	0.0E+00	AB018327.1	NT	CE22631 ;
199	12859	25342	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
199	12859	25343	1.88	0.0E+00	AB018327.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
208	12869	25355	92.14	0.0E+00	D50659.1	NT	Homo sapiens mRNA for KIAA0784 protein, partial cds
213	12874	25360	4.7	0.0E+00	AF273045.1	NT	Human gamma-cytoplasmic actin (ACTG9) pseudogene
213	12874	25361	4.7	0.0E+00	AF273045.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
215	12876	25363	8.92	0.0E+00	AF167174.1	NT	Homo sapiens CTCL tumor antigen se14-3 mRNA, complete cds
215	12876	25364	8.92	0.0E+00	AF167174.1	NT	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
225	15410	25371	33.35	0.0E+00	AI587308.1	EST_HUMAN	Homo sapiens chromosome X MSL3-2 protein mRNA, complete cds
225	15410	25372	33.35	0.0E+00	AI587308.1	EST_HUMAN	tp04f08.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
227	12887	25374	1.91	0.0E+00	AF195658.1	NT	tp04f08.x1 NCL_CGAP_U13 Homo sapiens cDNA clone IMAGE:2207847 3' similar to gb:J03191 PROFILIN I (HUMAN);
231	12891		44.25	0.0E+00	4506832	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
232	12892		8.88	0.0E+00	AF132000.1	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
239	12899	25382	2.84	0.0E+00	AB018264.1	NT	Homo sapiens TADA1 protein mRNA, complete cds
240	12899	25382	1.99	0.0E+00	AB018264.1	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
241	12900	25383	3.13	0.0E+00	6678444	NT	Homo sapiens mRNA for KIAA0721 protein, partial cds
248	12908	25387	0.78	0.0E+00	BE246780.1	EST_HUMAN	Mus musculus testis-specific protein, Y-encoded-like (Tspyl), mRNA
							TCBAP1E4466 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4466

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
248	12908	25388	0.78	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4468
248	12908	25389	0.78	0.0E+00	BE246780.1	EST_HUMAN	TCBAP1E4468 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP4468
256	12916	25400	0.97	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
256	12916	25401	0.97	0.0E+00	AB018301.1	NT	Homo sapiens mRNA for KIAA0758 protein, partial cds
259	12918	25405	9.57	0.0E+00	5453805	NT	Homo sapiens NS1-associated protein 1 (NSAP1) mRNA
261	12920		11.16	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
268	12925	25411	4.93	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
270	12927	25414	1.82	0.0E+00	X89772.1	NT	H. sapiens mRNA for interferon alpha/beta receptor (long form)
278	12935		7.37	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
291	12947	25433	1.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
291	12947	25434	1.28	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
293	12949	25436	1.66	0.0E+00	7706028	NT	Homo sapiens hypothetical protein (LOC51250), mRNA
304	12959		2.01	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
305	12960	25449	2.17	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
305	12960	25450	2.17	0.0E+00	D83327.1	NT	Homo sapiens DORR1 mRNA, partial cds
308	12981		1.14	0.0E+00	AW845293.1	EST_HUMAN	IL2-CT0031-181199-020-B03 CT0031 Homo sapiens cDNA
315	12969	25457	6.39	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
315	12969	25458	6.39	0.0E+00	4557029	NT	Homo sapiens potassium inwardly-rectifying channel, subfamily J, member 15 (KCNJ15) mRNA
326	12980	25468	8.1	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
327	12981	25469	4.44	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
328	15413		23.15	0.0E+00	4508728	NT	Homo sapiens ribosomal protein S5 (RP55) mRNA
329	12982	25470	0.99	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylamidimidazole synthetase (GART) mRNA
330	12983		2.5	0.0E+00	AA480002.1	EST_HUMAN	zyl8c06.r1 Soares, NIH-MIPu, S1 Homo sapiens cDNA clone IMAGE:753994 5'
331	12984	25471	18.8	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
332	12984	25471	19.33	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
336	12988	25475	3.18	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
348	13000	25484	1.64	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
349	13000	25485	1.64	0.0E+00	O14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
350	13001	25486	3.83	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA
351	13001	25486	1.41	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK) mRNA

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366	13015	25498	5.41	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (t(11q24) translocated to, 4 (MLLT4) mRNA
367	13018	25499	1.14	0.0E+00	4505256	NT	Homo sapiens moesin (MSN), mRNA
370	13018	25503	20.33	0.0E+00	4827057	NT	Homo sapiens X-box binding protein 1 (XBP1) mRNA
373	13022	25508	1.49	0.0E+00	U71600.1	NT	Human zinc finger protein Zfp31 (zfp31) mRNA, partial cds
378	13026	25512	2.59	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
378	13026	25513	2.59	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
379	15414	25514	2.86	0.0E+00	AF231919.1	NT	Homo sapiens chromosome 21 unknown mRNA
381	13028	25516	0.74	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
384	13031	25520	1.3	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60kD) (GABPA), mRNA
385	13032	25521	1.87	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
386	13032	25521	1.52	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
388	13034	25523	0.83	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
399	13043	25534	3.85	0.0E+00	AU134963.1	EST_HUMAN	AU134963 PLACE1 Homo sapiens cDNA clone PLAGE1000899 5'
410	13085	25578	8.92	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
411	13086	25579	2.03	0.0E+00	A1363014.1	EST_HUMAN	q961105.x1 NCL CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2018457 3' similar to gb.X54199
416	13051	25541	2.36	0.0E+00	AW754180.1	EST_HUMAN	PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (HUMAN);
419	13053	25544	1.95	0.0E+00	4503680	NT	RC2-CT0320-300100-016-a09 CT0320 Homo sapiens cDNA
420	13054	25545	2.21	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
420	13054	25546	2.21	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
421	13055	25547	1.1	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
422	13056	25548	1.46	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
422	13056	25549	1.46	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
423	13057	25550	0.95	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
424	13058	25551	2.9	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
425	13059	25552	1.17	0.0E+00	4503680	NT	Homo sapiens IgG Fc binding protein (FC(GAMMA)BP) mRNA
426	13060	25553	1.66	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
426	13060	25554	1.66	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
427	13060	25553	2.78	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
427	13060	25554	2.78	0.0E+00	X74870.1	NT	H. sapiens gene for RNA pol II largest subunit, exons 23-29
431	13084		96.04	0.0E+00	4506608	NT	Homo sapiens ribosomal protein L19 (RPL19) mRNA
445	12674	25130	1.11	0.0E+00	R17795.1	EST_HUMAN	yg09a02.r1 Soares infant brain INIB Homo sapiens cDNA clone IMAGE:31652 5'

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
453	13087	25580	1.82	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
454	13088		20.68	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S5 (RPS5) mRNA
455	13089	25581	5.49	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
456	13090	25582	10.07	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
456	13090	25583	10.07	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
457	13091	25584	5.34	0.0E+00	AF193607.1	NT	Mus musculus truncated SON protein (Son) mRNA, complete cds
469	13102		0.81	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
471	13104	25597	2.96	0.0E+00	4557879	NT	Homo sapiens interferon gamma receptor 1 (IFNGR1) mRNA
476	13109		0.92	0.0E+00	AA324262.1	EST_HUMAN	EST27054 Cerebellum II Homo sapiens cDNA 5' end
477	13110		1.1	0.0E+00	BE254447.1	EST_HUMAN	601111620F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3352348 5'
493	13126	25611	4.29	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
493	13126	25612	4.29	0.0E+00	4504532	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1B (HTR1B) mRNA
499	13131	25620	11.34	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
499	13131	25621	11.34	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
509	13142	25627	2.62	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
510	13143	25628	5.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
510	13143	25629	5.1	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C048
519	13151	25634	6.04	0.0E+00	AB033035.1	NT	Homo sapiens mRNA for KIAA1209 protein, partial cds
521	13153	25636	2.12	0.0E+00	AU132898.1	EST_HUMAN	AU132898 NT2RP4 Homo sapiens cDNA clone NT2RP4000837 5'
529	13181	25642	6.27	0.0E+00	BE385144.1	EST_HUMAN	601274951F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615756 5'
530	15417	25643	1.89	0.0E+00	AW938825.1	EST_HUMAN	PMO-DT0065-130400-002-c06 DT0065 Homo sapiens cDNA
533	13184	25645	1.33	0.0E+00	AL117233.1	NT	Novel human gene mapping to chromosome 1
534	13185	25646	1.42	0.0E+00	8923955	NT	Homo sapiens PC328 protein (PC328), mRNA
538	13189		0.72	0.0E+00	BF373403.1	EST_HUMAN	IL2-FT0159-070800-120-F07 FT0159 Homo sapiens cDNA
545	13176	25656	4.88	0.0E+00	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
552	15418	25660	1.31	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-H05 BT0635 Homo sapiens cDNA
556	13187	25685	1.27	0.0E+00	BF028005.1	EST_HUMAN	601764859F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996998 5'
562	13193	25672	1.12	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
565	13196	25675	14.24	0.0E+00	6006030	NT	Homo sapiens transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L) mRNA
566	13197	25676	4.05	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
568	13197	25677	4.05	0.0E+00	4504036	NT	Homo sapiens guanine nucleotide binding protein (G protein), alpha 11 (Gq class) (GNA11) mRNA
568	13199	25679	1.36	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA
569	13200	25680	0.96	0.0E+00	8923831	NT	Homo sapiens anillin (LOC54443), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
569	13200	25681	0.96	0.0E+00	8923631	NT	Homo sapiens anillin (LOC54443), mRNA
574	13204		4.55	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
582	13212	25690	1.45	0.0E+00	AW135324.1	EST_HUMAN	U1-H-B11-ecb-h-04-Q-U1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2713951 3'
592	13222		6.6	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
612	13240	25715	4.68	0.0E+00	5174742	NT	Homo sapiens ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCRCF1), nuclear gene encoding mitochondrial protein, mRNA
626	13252		6.05	0.0E+00	J04066.1	NT	Human apolipoprotein A-I (ApoA-I) gene, exon 1
628	13255	25729	2.19	0.0E+00	BF104898.1	EST_HUMAN	601822627F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4045447 5'
630	13257	25731	1.6	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
630	13257	25732	1.6	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
631	13257	25731	1.74	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
631	13257	25732	1.74	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
632	13257	25731	1.81	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
632	13257	25732	1.81	0.0E+00	8923631	NT	Homo sapiens hypothetical protein FLJ20701 (FLJ20701), mRNA
637	13260	25735	0.88	0.0E+00	4501854	NT	Homo sapiens acetyl-Coenzyme A carboxylase beta (ACACB), mRNA
642	13265	25741	0.94	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
642	13265	25742	0.94	0.0E+00	AF221712.1	NT	Homo sapiens Smad- and Olf-interacting zinc finger protein mRNA, partial cds
650	13273	25750	3.63	0.0E+00	AF149773.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
652	13275	25753	0.89	0.0E+00	AB037807.1	NT	Homo sapiens mRNA for KIAA1386 protein, partial cds
654	13277	25754	1.8	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
655	13278	25755	2.31	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
655	13278	25756	2.31	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
656	13279	25757	0.73	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
656	13279	25758	0.73	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
663	13287	25768	1.2	0.0E+00	AA398486.1	EST_HUMAN	z60c07.1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:726732 5'
667	13291	25772	6.55	0.0E+00	D11078.1	NT	Homo sapiens RGH2 gene, retrovirus-like element
671	13295	25775	48.91	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
671	13295	25776	48.91	0.0E+00	W78811.1	EST_HUMAN	zh51b04.r1 Soares fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:415567 5' similar to gb:A21187 ALPHA-2-MACROGLOBULIN PRECURSOR (HUMAN);
674	13298		3.09	0.0E+00	4885525	NT	Homo sapiens novel SH2-containing protein 3 (NSP3) mRNA
681	13305	25788	2.98	0.0E+00	6006003	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2B (GRIN2B) mRNA
683	13307	25791	1.7	0.0E+00	5031624	NT	Homo sapiens CCAAT-box-binding transcription factor (CBF2) mRNA

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686	13310	25795	1.77	0.0E+00	U05235.1	NT	Human neutral amino acid transporter (ASCT1) gene, exon 8
690	13314	25798	0.9	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
690	13314	25799	0.9	0.0E+00	AF108389.1	NT	Homo sapiens sodium/calcium exchanger isoform NaCa3 (NCX1) mRNA, complete cds
696	13319	25804	4.78	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
696	13319	25805	4.78	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
702	15421		1.23	0.0E+00	X57147.1	NT	Human endogenous retrovirus pHE.1 (ERV6)
711	13332	25819	21.02	0.0E+00	4504424	NT	Homo sapiens high-mobility group (nucleosome chromosomal) protein 1 (HMG1) mRNA
718	13337	25823	5.36	0.0E+00	AB028012.1	NT	Homo sapiens mRNA for KIAA1089 protein, partial cds
726	13346	25838	7.22	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
738	13358	25852	87.91	0.0E+00	AA614537.1	EST_HUMAN	np49d01.a1 NCI CGAP Br.1.1 Homo sapiens cDNA clone IMAGE:11296333 3' similar to gb:X57352
742	13362	25856	4.31	0.0E+00	M60875.1	NT	INTERFERON-INDUCIBLE PROTEIN 1-8J (HUMAN);
742	13362	25857	4.31	0.0E+00	M60875.1	NT	Human von Willebrand factor gene, exons 23 through 34
752	13372	25868	1.48	0.0E+00	5032182	NT	Homo sapiens TNF receptor-associated factor 1 (TRAF1) mRNA
758	13377	25872	4.75	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
758	13377	25873	4.75	0.0E+00	AF264750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
760	13379	25878	11.52	0.0E+00	11545800	NT	Homo sapiens hypothetical protein FLJ21634 (FLJ21634), mRNA
766	13385	25884	2.52	0.0E+00	BE241577.1	EST_HUMAN	TCAAP1D0779 Pediatr acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAP0779
766	13404	25808	1.47	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
766	13404	25909	1.47	0.0E+00	AF226990.2	NT	Homo sapiens MHC class I antigen (HLA-G) mRNA, HLA-G1 allele, complete cds
787	13405	25910	0.72	0.0E+00	AF170492.1	NT	Homo sapiens chloride channel CLC4 (ClC4) mRNA, complete cds
780	13408	25913	19.87	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
780	13408	25914	19.87	0.0E+00	J03784.1	NT	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9
783	13411	25915	1.06	0.0E+00	AB037760.1	NT	Homo sapiens mRNA for KIAA1339 protein, partial cds
794	13412	25916	1.82	0.0E+00	6912749	NT	Homo sapiens zinc finger protein 212 (ZNF212), mRNA
798	15425	25918	2.4	0.0E+00	D30612.1	NT	Homo sapiens mRNA for repressor protein, partial cds
797	13414	25919	3.29	0.0E+00	BE689735.1	EST_HUMAN	601445647F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3849803 5'
801	13418	25923	2.87	0.0E+00	R48915.1	EST_HUMAN	y66908.r1 Scores breast 2NblBst Homo sapiens cDNA clone IMAGE:154046 5'
802	13419	25924	4.63	0.0E+00	5032088	NT	Homo sapiens splicing factor 3a, subunit 1, 120KD (SF3A1), mRNA
811	13428	25933	1.72	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
814	13432	25937	3.28	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
825	13442	25949	1.15	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds
825	13442	25950	1.15	0.0E+00	D80006.1	NT	Human mRNA for KIAA0184 gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
830	13447	25954	2.88	0.0E+00	X89772.1	NT	H sapiens mRNA for interferon alpha/beta receptor (long form)
834	13451	25958	2.77	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
834	13451	25959	2.77	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
839	13455	25965	9.17	0.0E+00	5174478	NT	Homo sapiens pericentrin (PCNT) mRNA
840	13456		8.31	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
857	13473	25986	1.71	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
858	13474	25987	2.61	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
860	13476	25989	2.3	0.0E+00	4557686	NT	Homo sapiens voltage-gated channel, Isk-related family, member 1 (KCNE1) mRNA
866	13481	25996	1.58	0.0E+00	AF106830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
867	13482	25997	0.95	0.0E+00	AF106830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
872	13487	26002	2.8	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (GABPA), mRNA
876	13490	26007	1.96	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
876	13490	26008	1.96	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
883	13497		1.72	0.0E+00	AF027193.1	NT	Homo sapiens sodium/myo-inositol cotransporter (SLC5A3) gene, complete cds
887	13501	26019	6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
887	13501	26020	6	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
888	13502	26021	12.68	0.0E+00	4507152	NT	Homo sapiens SON DNA binding protein (SON) mRNA
889	13503	26022	6.37	0.0E+00	AB028942.1	NT	Homo sapiens mRNA for KIAA1019 protein, partial cds
890	13504	26023	15.55	0.0E+00	4506728	NT	Homo sapiens ribosomal protein S6 (RPS6) mRNA
894	13508	26026	1.64	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
894	13508	26027	1.64	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
895	13509	26028	2.12	0.0E+00	AA533272.1	EST_HUMAN	h186407 s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997453
895	13509	26029	2.12	0.0E+00	AA533272.1	EST_HUMAN	h186407 s1 NCI_CGAP_P10 Homo sapiens cDNA clone IMAGE:997453
896	13510		6.29	0.0E+00	BF677694.1	EST_HUMAN	802085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
900	13514	26030	1.67	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
900	13514	26031	1.67	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
901	13515	26032	2.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
901	13515	26033	2.03	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
924	13537	26056	0.95	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
931	13544	26061	1.84	0.0E+00	BE089592.1	EST_HUMAN	QV0-B10703-280400-211-g11 B10703 Homo sapiens cDNA
931	13544	26062	1.84	0.0E+00	BE089592.1	EST_HUMAN	QV0-B10703-280400-211-g11 B10703 Homo sapiens cDNA
941	13554	26071	2.92	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
951	13563		32.19	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
954	13568	26078	6.19	0.0E+00	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
954	13568	26080	6.19	0.0E+00	U35464.1	NT	Human protein C inhibitor (PCI-B) mRNA, complete cds
956	13563		27.9	0.0E+00	4504958	NT	Homo sapiens laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1), mRNA
957	13568	26082	269.29	0.0E+00	AF089747.1	NT	Homo sapiens alpha-1-antichymotrypsin precursor, mRNA, partial cds
958	13569	26083	16.83	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
958	13569	26084	16.83	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
958	13569	26085	16.83	0.0E+00	S69364.1	NT	protein C inhibitor [human, leukocytes, Genomic, 1216 nt, segment 2 of 5]
959	13570	26086	12.58	0.0E+00	L28101.1	NT	Homo sapiens kallistatin (Pl4) gene, exons 1-4, complete cds
966	13598	26111	0.9	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
987	13599	26112	8.4	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
988	13600	26113	0.6	0.0E+00	M37190.1	NT	Human ras inhibitor mRNA, 3' end
989	13601	26114	1.26	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
989	13601	26115	1.26	0.0E+00	4507430	NT	Homo sapiens thyrotrophic embryonic factor (TEF), mRNA
997	15430	26122	6.65	0.0E+00	A1001848.1	EST_HUMAN	os98603.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
997	15430	26123	6.65	0.0E+00	A1001848.1	EST_HUMAN	os98603.s1 NCI_CGAP_GC3 Homo sapiens cDNA clone IMAGE:1613404 3'
999	13610	26126	8.95	0.0E+00	7657266	NT	Homo sapiens KIAA0929 protein Mox2 interacting nuclear target (MINT) homolog (KIAA0929), mRNA
1010	13620	26135	2.35	0.0E+00	AB030568.1	NT	Homo sapiens mRNA for PSP24, complete cds
1019	13629	26142	1.56	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050800-001-f02 GN0014 Homo sapiens cDNA
1019	13629	26143	1.56	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050800-001-f02 GN0014 Homo sapiens cDNA
1019	13629	26144	1.56	0.0E+00	BF366974.1	EST_HUMAN	PM2-GN0014-050800-001-f02 GN0014 Homo sapiens cDNA
1021	13631	26147	2.54	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1021	13631	26148	2.54	0.0E+00	X52207.1	NT	Homo sapiens partial c-fgr gene, exons 2 and 3
1030	13640	26155	2.14	0.0E+00	4757969	NT	Homo sapiens chromodomain protein, Y chromosome-like (CDYL) mRNA
1042	13651	26163	1.99	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1043	13652	26164	31.97	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1044	13652	26164	15.2	0.0E+00	U83668.1	NT	Human beta-tubulin (TUB4q) gene, complete cds
1047	13655		5.72	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1048	13655		7.75	0.0E+00	AF198490.1	NT	Homo sapiens 8q22.1 region and MTG8 (CBFA2T1) gene, partial cds
1052	13659	26170	1.6	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
1053	13659	26170	2.85	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
1054	13659	26170	2.84	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
1055	13660	26171	2.67	0.0E+00	AF111170.3	NT	Homo sapiens 14q32 Jagged2 gene, complete cds, and unknown gene
1058	13663	26174	1.69	0.0E+00	7661685	NT	Homo sapiens DKFZP586M0122 protein (DKFZP586M0122), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1062	13667	26178	3.66	0.0E+00	5803114	NT	Homo sapiens inner membrane protein, mitochondrial (mitofilin) (IMMT), mRNA
1063	13668		2.66	0.0E+00	AA458680.1	EST_HUMAN	aa8607.s1 Stratogene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838236 3' similar to SW:PRSB_HUMAN P47210 26S PROTEASE REGULATORY SUBUNIT 8:
1066	13671	26182	0.94	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1066	13671	26183	0.94	0.0E+00	N43182.1	EST_HUMAN	EST5124 WATM1 Homo sapiens cDNA clone 5124 similar to DNA-DIRECTED RNA POLYMERASE II (alignment Ser and Pro with BLASTx or p)
1067	13672	26184	2.11	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1067	13672	26185	2.11	0.0E+00	4759249	NT	Homo sapiens TRAF family member-associated NFKB activator (TANK) mRNA
1071	13676		2.96	0.0E+00	8922633	NT	Homo sapiens hypothetical protein FLJ11196 (FLJ11196), mRNA
1085	13680	26200	5.51	0.0E+00	4759569	NT	Homo sapiens heat shock 70kD protein 9B (mortalin-2) (HSPA9B) mRNA
1103	13707	26215	2.09	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1103	13707	26216	2.09	0.0E+00	4826872	NT	Homo sapiens cadherin 6, K-cadherin (fetal kidney) (CDH6) mRNA
1107	13711	26220	3.31	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1107	13711	26221	3.31	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
1108	13712	26222	72.04	0.0E+00	AJ245922.1	NT	Homo sapiens mRNA for alpha-tubulin 8 (TUBA8 gene)
1110	13714		1.08	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
1112	13716	26226	4.16	0.0E+00	5174384	NT	Homo sapiens alkylation repair, alkB homolog (ABH), mRNA
1121	13724	26237	4.89	0.0E+00	4758117	NT	Homo sapiens Death associated protein 3 (DAP3) mRNA
1135	13738	26247	2.88	0.0E+00	BE005208.1	EST_HUMAN	MR0-BN0115-200300-003-h08 BN0115 Homo sapiens cDNA
1158	13761	26271	4.25	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1158	13761	26272	4.25	0.0E+00	7706134	NT	Homo sapiens potassium channel, subfamily K, member 9 (KCNK9), mRNA
1171	13773	26282	1.29	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1171	13773	26283	1.29	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
1172	13774	26284	23.49	0.0E+00	4306712	NT	Homo sapiens ribosomal protein S27a (RPS27A) mRNA
1174	13776	26286	1.24	0.0E+00	8923290	NT	Homo sapiens hypothetical protein FLJ20309 (FLJ20309), mRNA
1174	13776	26289	15.95	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1179	13781	26290	37.33	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
1180	13782	26291	6.32	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1180	13782	26292	6.32	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
1184	13785	26295	2.19	0.0E+00	7706500	NT	Homo sapiens Npw38-binding protein NpwBP (LOC51728), mRNA
1185	13786	26296	1.92	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1185	13786	26297	1.92	0.0E+00	X95826.1	NT	H. sapiens ART4 gene
1186	13787	26298	2.16	0.0E+00	A1147650.1	EST_HUMAN	qb22d10.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:1697011 3'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1188	13789	26300	1.59	0.0E+00	AB020710.1	NT	Homo sapiens mRNA for KIAA0903 protein, partial cds
1197	13798	26309	0.7	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1197	13798	26310	0.7	0.0E+00	4758081	NT	Homo sapiens chondroitin sulfate proteoglycan 2 (versican) (CSPG2) mRNA
1198	13799	26311	1	0.0E+00	9968944	NT	Homo sapiens chromosome 12 open reading frame 3 (C12ORF3), mRNA
1210	13810	26323	3.09	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1210	13810	26324	3.09	0.0E+00	7305076	NT	Homo sapiens glutamate decarboxylase 1 (brain, 67kD) (GAD1), transcript variant GAD25, mRNA
1213	13813	26327	1.78	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
1220	13820	26336	8.63	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18), mRNA
1251	13848		0.85	0.0E+00	7657338	NT	Homo sapiens mult. (E. coli) homolog 3 (MLH3), mRNA
1265	13862	26379	0.63	0.0E+00	8922593	NT	Homo sapiens hypothetical protein FLJ10897 (FLJ10897), mRNA
1269	13866	26383	2.13	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1269	13866	26384	2.13	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1270	13867	26385	2.51	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1271	15436	26386	2.03	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
1269	13884	26409	6.85	0.0E+00	AF109718.1	NT	Homo sapiens chromosome 3 subtelomeric region
1290	13885	26410	1.33	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1300	13894	26416	0.83	0.0E+00	4505740	NT	Homo sapiens prefoldin 4 (PF4D4) mRNA
1309	13903		2.3	0.0E+00	Y18000.1	NT	Homo sapiens NF2 gene
1317	13911	26431	160.44	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1324	13918	26440	3.35	0.0E+00	AF084478.1	NT	Homo sapiens Williams-Beuren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
1331	13925	26445	1.6	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1331	13925	26446	1.6	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
1343	13938	26459	2.36	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1343	13938	26460	2.36	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1343	13938	26461	2.36	0.0E+00	5174748	NT	Homo sapiens Wolfram syndrome (WFS) mRNA
1344	13939		2.61	0.0E+00	AF086156.1	NT	Homo sapiens protein phosphatase 2A BR gamma subunit gene, exon 5
1354	15438	26473	2.05	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1354	15438	26474	2.05	0.0E+00	7657529	NT	Homo sapiens rhabdoid tumor deletion region protein 1 (RTDR1), mRNA
1360	13954	26480	4.79	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1361	13955	26481	1.2	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1363	13957	26482	0.97	0.0E+00	Y07829.2	NT	Homo sapiens RFB30 gene for RING finger protein
1364	13958	26483	4.9	0.0E+00	5803146	NT	Homo sapiens ring finger protein 9 (RNF9), mRNA
1365	13959	26484	1.23	0.0E+00	4508004	NT	Homo sapiens zinc finger protein 173 (ZNF173) mRNA
1367	13961	26486	3.51	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1368	13982	26487	2.76	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1369	13983	26488	4.67	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1370	13984	26489	4.11	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1370	13984	26490	4.11	0.0E+00	8567387	NT	Homo sapiens period (Drosophila) homolog 3 (PER3), mRNA
1382	13975	26503	1	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
1442	14035	26563	0.96	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350471 5'
1442	14035	26564	0.96	0.0E+00	BE257955.1	EST_HUMAN	601109792F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:3350471 5'
1454	14048	26576	0.92	0.0E+00	AJ250014.1	NT	Homo sapiens mRNA for Familial Cylindromatosis cyd gene
1462	14054	26587	1.2	0.0E+00	AJ208756.1	EST_HUMAN	qg38b06.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837427 3' similar to WP:127A1.5
1463	14055	26588	11.41	0.0E+00	6042208	NT	RAN, member RAS oncogene family/Homo sapiens RAN, member RAS oncogene family (RAN), mRNA
1472	14064	26599	1	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1472	14064	26600	1	0.0E+00	4505646	NT	Homo sapiens protein convertase subtilisin/kexin type 2 (PCSK2) mRNA
1474	14066	26603	3.26	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1474	14066	26604	3.26	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
1477	14089	26608	7.19	0.0E+00	AJ238093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and Alu repeat elements
1488	14081	26620	3.54	0.0E+00	AF038280.1	NT	Homo sapiens alpha1-6fucosyltransferase (alpha1-6FucT) gene, exon 7
1510	14102	26638	3.27	0.0E+00	AL132699.1	NT	Novel human gene on chromosome 20
1512	14104	26639	1.4	0.0E+00	AL137764.1	NT	Novel human gene mapping to chromosome 1
1516	14108	26644	1.45	0.0E+00	DB7077.1	NT	Human mRNA for KIAA0240 gene, partial cds
1519	14111	26647	9.86	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
1521	14113	26649	2.74	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1521	14113	26650	2.74	0.0E+00	7661965	NT	Homo sapiens KIAA0170 gene product (KIAA0170), mRNA
1558	14150	26682	1.6	0.0E+00	7708434	NT	Homo sapiens hHDC for homolog of Drosophila headcase (LOC51698), mRNA
1573	14166	26697	1.46	0.0E+00	AA481172.1	EST_HUMAN	aa34a03.11 NCI_OGAP_GCB1 Homo sapiens cDNA clone IMAGE:815118 5'
1579	14172	26701	23.67	0.0E+00	AF023860.1	NT	Carcopithecus aethiops cyclophilin A mRNA, complete cds
1579	14172	26702	23.67	0.0E+00	AF023860.1	NT	Carcopithecus aethiops cyclophilin A mRNA, complete cds
1581	14174	26705	1.2	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1581	14174	26706	1.2	0.0E+00	AW976097.1	EST_HUMAN	EST388206 MAGE resequences, MAGN Homo sapiens cDNA
1582	14175	26707	1.02	0.0E+00	D10884.1	NT	Bovine mRNA for neurocalcin
1584	14177		3.69	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
1585	14178	26710	1.89	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB) mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1585	14178	26711	1.89	0.0E+00	4505404	NT	Homo sapiens transmembrane glycoprotein (GPNMB), mRNA
1586	14179	26712	3.3	0.0E+00	7692405	NT	Homo sapiens KIAA0957 protein (KIAA0957), mRNA
1587	14180		8.59	0.0E+00	7656972	NT	Homo sapiens TNF-inducible protein CG12-1 (CG12-1), mRNA
1583	14188	26718	8.98	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1596	15445		25.62	0.0E+00	4506654	NT	Homo sapiens ribosomal protein L5 (RPL5), mRNA
1597	14189	26720	28.65	0.0E+00	M14199.1	NT	Human laminin receptor (2H5 epitope) mRNA, 5' end
1609	14202	26735	11.52	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
1617	14210		1.58	0.0E+00	D00333.1	NT	Human c-yes-2 gene
1624	14217	26749	10.11	0.0E+00	Z83738.1	NT	H. sapiens HH2B/e gene
1625	14218	26750	2.24	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1625	14218	26751	2.24	0.0E+00	5921460	NT	Homo sapiens butyrophilin, subfamily 2, member A1 (BTN2A1), mRNA
1626	14219	26752	7.63	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1626	14219	26753	7.63	0.0E+00	AV690831.1	EST_HUMAN	AV690831 GKC Homo sapiens cDNA clone GKCBOF02 5'
1628	15446	26754	2.78	0.0E+00	AB040905.1	NT	Homo sapiens mRNA for KIAA1472 protein, partial cds
1632	14224	26755	1.01	0.0E+00	AF157478.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3), mRNA, complete cds
1634	14226	26758	3.22	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1634	14228	26759	3.22	0.0E+00	7682183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
1636	14228	26760	37.34	0.0E+00	5728878	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1636	14228	26761	37.34	0.0E+00	5728878	NT	Homo sapiens heat shock 70kD protein 10 (HSC71) (HSPA10), mRNA
1638	14230	26763	0.87	0.0E+00	M91803.1	NT	Human sodium channel mRNA
1652	14244	26778	7.35	0.0E+00	H28973.1	EST_HUMAN	yo76c05.s1 Scores adult brain N2b4HB55Y Homo sapiens cDNA clone IMAGE:183848 3'
1661	14254	26789	1.46	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1661	14254	26790	1.46	0.0E+00	AB046829.1	NT	Homo sapiens mRNA for KIAA1609 protein, partial cds
1680	14272	26805	0.9	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-ajw-c-04-0-U1.s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733294 3'
1708	14301	26838					wg81b07.x1 Scores NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2733294 3'
1709	14302	26839					TR:Q62788 Q62788 CYS2/HIS2 ZINC FINGER PROTEIN ;
1713	14305	26843	1.38	0.0E+00	M28580.1	NT	Homo sapiens T-cell receptor gamma V1 gene region
1713	14305	26844	1.38	0.0E+00	M29580.1	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1715	14307	26846	6.78	0.0E+00	4557887	NT	Human zinc-finger protein 7 (ZFP7) mRNA, complete cds
1716	14308	26847	0.95	0.0E+00	7657065	NT	Homo sapiens keratin 18 (KRT18) mRNA
1720	14312	26850	0.95	0.0E+00	BE222374.1	EST_HUMAN	Hu11d05.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;

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Single Exon Probes Expressed in Fetal Liver.

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1720	14312	26851	0.95	0.0E+00	BE222374.1	EST_HUMAN	hu11d05.x1 NCLCGAP_Lu24 Homo sapiens cDNA clone IMAGE:3166281 3' similar to TR:O95147 O95147 MKP-1 LIKE PROTEIN TYROSINE PHOSPHATASE ;
1723	14314	26855	3.69	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1723	14314	26856	3.69	0.0E+00	H30132.1	EST_HUMAN	yc59e08.r1 Soares breast 3NHBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb:M64099 GAMMA-GLUTAMYL TRANSPEPTIDASE 5 PRECURSOR (HUMAN);
1725	14316	26858	6.58	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
1725	14316	26859	6.58	0.0E+00	Z80780.1	NT	H. sapiens H2B/h gene
1728	14318		20.47	0.0E+00	5031748	NT	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17), mRNA
1737	14327	26871	4.36	0.0E+00	8923841	NT	Homo sapiens FOXJ2 forkhead factor (LOC55810), mRNA
1742	14332	26877	0.92	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1742	14332	26878	0.92	0.0E+00	M75980.1	NT	Human hepatocyte growth factor gene, exon 15
1745	14335	26882	1.17	0.0E+00	4826673	NT	Homo sapiens RNA binding motif protein, Y chromosome, family 1, member A1 (RBM1A1) mRNA
1751	14341	26889	3.79	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP-family protein, complete cds
1753	14343		3.16	0.0E+00	S94400.1	NT	TCR zeta [human, Genomic/mRNA, 365 nt, segment 1 of 8]
1762	14352	26898	1.05	0.0E+00	4557538	NT	Homo sapiens solute carrier family 28 (sulfate transporter), member 2 (SLC26A2) mRNA
1781	14371	26916	2.35	0.0E+00	AF273841.1	NT	Homo sapiens SMCY (SMCY) gene, complete cds
1820	15450		35.11	0.0E+00	4506718	NT	Homo sapiens ribosomal protein S2 (RPS2) mRNA
1825	14414	26960	1.31	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1825	14414	26961	1.31	0.0E+00	4557556	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
1828	14417	26965	1.47	0.0E+00	U63963.1	NT	Human CSF-1 receptor (FMS) gene, complete cds, and (SMF) gene, partial cds
1831	15451	26969	5.45	0.0E+00	4505332	NT	Homo sapiens nuclear autoantigenic sperm protein (histone-binding) (NASP) mRNA
1843	14431	26984	13.82	0.0E+00	U14987.1	NT	Human ribosomal protein L21 mRNA, complete cds
1845	14433	26987	7.44	0.0E+00	AB002331.1	NT	Human mRNA for KIAA0333 gene, partial cds
1846	14434	26988	9.59	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1848	14434	26989	9.59	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1846	14434	26990	9.59	0.0E+00	4502284	NT	Homo sapiens activating transcription factor 4 (tax-responsive enhancer element B67) (ATF4) mRNA
1857	14445	27001	1.57	0.0E+00	4505328	NT	Homo sapiens protein tyrosine phosphatase, receptor-type, zeta polypeptide 1 (PTPRZ1) mRNA
1863	14450	27009	1.38	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1863	14450	27010	1.38	0.0E+00	4504626	NT	Homo sapiens immunoglobulin superfamily, member 3 (IGSF3) mRNA, and translated products
1874	14460	27016	7.62	0.0E+00	6003955	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1874	14460	27017	7.62	0.0E+00	6005855	NT	Homo sapiens Retina-derived POU-domain factor-1 (RPF-1), mRNA
1884	14470	27027	0.93	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1884	14470	27028	0.93	0.0E+00	AB032978.1	NT	Homo sapiens mRNA for KIAA1152 protein, partial cds
1888	14473	27030	5	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1888	14473	27031	5	0.0E+00	4826783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
1889	14474	27032	8.6	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1889	14474	27033	8.6	0.0E+00	U07147.1	NT	Human retinal degeneration slow (RDS) gene, exon 1
1889	14474	27036	1.32	0.0E+00	AW207280.1	EST_HUMAN	UIH-B11-afn-f07-q-U1 st NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1892	14477	27037	1.32	0.0E+00	AW207280.1	EST_HUMAN	UIH-B11-afn-f07-q-U1 st NCI CGAP Sub3 Homo sapiens cDNA clone IMAGE:2722333 3'
1916	14501	27056	3.38	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1916	14501	27057	3.38	0.0E+00	BE277465.1	EST_HUMAN	601179164F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3547239 5'
1939	14523	27079	1.77	0.0E+00	BE006292.1	EST_HUMAN	RC2-BN0128-200300-012-504 BN0128 Homo sapiens cDNA
1967	14551	27106	2.92	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1967	14551	27107	2.92	0.0E+00	4506384	NT	Homo sapiens RAD1 (S. pombe) homolog (RAD1) mRNA, and translated products
1975	14559		1.84	0.0E+00	AF157476.1	NT	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
1978	15455	27116	2.72	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1976	15455	27117	2.72	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
1981	14564	27124	1.69	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1981	14564	27125	1.69	0.0E+00	4507464	NT	Homo sapiens transforming growth factor, beta 3 (TGFB3), mRNA
1985	14567		5.68	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 1 (GSTT1) genes, complete cds
1990	14572		5.14	0.0E+00	M55632.1	NT	Human topoisomerase I pseudogene 1
1999	14581	27139	3.45	0.0E+00	4809282	NT	Homo sapiens histidine ammoniase-lyase (HAL) mRNA
1999	14581	27140	3.45	0.0E+00	4809282	NT	Homo sapiens histidine ammoniase-lyase (HAL) mRNA
2009	14591		0.99	0.0E+00	AL163252.2	NT	Homo sapiens chromosome 21 segment HS21C062
2011	14593	27153	1.13	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2011	14593	27154	1.13	0.0E+00	8400716	NT	Homo sapiens nebulin (NEB), mRNA
2012	14594	27155	2.07	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2012	14594	27156	2.07	0.0E+00	4826638	NT	Homo sapiens actinin, alpha 4 (ACTN4) mRNA
2024	14606	27171	1.03	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2024	14606	27172	1.03	0.0E+00	AB018333.1	NT	Homo sapiens mRNA for KIAA0790 protein, partial cds
2030	14612	27176	1.43	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2030	14612	27177	1.43	0.0E+00	M33782.1	NT	Human TFEB protein mRNA, partial cds
2032	14614	27178	0.89	0.0E+00	AW193024.1	EST_HUMAN	x169501.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
2032	14614	27179	0.89	0.0E+00	AW193024.1	EST_HUMAN	x169501.x1 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2679913 3'
2033	14615	27180	7.94	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2033	14615	27181	7.94	0.0E+00	6912457	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
2035	14617	27183	0.88	0.0E+00	AB011149.1	NT	Homo sapiens mRNA for KIAA0577 protein, complete cds
2036	14618	27184	0.92	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2036	14618	27185	0.92	0.0E+00	Z47558.1	NT	H. sapiens genes for semenogelin I and semenogelin II
2043	14625	27194	2.25	0.0E+00	AB040946.1	NT	Homo sapiens mRNA for KIAA1513 protein, partial cds
2097	14676	27245	0.94	0.0E+00	7708742	NT	Homo sapiens TP53TG3a (TP53TG3a), mRNA
2102	14681	27249	2.71	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2102	14681	27250	2.71	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
2104	14683	27251	1.39	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
2105	14684	27252	3.79	0.0E+00	AU140831.1	EST_HUMAN	AU140831 PLACE4 Homo sapiens cDNA clone PLAGE4000321 5'
2106	14066	26603	1.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2106	14066	26604	1.97	0.0E+00	7705565	NT	Homo sapiens KIAA1114 protein (KIAA1114), mRNA
2108	14886	27254	1.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2108	14886	27255	1.59	0.0E+00	AA077589.1	EST_HUMAN	7B22E10 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B22E10
2110	14688		1.75	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2112	14690		1.76	0.0E+00	4585963	NT	Homo sapiens phosphodiesterase 6A, cGMP-specific, rod, alpha (PDE6A), mRNA
2114	14692		2.2	0.0E+00	A1244247.1	EST_HUMAN	q160008.x1 NCL CGAP_U12 Homo sapiens cDNA clone IMAGE:1988871 3' similar to contains Alu repetitive element
2119	14697	27266	2.72	0.0E+00	BE877225.1	EST_HUMAN	601485146F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887747 5'
2121	14699	27268	1.8	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2121	14699	27269	1.8	0.0E+00	BF315325.1	EST_HUMAN	601902804F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4135320 5'
2126	14704	27276	2.31	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2128	14704	27276	2.31	0.0E+00	BE697125.1	EST_HUMAN	RC3-CT0413-270700-022-410 CT0413 Homo sapiens cDNA
2133	14711	27283	2.79	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2133	14711	27284	2.79	0.0E+00	L00620.1	NT	Human plasma membrane calcium ATPase isoform 2 (APT2B2) mRNA, complete cds
2134	14712	27285	1.81	0.0E+00	AJ297709.1	NT	Homo sapiens mRNA for CDC2L5 protein kinase, (CDC2L5 gene), isoform 1
2139	14717	27289	1.28	0.0E+00	4758483	NT	Homo sapiens GTP binding protein 1 (GTPBP1) mRNA
2143	14721	27292	34.67	0.0E+00	BE500995.1	EST_HUMAN	7a34c-02.x1 NCL CGAP_GC8 Homo sapiens cDNA clone IMAGE:3220610 3' similar to SW:DTD_HUMAN P50443 SULFATE TRANSPORTER;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2160	14737		2.08	0.0E+00	BE767864.1	EST_HUMAN	QV1-GN0065-140800-318-c10 GN0065 Homo sapiens cDNA
2161	14738		1.8	0.0E+00	AF018963.1	NT	Homo sapiens X-linked juvenile retinoschisis protein (XLR31) gene, exon 6 and complete cds
2163	14740	27310	3.84	0.0E+00	BF027562.1	EST_HUMAN	601672066F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3954785 5'
2165	14742	27311	0.98	0.0E+00	AF240788.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
2166	14743	27312	1.35	0.0E+00	AW752708.1	EST_HUMAN	IL3-CT0219-271099-022-G10 CT0219 Homo sapiens cDNA
2168	14745	27314	6.51	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2168	14745	27315	6.51	0.0E+00	A1904640.1	EST_HUMAN	QV-BT065-020399-092 BT065 Homo sapiens cDNA
2202	14778		0.97	0.0E+00	7657252	NT	Homo sapiens potassium large conductance calcium-activated channel, subfamily M, beta member 3-like (KCNMB3L), mRNA
2204	14799		1.37	0.0E+00	L14787.1	NT	Human DNA-binding protein mRNA, 3'end
2230	14805	27377	10.57	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2230	14805	27378	10.57	0.0E+00	AV738288.1	EST_HUMAN	AV738288 CB Homo sapiens cDNA clone CBNBDE08 5'
2232	14807	27380	1.12	0.0E+00	AA931691.1	EST_HUMAN	oc32e01.s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1567896 3'
2234	14809		7.75	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 28
2236	14811	27383	10.88	0.0E+00	BF344434.1	EST_HUMAN	602014829F1 NCI CGAP Bm64 Homo sapiens cDNA clone IMAGE:4150734 5'
2237	14812	27384	20.34	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
2240	14815	27387	2.59	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2240	14815	27388	2.59	0.0E+00	BF377897.1	EST_HUMAN	GM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2244	15461	27393	2.04	0.0E+00	BF313617.1	EST_HUMAN	601900281F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128622 5'
2247	14821	27396	1.56	0.0E+00	BE018750.1	EST_HUMAN	b684e02.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049082 5' similar to TR:Q15170 Q15170 TRANSCRIPTION FACTOR S-II-RELATED PROTEIN
2248	14822	27397	0.94	0.0E+00	AA042813.1	EST_HUMAN	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2248	14822	27398	0.94	0.0E+00	AA042813.1	EST_HUMAN	z63c07.s1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:486540 3' similar to gb:X65867_cds1 OLFACTORY RECEPTOR-LIKE PROTEIN HGMP07E (HUMAN);
2256	14830	27406	2.87	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2256	14830	27407	2.87	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
2257	14831	27408	0.98	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2257	14831	27409	0.98	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2262	14836		1.58	0.0E+00	U38284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
2263	14837	27414	0.91	0.0E+00	AA282281.1	EST_HUMAN	z12b10.r1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712891 5'
2270	14844	27420	0.92	0.0E+00	BE897487.1	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
2271	14845		4.79	0.0E+00	M20903.1	NT	Human apolipoprotein C-I pseudogene, complete cds

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2282	14856	27433	6.28	0.0E+00	4557558	NT	Homo sapiens E1A binding protein p300 (EP300) mRNA
2288	14862	27437	1.15	0.0E+00	7682401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
2295	14889	27445	1.05	0.0E+00	BE965281.1	EST_HUMAN	601433525F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3918607 5'
2298	14872	27448	1.26	0.0E+00	AB037784.1	NT	Homo sapiens mRNA for KIAA1363 protein, partial cds
2339	14910	27482	3.84	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2339	14910	27483	3.84	0.0E+00	11545748	NT	Homo sapiens differentially expressed in FDCP (mouse homolog) 6 (DEF6), mRNA
2340	14911	27484	2.06	0.0E+00	AI076404.1	EST_HUMAN	ox09c07.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1674828 3'
2342	14913	27486	1.81	0.0E+00	AA429001.1	EST_HUMAN	z778a11.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:759740 5'
2342	14913	27487	1.81	0.0E+00	AA429001.1	EST_HUMAN	z778a11.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:759740 5'
2344	14915	27489	1.98	0.0E+00	AA680367.1	EST_HUMAN	z11e12.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:430510 3'
2345	14916	27490	3.65	0.0E+00	BF347039.1	EST_HUMAN	602021846F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4157339 5'
2350	14921	27498	3.07	0.0E+00	L02840.1	NT	Homo sapiens potassium channel Kv2.1 mRNA, complete cds
2351	14922	27497	1.6	0.0E+00	6325468	NT	Homo sapiens flavin containing monooxygenase 3 (FMO3), mRNA
2358	14929	27503	1.17	0.0E+00	BE876095.1	EST_HUMAN	7122a02.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295370 3' similar to TR:094939 094939 KIAA0857 PROTEIN
2360	14931	27504	5.89	0.0E+00	AF044571.1	NT	Homo sapiens phosphatase kinase alpha subunit (PHKA2) gene, exon 32
2361	14932	27505	2.94	0.0E+00	AI625542.1	EST_HUMAN	ly67c08.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2283192 3'
2366	14937	27509	1.72	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2366	14937	27510	1.72	0.0E+00	5803178	NT	Homo sapiens sperm specific antigen 2 (SSFA2), mRNA
2377	14946	27520	0.99	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2377	14946	27521	0.99	0.0E+00	D83778.1	NT	Human mRNA for KIAA0194 gene, partial cds
2378	14947		1.07	0.0E+00	4557521	NT	Human mRNA for KIAA0194 gene, partial cds
2387	14956	27527	2.83	0.0E+00	5174678	NT	Homo sapiens deiodinase, iodothyronine, type 1 (DIO1) mRNA
2391	14959	27531	1.95	0.0E+00	AU131142.1	EST_HUMAN	Homo sapiens signal regulatory protein, beta, 1 (SIRP-BETA-1) mRNA
2392	14960		8.95	0.0E+00	BE784026.1	EST_HUMAN	AU131142 NT2RP3 Homo sapiens cDNA clone NT2RP3002064 5'
2393	14961	27532	0.98	0.0E+00	AW867076.1	EST_HUMAN	601586843F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941003 5'
2394	14982	27533	5.08	0.0E+00	- 76652017	NT	MR1-SND033-120400-002-e04 SN0033 Homo sapiens cDNA
2395	14983	27534	1.69	0.0E+00	4758497	NT	Homo sapiens KIAA0244 protein (KIAA0244), mRNA
2395	14983	27535	1.69	0.0E+00	4758497	NT	Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
							Homo sapiens hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) (H6PD), mRNA
2396	14964		3.28	0.0E+00	AF280107.1	NT	Homo sapiens cytochrome P450 polypeptide 43 (CYP3A43) gene, partial cds; cytochrome P450 polypeptide 4 (CYP3A4) and cytochrome P450 polypeptide 7 (CYP3A7) genes, complete cds; and cytochrome P450
2398	14966	27537	10.16	0.0E+00	AU118082.1	EST_HUMAN	polypeptide 5 (CYP3A5) gene, partial cds
2398	14966	27538	10.16	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
							AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2398	14968	27539	10.16	0.0E+00	AU118082.1	EST_HUMAN	AU118082 HEMBA1 Homo sapiens cDNA clone HEMBA1002839 5'
2458	15025	27595	4.3	0.0E+00	AU119582.1	EST_HUMAN	AU119582 HEMBA1 Homo sapiens cDNA clone HEMBA1006155 5'
2459	15026		3.3	0.0E+00	AI042035.1	EST_HUMAN	ox0302.x1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:1680683 3' similar to TR:O08662
2460	15027	27588	1.06	0.0E+00	8923820	NT	O08662 230KDA PHOSPHATIDYLINOSITOL 4-KINASE ; Homo sapiens hypothetical protein FLJ20693 (FLJ20693), mRNA
2463	15030	27588	1.3	0.0E+00	AW303998.1	EST_HUMAN	xv1507.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2813221 3' similar to TR:O54924
2465	15032		1.28	0.0E+00	BE895805.1	EST_HUMAN	O54924 EXO84 ;
2476	15043		1.17	0.0E+00	AB005822.1	EST_HUMAN	601432608F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916168 5'
2480	15046	27615	8.35	0.0E+00	6006002	NT	AB005822 Hela cDNA (T.Noma) Homo sapiens cDNA similar to adenylate kinase isozyme 2
2484	15049	27619	1.94	0.0E+00	D85606.1	NT	Homo sapiens glutamate receptor, ionotropic, N-methyl D-aspartate 2A (GRIN2A) mRNA
2484	15049	27620	1.94	0.0E+00	D85606.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2491	15056	27629	3.24	0.0E+00	AF108275.1	NT	Homo sapiens gene for cholecystokinin type-A receptor, complete cds
2499	15063	27638	3.07	0.0E+00	5729777	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
2507	15071	27644	4.18	0.0E+00	BF569144.1	EST_HUMAN	Homo sapiens collagen, type XII, alpha 1 (COL12A1), mRNA
2518	15082	27655	2.85	0.0E+00	AW466922.1	EST_HUMAN	602184558T1 NIH_MGC_42 Homo sapiens cDNA clone IMAGE:4300383 3'
2520	15084	27656	2.91	0.0E+00	AW501010.1	EST_HUMAN	ha04h04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2872759 3'
2529	15093		1.39	0.0E+00	AI287878.1	EST_HUMAN	UJHF-BP0p-als-c-07-Q-UJ.r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072780 5'
2537	15101	27674	1.54	0.0E+00	5453965	NT	qv23r06.x1 NCI_CGAP_Lym6 Homo sapiens cDNA clone IMAGE:1882435 3' similar to contains element
2537	15101	27675	1.54	0.0E+00	5453965	NT	MIR repetitive element ;
2548	15112		1.81	0.0E+00	AW813853.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2552	15118	27686	9.72	0.0E+00	BE795542.1	EST_HUMAN	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
2553	15117	27687	1.32	0.0E+00	BF508482.1	EST_HUMAN	RC3-ST0197:300300-016-c04 ST0197 Homo sapiens cDNA
2553	15119	27689	1.52	0.0E+00	Z32684.2	NT	601592530F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3848518 5'
2557	15121		3.57	0.0E+00	5453871	NT	UJH-B14-eoz-b-08-Q-UJ.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3086535 3'
2559	15123	27692	0.89	0.0E+00	BE910378.1	EST_HUMAN	Homo sapiens mRNA for membrane transport protein (XK gene)
2560	15124	27693	3.1	0.0E+00	7657468	NT	Homo sapiens platelet-derived growth factor receptor-like (PDGFR) mRNA
2561	15125	27694	3.56	0.0E+00	BE150895.1	EST_HUMAN	601503356F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3905148 5'
2562	15126	27695	1.24	0.0E+00	8923340	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
2563	15127	27698	3	0.0E+00	U93239.1	NT	RC4-HT0276-160200-019-405 HT0276 Homo sapiens cDNA
2568	15132	27700	1.34	0.0E+00	BE898490.1	EST_HUMAN	Homo sapiens hypothetical protein FLJ20366 (FLJ20366), mRNA
2571	15134	27704	4.84	0.0E+00	BE875511.1	EST_HUMAN	Human Sec62 (Sec62) mRNA, complete cds
2571	15134	27705	4.84	0.0E+00	BE875511.1	EST_HUMAN	601508211F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3909866 5'
							601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'
							601489241F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3891371 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2587	15150	27714	0.9	0.0E+00	BE536921.1	EST_HUMAN	601064738F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451161 5'
2592	15154	27721	9.34	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2592	15154	27722	9.34	0.0E+00	AU143277.1	EST_HUMAN	AU143277 Y79AA1 Homo sapiens cDNA clone Y79AA1001673 5'
2593	15155	27723	0.9	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987855 5'
2593	15155	27724	0.9	0.0E+00	BE292896.1	EST_HUMAN	601105312F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987855 5'
2596	15158	27726	8.62	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
2633	15402	27766	1.76	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2633	15402	27767	1.76	0.0E+00	AB037836.1	NT	Homo sapiens mRNA for KIAA1415 protein, partial cds
2634	15194		3.12	0.0E+00	BF513835.1	EST_HUMAN	UI-H-BW1-amp-T-12-0-UI.s1 NCI CGAP_Sub57 Homo sapiens cDNA clone IMAGE:3070631 3'
2643	15202	27775	1.24	0.0E+00	AI571737.1	EST_HUMAN	tn18p08.x1 NCI CGAP_Bn25 Homo sapiens cDNA clone IMAGE:2168055 3' similar to gb.L20977 CALCIUM-TRANSPORTING ATPASE PLASMA MEMBRANE, BRAIN ISOFORM 2 (HUMAN);
2644	15203	27776	2.06	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 28kD (TAF21) mRNA
2647	15206	27779	6.91	0.0E+00	AB037859.1	NT	Homo sapiens mRNA for KIAA1438 protein, partial cds
2648	15207	27780	0.99	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3844304 5'
2648	15207	27781	0.99	0.0E+00	BE795445.1	EST_HUMAN	601590108F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3844304 5'
2651	15210	27782	1.16	0.0E+00	BE283328.1	EST_HUMAN	601143722F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051389 5'
2655	15214		5.98	0.0E+00	BE782472.1	EST_HUMAN	601594830F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939222 5'
2663	15221	27793	1.73	0.0E+00	4504686	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1) mRNA
2671	15228		1.65	0.0E+00	U78027.1	NT	Homo sapiens Bruton's tyrosine kinase (BTK), alpha-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and FTP3 (FTP3) genes, complete cds
2672	15230	27800	6.98	0.0E+00	AF173227.1	NT	Homo sapiens guanylate cyclase-activating protein 2 (GUCA1B) gene, exon 1
2676	15234	27801	2.15	0.0E+00	AB011108.1	NT	Homo sapiens mRNA for KIAA0536 protein, partial cds
2680	15238	27805	1.01	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2680	15238	27806	1.01	0.0E+00	AU130403.1	EST_HUMAN	AU130403 NT2RP3 Homo sapiens cDNA clone NT2RP3000779 5'
2682	15240	27808	1.22	0.0E+00	AW887016.1	EST_HUMAN	RC1-OT0086-220300-011-407 OT0086 Homo sapiens cDNA
2685	15243	27811	3.43	0.0E+00	BE383165.1	EST_HUMAN	601298714F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3828923 5'
2686	15244		2.17	0.0E+00	BE531263.1	EST_HUMAN	601276373F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3610267 5'
2712	15269	27837	1.4	0.0E+00	8922843	NT	Homo sapiens hypothetical protein FLJ11052 (FLJ11052), mRNA
2748	15303		9.58	0.0E+00	AA316723.1	EST_HUMAN	EST188414 HCC cell line (metastasis to liver in mouse) II Homo sapiens cDNA 5' end similar to ribosomal protein L29
2749	15304	27868	12.57	0.0E+00	BE794984.1	EST_HUMAN	601589625F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3843591 5'
2755	15310	27876	2.37	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
2757	15312	27878	0.97	0.0E+00	7669517	NT	Homo sapiens neuregulin 1 (NRG1), transcript variant SMDF, mRNA

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2758	15313	27878	1.42	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
2760	15315	27881	1.23	0.0E+00	AB051826.1	NT	Homo sapiens hG28K mRNA for GTP-binding protein like 1, complete cds
2765	15319	27885	20.41	0.0E+00	BE798376.1	EST_HUMAN	601591991F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945983 5'
2766	15320	27886	2.11	0.0E+00	BF680632.1	EST_HUMAN	60215923F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297132 5'
2769	15376	27890	14.33	0.0E+00	BE593433.1	EST_HUMAN	601335485F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689564 5'
2770	15323		1.77	0.0E+00	AV721647.1	EST_HUMAN	AV721647 HTB Homo sapiens cDNA clone HTBBYE08 5'
2772	15325	27893	2.47	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2773	15325	27894	2.47	0.0E+00	5174486	NT	Homo sapiens spermatogenesis associated PD1 (KIAA0757) mRNA
2773	15326	27895	1.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477). mRNA
2773	15328	27896	1.25	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477). mRNA
2774	15327	27897	2.27	0.0E+00	AF280195.1	NT	Homo sapiens hypertension-related calcium-regulated gene mRNA, complete cds
2775	15328		131.05	0.0E+00	AV651066.1	EST_HUMAN	AV651066 GLC Homo sapiens cDNA clone GLC007 3'
2776	15329	27898	4.94	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2776	15329	27899	4.94	0.0E+00	BF377897.1	EST_HUMAN	CM1-TN0141-250900-439-b08 TN0141 Homo sapiens cDNA
2780	15333	27902	7.42	0.0E+00	4757963	NT	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2784	15337	27908	3.11	0.0E+00	BE747193.1	EST_HUMAN	Homo sapiens cerebellar degeneration-related protein (34kD) (CDR1) mRNA
2796	15349		0.98	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2797	15350	27919	2.78	0.0E+00	BF514110.1	EST_HUMAN	UI-H-BW1-armw-e-07-d-JL1 NCI_CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3071340 3'
2804	15356		0.88	0.0E+00	4503098	NT	Homo sapiens chondrin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2808	15361	27928	1.76	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2809	15361	27929	1.76	0.0E+00	7705275	NT	Homo sapiens angiotensin-3 (ANG-3), mRNA
2810	15362	27930	4.3	0.0E+00	BF677694.1	EST_HUMAN	602085579F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249915 5'
2814	15366	27936	1.1	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA
2817	15369	27938	17.28	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2817	15369	27939	17.28	0.0E+00	AV725534.1	EST_HUMAN	AV725534 HTC Homo sapiens cDNA clone HTCCCA03 5'
2819	15371		9.44	0.0E+00	AI679163.1	EST_HUMAN	ai55404.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2518663 5' similar to SW:R13A HUMAN P40429 60S RIBOSOMAL PROTEIN L13A:
2822	15374	27944	1.69	0.0E+00	BF530661.1	EST_HUMAN	602071957F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4214679 5'
2823	15375	27945	7.68	0.0E+00	BE872768.1	EST_HUMAN	601450812F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3854842 5'
2825	15377	27946	1.55	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2825	15377	27947	1.55	0.0E+00	AU131494.1	EST_HUMAN	AU131494 NT2RP3 Homo sapiens cDNA clone NT2RP3002672 5'
2826	15378	27948	34.11	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'
2826	15378	27949	34.11	0.0E+00	BE300344.1	EST_HUMAN	600944794F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960806 5'

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2832	12881	25345	7.88	0.0E+00	S76830.1	NT	glycoprotein D=Duffy group antigen [human, blood, Genomic DNA, 3088 nt]
2835	15385		1.75	0.0E+00	AB033281.1	NT	Homo sapiens BTROP2 mRNA for F-box and WD-repeats protein isoform C, complete cds
2841	13382	25881	1.88	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2841	13382	25882	1.88	0.0E+00	AF284750.1	NT	Homo sapiens ALR-like protein mRNA, partial cds
2846	13682	26192	3.33	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2846	13682	26193	3.33	0.0E+00	4503202	NT	Homo sapiens cytochrome P450, subfamily 1 (dioxin-inducible), polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1) mRNA
2861	15480	27856	4.7	0.0E+00	X85980.1	NT	H. sapiens serine hydroxymethyltransferase pseudogene
2862	15481		2.28	0.0E+00	AF068824.1	NT	Homo sapiens 5-aminolevulinate synthase 2 (ALAS2) gene, complete cds
2863	15482		1.83	0.0E+00	AB040960.1	NT	Homo sapiens mRNA for KIAA1527 protein, partial cds
2870	15488		1.06	0.0E+00	AJ238852.1	NT	Homo sapiens partial tp13 gene for ribosomal protein L3, U82 snRNA, U83a snRNA and U83b snRNA genes
2871	15489	27860	2.43	0.0E+00	AL163201.2	NT	Homo sapiens chromosome 21 segment HS21C001
2875	15493	27863	1.99	0.0E+00	M80902.1	NT	Human AHNAK nucleoprotein mRNA, 5' end
2877	15495	27865	1.25	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281268-003-002 HT0343 Homo sapiens cDNA
2877	15495	27866	1.26	0.0E+00	BE154504.1	EST_HUMAN	PM0-HT0343-281268-003-002 HT0343 Homo sapiens cDNA
2879	15497		1	0.0E+00	X73428.1	NT	H. sapiens lds gene for HLH type transcription factor
2881	15499		2.76	0.0E+00	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C088
2882	15500	27869	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2882	15500	27870	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2882	15500	27871	1.01	0.0E+00	7019584	NT	Homo sapiens zinc finger protein 221 (ZNF221), mRNA
2884	15502	27872	2.39	0.0E+00	M98478.1	NT	Human transglutaminase mRNA, complete cds
2888	15505	27875	15.68	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2888	15505	27876	15.68	0.0E+00	D50657.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
2891	15508	27879	1.95	0.0E+00	AL086857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
2892	15509		7.43	0.0E+00	Y10658.1	NT	H. sapiens mRNA for nuclear DNA helicase II
2893	15510		1.17	0.0E+00	AF152303.1	NT	Homo sapiens protocadherin alpha C1 (PCDH-alpha-C1) mRNA, complete cds
2894	15511	27880	112.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2894	15511	27881	112.87	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2894	15521	27891	2.68	0.0E+00	4507280	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2907	15524	27895	1.03	0.0E+00	AL047599.1	EST_HUMAN	DKFZp586G0621_r1 586 (synonym: hule1) Homo sapiens cDNA clone DKFZp586G0621
2908	15525	27898	1.84	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA
2908	15525	27897	1.64	0.0E+00	7661883	NT	Homo sapiens KIAA0054 gene product; Helicase (KIAA0054), mRNA

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2909	15526		2.8	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
2912	15529	27999	6.04	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-103 BT0636 Homo sapiens cDNA
2912	15529	28000	6.04	0.0E+00	BE081896.1	EST_HUMAN	QV2-BT0636-130400-138-103 BT0636 Homo sapiens cDNA
2918	15535	28008	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2918	15535	28009	0.71	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
2921	15538	28013	2.25	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2921	15538	28014	2.25	0.0E+00	AL163206.2	NT	Homo sapiens chromosome 21 segment HS21C006
2922	15539	28015	1.29	0.0E+00	AA215579.1	EST_HUMAN	z96b11.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683517 3' similar to contains Alu repetitive element;
2928	15545		4.1	0.0E+00	Y19210.1	NT	Homo sapiens HHb5 gene for hair keratin, exons 1 to 9
2932	15548	28024	1.24	0.0E+00	4758279	NT	Homo sapiens EphA4 (EPHA4) mRNA
2934	15550	28027	41.84	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
2936	15552	28029	1.65	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
2937	15553	28030	1.25	0.0E+00	AF152338.1	NT	Homo sapiens protocadherin gamma C4 (PCDH-gamma-C4) mRNA, complete cds
2946	15562	28037	0.92	0.0E+00	AI209084.1	EST_HUMAN	q94904.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1838527 3' similar to SW:CB20_HUMAN P52288 20 KD NUCLEAR CAP BINDING PROTEIN ;
2954	15570	28045	1.78	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2954	15570	28046	1.78	0.0E+00	AB033093.1	NT	Homo sapiens mRNA for KIAA1267 protein, partial cds
2955	15571	28047	6.84	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2955	15571	28048	6.84	0.0E+00	AB040941.1	NT	Homo sapiens mRNA for KIAA1508 protein, partial cds
2958	15574	28051	3.14	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2958	15574	28052	3.14	0.0E+00	7661903	NT	Homo sapiens KIAA0100 gene product (KIAA0100), mRNA
2959	15575	28053	3.48	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2959	15575	28054	3.48	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog), translocated to, 4 (MLLT4) mRNA
2964	15579	28058	1.12	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2964	15579	28059	1.12	0.0E+00	BF110702.1	EST_HUMAN	7n40d03.x1 NCL CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3567028 3' similar to TR:Q9VLN1
2972	15586	28070	2.98	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2972	15588	28071	2.98	0.0E+00	4505084	NT	Homo sapiens melanoma antigen, family B, 4 (MAGEB4), mRNA
2981	15597	28077	1.82	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
2985	15601	28080	1.33	0.0E+00	X15308.1	NT	H. sapiens NF-H gene, exon 4

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2985	15601	28081	1.33	0.0E+00	X15309.1	NT	H. sapiens NF-H gene, exon 4
2987	15603	28083	9.28	0.0E+00	AF108275.1	NT	Homo sapiens immunoglobulin-like transcript 1c variant 4 (ILT1c) gene, exon 6
3001	15617		1.26	0.0E+00	A1149880.1	EST_HUMAN	qf43f09.x1 Scores_testis NHT Homo sapiens cDNA clone IMAGE:1752809 3'
3009	15625	28103	0.72	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3009	15625	28104	0.72	0.0E+00	AF281074.1	NT	Homo sapiens neuropilin 2 (NRP2) gene, complete cds, alternatively spliced
3010	15628	28105	1.24	0.0E+00	4506118	NT	Homo sapiens prospero-related homeobox 1 (PROX1) mRNA
3011	15627	28106	2.29	0.0E+00	AB004884.1	NT	Homo sapiens mRNA for PKU-alpha, partial cds
3023	15639	28110	1.93	0.0E+00	7682273	NT	Homo sapiens KIAA0737 gene product (KIAA0737), mRNA
3025	15641	28118	2.52	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3025	15641	28119	2.52	0.0E+00	5729755	NT	Homo sapiens calcium channel, voltage-dependent, gamma subunit 3 (CACNG3), mRNA
3036	15652	28130	1.45	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
3036	15652	28131	1.45	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN), complete cds
3060	15676		0.73	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
3062	15678	28152	1.4	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
3072	15687	28159	0.72	0.0E+00	4506882	NT	Homo sapiens semenogelin 1 (SEMG1) mRNA
3075	15690	28163	0.66	0.0E+00	AW976266.1	EST_HUMAN	EST388375 MAGe resequences, MAGN Homo sapiens cDNA
3080	15695		3.96	0.0E+00	AF185953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
3083	15698	28171	20.17	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3083	15698	28172	20.17	0.0E+00	5579469	NT	Homo sapiens heat shock 70kD protein 1 (HSPA1A), mRNA
3085	15700		7.12	0.0E+00	AL359403.1	NT	Isoform 2 of a novel human mRNA from chromosome 22
3089	15704	28176	2.79	0.0E+00	AF017433.1	NT	Homo sapiens putative transcription factor CR53 (CR53) mRNA, partial cds
3092	15707						Homo sapiens transcription factor GHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel α_2
3112	15727	28198	2.39	0.0E+00	AF198779.1	NT	Human germline gene 16.1 for Ig lambda L-chain C region (IgLC16.1)
3118	15732		3.45	0.0E+00	X03529.1	NT	Homo sapiens F-box protein FBL5 (FBL5) mRNA, complete cds
3122	15736	28205	1.69	0.0E+00	AF198955.1	NT	Homo sapiens melanoma-associated antigen (MAGE-C1) gene, complete cds
3140	15754	28221	1.74	0.0E+00	AF064589.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds
3141	15755	28222	3.56	0.0E+00	AF265208.1	NT	Homo sapiens NOD1 protein (NOD1) gene, exons 1, 2, and 3
3146	15760	28226	5.25	0.0E+00	AF149773.1	NT	Homo sapiens KIAA0469 gene product (KIAA0469), mRNA
3147	15761	28227	4.35	0.0E+00	7662139	NT	Homo sapiens olfactory receptor-like protein (OLFR 42B) gene, OLFR 42B-9110 allele, partial cds
3175	15788	28260	1.46	0.0E+00	AF042075.1	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3185	15797	28269	3.49	0.0E+00	4926783	NT	Human ferritin heavy chain mRNA, complete cds
			48.14	0.0E+00	L20941.1	NT	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3188	15800	28272	2.08	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3188	15800	28273	2.08	0.0E+00	AB011121.1	NT	Homo sapiens mRNA for KIAA0549 protein, partial cds
3196	15808	28281	18.48	0.0E+00	T94870.1	EST_HUMAN	ye32703.s1 Stragene lung (4937210) Homo sapiens cDNA clone IMAGE:119453 3' similar to SP:S29539
3210	15822	28298	1.23	0.0E+00	BF243336.1	EST_HUMAN	601878507F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4107433 5'
3211	15823	28298	1.28	0.0E+00	A1968086.1	EST_HUMAN	wu12h10.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2516803 3'
3216	15828	28306	4.69	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3216	15828	28307	4.69	0.0E+00	X98922.1	NT	H.sapiens mRNA for gamma-glutamyltransferase
3218	15830	28309	0.63	0.0E+00	A1985950.1	EST_HUMAN	tu3809.x1 NCL_CGAP_P128 Homo sapiens cDNA clone IMAGE:2253376 3' similar to SW:RASD_DICD1
3226	15838	28317	1.57	0.0E+00	4758827	NT	P03987 RAS-LIKE PROTEIN RASD
3226	15838	28318	1.57	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3233	15845	28325	10.75	0.0E+00	4504658	NT	Homo sapiens neuroxin III (NRXN3) mRNA
3234	15846	28326	0.92	0.0E+00	4507720	NT	Homo sapiens interleukin 1 receptor, type I (IL1R1) mRNA
3234	15846	28327	0.92	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3245	15857	28340	1	0.0E+00	AJ277892.1	NT	Homo sapiens titin (TTN) mRNA
3253	15865	28346	2.88	0.0E+00	M28699.1	NT	Homo sapiens partial TTN gene for titin
3257	15869	28349	2.27	0.0E+00	4502098	NT	Homo sapiens nucleolar phosphoprotein B23 (NPM1) mRNA, complete cds
3263	15875	28357	0.96	0.0E+00	4758055	NT	(SLC25A5), nuclear gene encoding mitochondrial carrier, adenine nucleotide translocator, member 5
3263	15875	28358	0.96	0.0E+00	4758055	NT	Homo sapiens CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP) mRNA
3265	15877	28359	4.57	0.0E+00	AA774783.1	EST_HUMAN	ae97b11.s1 Stragene schizo brain S11 Homo sapiens cDNA clone IMAGE:971133 3'
3273	15885	28367	4.14	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3273	15885	28368	4.14	0.0E+00	AF286598.1	NT	Homo sapiens angiotensin binding protein 1 mRNA, complete cds
3285	15896	28374	1.44	0.0E+00	4557590	NT	Homo sapiens fibrillin 1 (Marfan syndrome) (FBN1) mRNA
3292	15903	28383	1.09	0.0E+00	4507720	NT	Homo sapiens titin (TTN) mRNA
3300	15911		0.96	0.0E+00	M65189.1	NT	Human connexin 43 processed pseudogene
3301	15912	28390	1.7	0.0E+00	AF019413.1	NT	Homo sapiens HLA class III region containing tenascin X (tenascin-X) gene, partial cds; cytochrome P450 21-hydroxylase (CYP21B), complement component C4 (C4B) G11, helicase (SKI2W), RD, complement factor B (Bf), and complement component C2 (C2) genes,>
3303	15914	28392	4.47	0.0E+00	AF050084.1	NT	Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA, complete cds
3313	18001	28400	2.26	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3313	18001	28401	2.26	0.0E+00	4502014	NT	Homo sapiens A kinase (PRKA) anchor protein 1 (AKAP1), mRNA
3328	15939	28415	2.57	0.0E+00	AF285208.1	NT	Homo sapiens SWI-SNF complex protein p270 mRNA, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3330	15940	28418	1.66	0.0E+00	8923624	NT	Homo sapiens hypothetical protein FLJ20695 (FLJ20695), mRNA
3355	15963	28440	1.02	0.0E+00	4885312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
3368	15974	28451	5.6	0.0E+00	AI589284.1	EST_HUMAN	t58908.x2 NCL CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2222535 3' similar to SW:RL11_RAT
3369	15977	28454	1.4	0.0E+00	AW955400.1	EST_HUMAN	P25121 60S RIBOSOMAL PROTEIN L11; contains Alu repetitive element;
3374	15983	28460	2.28	0.0E+00	AF128893.1	NT	EST367470 IMAGE resequencing, MAGD Homo sapiens cDNA
3374	15983	28461	2.28	0.0E+00	AF128893.1	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3375	15984	28462	0.91	0.0E+00	7657213	NT	Homo sapiens telomerase reverse transcriptase (TERT) gene, exons 1-6
3375	15984	28463	0.91	0.0E+00	7657213	NT	Homo sapiens hormonally upregulated neu tumor-associated kinase (HUNK), mRNA
3378	15987	28465	1.23	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), mRNA
3378	15987	28466	1.23	0.0E+00	4502582	NT	Homo sapiens caspase 8, apoptosis-related cysteine protease (CASP8), mRNA
3382	15991	28469	13.03	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
3384	15993	28471	0.89	0.0E+00	AB040940.1	NT	Homo sapiens mRNA for KIAA1507 protein, partial cds
3403	16012	28491	1.08	0.0E+00	AI632569.1	EST_HUMAN	wb10f04.x1 NCL CGAP_GCB Homo sapiens cDNA clone IMAGE:2305279 3' similar to TR:Q91928 Q91928
3443	16051	28526	3.18	0.0E+00	AU123664.1	EST_HUMAN	ZINC FINGER PROTEIN
3450	16057	28532	0.94	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3450	16057	28533	0.94	0.0E+00	7363436	NT	Homo sapiens olfactory receptor, family 10, subfamily C, member 1 (OR10C1), mRNA
3453	16060	28535	1.88	0.0E+00	7708239	NT	Homo sapiens neuroblastoma-amplified protein (LOC51594), mRNA
3454	16081	28536	1.04	0.0E+00	AF211189.1	NT	Homo sapiens T-type calcium channel alpha1 subunit Alpha1a isoform (CACNA1I) mRNA, complete cds
3458	16065		1.03	0.0E+00	AW867015.1	EST_HUMAN	MR1-SN0033-100400-001-c08 SN0033 Homo sapiens cDNA
3471	16077	28550	1.28	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3471	16077	28551	1.28	0.0E+00	7662401	NT	Homo sapiens KIAA0952 protein (KIAA0952), mRNA
3472	16078	28552	1.05	0.0E+00	4502398	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1) mRNA
3475	16081	28554	1.72	0.0E+00	5803067	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2 (LILRA2), mRNA
3484	15313	27879	1.56	0.0E+00	AF110763.1	NT	Homo sapiens skeletal muscle LIM-protein 1 (FHL1) gene, complete cds
3489	16084	28557	2.36	0.0E+00	7657038	NT	Homo sapiens death receptor 6 (DR6), mRNA
3490	16095	28568	0.97	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3490	16095	28569	0.97	0.0E+00	5453965	NT	Homo sapiens protein kinase, AMP-activated, alpha 2 catalytic subunit (PRKAA2) mRNA
3493	16098	28573	5.92	0.0E+00	K02980.1	NT	Bacteriophage P1 replication region including repA, parA, and parB genes and incA, incB, and incC
3495	16100	28575	1.2	0.0E+00	7427522	NT	Homo sapiens protein tyrosine phosphatase, receptor type, T (PTPRT), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3497	16102	28577	1	0.0E+00	4557748	NT	Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET) mRNA
3501	16108	28581	3.89	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE :
3501	16108	28582	3.89	0.0E+00	AI935159.1	EST_HUMAN	wp14d10.x1 NCL CGAP_Lu19 Homo sapiens cDNA clone IMAGE:2464819 3' similar to TR:O73634 O73634 NEURAL CELL ADHESION MOLECULE :
3505	16110	28587	2.13	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
3508	16111	28588	1.12	0.0E+00	7706378	NT	Homo sapiens ASB-4 protein (LOC51686), mRNA
3512	16117	28598	2.09	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3512	16117	28597	2.09	0.0E+00	6552332	NT	Homo sapiens v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS), mRNA
3518	16123	28603	1.4	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10
3523	16128	28608	8.45	0.0E+00	U43283.1	NT	Human MDS1A (AML1/MDST fusion) mRNA, partial cds
3528	16133	28612	0.94	0.0E+00	9558718	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3532	16137	28618	2.45	0.0E+00	AF045452.1	NT	Homo sapiens hypothetical protein (AF038169), mRNA
3532	16137	28619	2.45	0.0E+00	AF045452.1	NT	Homo sapiens cell-line K31 transcriptional regulatory protein p54 mRNA, complete cds
3540	16145	28628	1.19	0.0E+00	AF231922.1	NT	Homo sapiens chromosome 21 unknown mRNA
3547	16151	28631	0.95	0.0E+00	AA628677.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3547	16151	28632	0.95	0.0E+00	AA628677.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3547	16151	28633	0.95	0.0E+00	AA628677.1	EST_HUMAN	ab51112.1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:844367 5'
3553	16157	28639	1.53	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3553	16157	28640	1.53	0.0E+00	BE304791.1	EST_HUMAN	601143853F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:3051373 5'
3558	16160	28643	2.51	0.0E+00	4503648	NT	Homo sapiens coagulation factor IX (plasma thromboplastic component, Christmas disease, hemophilia B) (F9) mRNA
3557	16161	28644	1.08	0.0E+00	4826785	NT	Homo sapiens potassium voltage-gated channel, Isk-related family, member 2 (KCNE2) mRNA
3560	16164	28647	1.98	0.0E+00	O14887	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3565	16169	28651	0.93	0.0E+00	AJ384007.1	EST_HUMAN	ts35g12.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:2088742 3' similar to TR:O00498
3568	16172	28654	1.52	0.0E+00	M10976.1	NT	Human endogenous retroviral DNA (4-1), complete retroviral segment
3585	16189	28672	0.74	0.0E+00	AA456282.1	EST_HUMAN	z89h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3585	16189	28673	0.74	0.0E+00	AA456282.1	EST_HUMAN	z89h04.r1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:811927 5'
3594	16198	28681	1	0.0E+00	AV701869.1	EST_HUMAN	AV701869 ADB Homo sapiens cDNA clone ABDAH06 5'
3595	16199	28682	0.73	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
3597	16201	28686	1.47	0.0E+00	AF078868.1	NT	Homo sapiens homologous yeast-44.2 protein mRNA, complete cds
3608	16210	28690	1.07	0.0E+00	AL133204.1	NT	Novel human gene mapping to chromosome X

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3610	16213	28693	0.89	0.0E+00	AB040909.1	NT	Homo sapiens mRNA for KIAA1476 protein, partial cds
3622	16225	28703	1.1	0.0E+00	8923087	NT	Homo sapiens hypothetical protein FLJ20080 (FLJ20080), mRNA
3633	16236	28711	1.16	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3633	16236	28712	1.16	0.0E+00	6997248	NT	Homo sapiens sal (Drosophila)-like 1 (SALL1), mRNA
3634	16237		1.14	0.0E+00	AI081907.1	EST_HUMAN	α77c11.x1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:1662356 3' similar to WP.T18B4.4 CE13742.
3636	16239	28715	1.26	0.0E+00	6325463	NT	Homo sapiens butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA
3641	16244		5.41	0.0E+00	AW852217.1	EST_HUMAN	QV0-C10225-230300-169-e01 G10225 Homo sapiens cDNA
3645	16248	28724	1.08	0.0E+00	4504294	NT	Homo sapiens H3 histone family, member K (H3FK), mRNA
3649	16252		1.74	0.0E+00	AF118846.1	NT	Homo sapiens gamma-glutamylcysteine synthetase (GLCLO) gene, partial cds
3650	16253	28725	8.35	0.0E+00	BF676393.1	EST_HUMAN	602084583F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4248596 5'
3653	16256						α94M06.s1 NCI_CGAP_Kid6 Homo sapiens cDNA clone IMAGE:1694043 3' similar to contains MER29.b2
3653	16256		0.98	0.0E+00	AA988715.1	EST_HUMAN	MER29 repetitive element.
3663	16265	28737	0.9	0.0E+00	AW937977.1	EST_HUMAN	QV0-DT0047-170200-123-g01 DT0047 Homo sapiens cDNA
3675	16276	28743	0.8	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283845 5'
3675	16276	28744	0.8	0.0E+00	BF672054.1	EST_HUMAN	602152486F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4283845 5'
3676	16277		1.3	0.0E+00	4826987	NT	Homo sapiens retinoblastoma-binding protein 2 (RBBP2), mRNA
3678	16278	28746	0.96	0.0E+00	AW684693.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3678	16278	28747	0.96	0.0E+00	AW684693.1	EST_HUMAN	h184g01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2978024 3'
3682	16283	28751	0.8	0.0E+00	4828763	NT	Homo sapiens heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (HS3ST1), mRNA
3684	16285	28754	0.91	0.0E+00			Homo sapiens KIAA0808 gene product (KIAA0808), mRNA
3692	16293	28762	0.72	0.0E+00	7662319	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
3692	16293	28763	0.72	0.0E+00	4557752	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
3709	16310	28777	1.47	0.0E+00	D87327.1	NT	Homo sapiens midline 1 (Opitz/BBB syndrome) (MID1), mRNA
3712	16313		20.4	0.0E+00	7669491	NT	Homo sapiens glyceraldehyde-3-phosphate dehydrogenase (GAPD), mRNA
3730	16331	28797	2.49	0.0E+00	AB026542.1	NT	Homo sapiens WAVE2 mRNA for WASP family protein, complete cds
3732	16333	28799	0.93	0.0E+00	AB007868.2	NT	Homo sapiens mRNA for KIAA0406 protein, partial cds
3734	16335	28800	2.62	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3734	16335	28801	2.62	0.0E+00	AF124250.1	NT	Homo sapiens SH2-containing protein Nsp2 mRNA, complete cds
3739	16340	28807	2.63	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3739	16340	28808	2.63	0.0E+00	AA852743.1	EST_HUMAN	NHTBCae15g09f1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBCae15g09
3743	16344	28811	1.66	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3743	16344	28812	1.66	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
3746	16347	28815	1.08	0.0E+00	AW851714.1	EST_HUMAN	MR2-CT0222-281099-005-e05 CT0222 Homo sapiens cDNA
3748	16349	28817	1.4	0.0E+00	5729928	NT	Homo sapiens matrix metalloproteinase 24 (membrane-inserted) (MMP24), mRNA
3750	16351	28819	1.23	0.0E+00	AB018339.1	NT	Homo sapiens mRNA for KIAA0786 protein, partial cds
3752	16353	28821	1.56	0.0E+00	Q14867	SWISSPROT	TRANSCRIPTION REGULATOR PROTEIN BACH1 (BTB AND CNC HOMOLOG 1) (HA2303)
3754	16355	28823	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3756	16356	28824	0.83	0.0E+00	AB020717.1	NT	Homo sapiens mRNA for KIAA0910 protein, partial cds
3767	16368	28833	4.72	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-qls-e-12-0-J1.s1 NCJ CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3767	16368	28834	4.72	0.0E+00	AW298134.1	EST_HUMAN	UI-H-BW0-qls-e-12-0-J1.s1 NCJ CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2733022 3'
3792	16392	28857	1.06	0.0E+00	AB004630.1	NT	Human gene for Type XIX collagen a1 chain, exon 8
3793	16393	28858	0.87	0.0E+00	AA463659.1	EST_HUMAN	es08q01.r1 Soares, NIH-MP, S1 Homo sapiens cDNA clone IMAGE:812496 5' similar to
3798	16398	28863	1.04	0.0E+00	AB020710.1	NT	SW:KRB4_SHEEP P02445 KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIB4, [1];
3801	16401	28865	4.05	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3810	16408	28874	0.95	0.0E+00	AB037835.1	NT	Homo sapiens mRNA for KIAA1414 protein, partial cds
3828	16426	28888	7.87	0.0E+00	7662183	NT	Homo sapiens KIAA0669 gene product (KIAA0669), mRNA
3834	16433	28894	23.27	0.0E+00	4508718	NT	Homo sapiens ribosomal protein S2 (RPS2), mRNA
3834	16433	28895	1.04	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3834	16433	28895	1.04	0.0E+00	7657065	NT	Homo sapiens v-ets avian erythroblastosis virus E26 oncogene related (ERG), mRNA
3873	16471	28935	0.92	0.0E+00	7681867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3873	16471	28936	0.92	0.0E+00	7681867	NT	Homo sapiens KIAA0022 gene product (KIAA0022), mRNA
3892	16491	28951	2.65	0.0E+00	AF179733.1	NT	Pan troglodytes olfactory receptor (PTR208) gene, partial cds
3896	16495	28956	1.55	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3896	16495	28957	1.55	0.0E+00	7657468	NT	Homo sapiens similar to rat integral membrane glycoprotein POM121 (POM121L1), mRNA
3900	16498	28962	1.35	0.0E+00	A1377699.1	EST_HUMAN	te62f10.x1 Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2091307 3'
3901	16500	28971	1.09	0.0E+00	AF152498.1	NT	Homo sapiens protocadherin beta 3 (PCDH-beta3), mRNA, complete cds
3902	16501	28963	2.32	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPLI) (DSP), mRNA
3905	16504	28966	10.94	0.0E+00	S79685.1	NT	Homo sapiens ATP-sensitive inwardly rectifying K-channel subunit (KCNJB1/BIR1) gene, complete cds
3906	16505	28967	2.15	0.0E+00	7710148	NT	Homo sapiens methyl CpG binding protein 2 (MECP2), mRNA
3907	16506	28968	2.69	0.0E+00	7662183	NT	Homo sapiens KIAA0569 gene product (KIAA0569), mRNA
3910	16509	28970	1.1	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3910	16509	28971	1.1	0.0E+00	AF069601.2	NT	Homo sapiens myosin light chain kinase isoform 2 (MLCK) mRNA, complete cds
3916	16514	28977	0.84	0.0E+00	6812735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3921	16519	28985	6.15	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3921	16519	28986	6.15	0.0E+00	4503178	NT	Homo sapiens chromosome X open reading frame 5 (CXORF5) mRNA
3923	16521	28989	4.15	0.0E+00	U09412.1	NT	Human zinc finger protein ZNF134 mRNA, complete cds
3924	16522	28990	32.21	0.0E+00	AF114488.1	NT	Homo sapiens intersectin short isoform (ITSN) mRNA, complete cds
3927	16525	28992	1.48	0.0E+00	4828783	NT	Homo sapiens potassium voltage-gated channel, Shab-related subfamily, member 1 (KCNB1) mRNA
3930	16528	28995	1.1	0.0E+00	AF012815.1	NT	Homo sapiens familial mental retardation protein 2 (FMR2) gene, exon 11
3931	16529	28996	1.83	0.0E+00	4759171	NT	Homo sapiens SC35-interacting protein 1 (SRRP129), mRNA
3933	16531	28998	1.09	0.0E+00	AF098117.1	NT	Homo sapiens amphiphysin gene, partial cds
3944	16542	29009	2.45	0.0E+00	AI864727.1	EST_HUMAN	wk0101.1 NCI CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411065 3' similar to TR-O43340
3947	16545	29013	16.56	0.0E+00	4508742	NT	O43340 R28830.2, contains element PTR7 repetitive element;
3952	16550	29019	1.8	0.0E+00	AL040338.1	EST_HUMAN	Homo sapiens ribosomal protein S8 (RPS8), mRNA
3957	16555	29025	1.03	0.0E+00	6005887	NT	DKFZp434N0413.1 434 (synonym: hras3) Homo sapiens cDNA clone DKFZp434N0413 5'
3957	16555	29026	1.03	0.0E+00	6005887	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3958	16556	29027	2.86	0.0E+00	4504138	NT	Homo sapiens AP1 gamma subunit binding protein 1 (AP1GBP1), mRNA
3960	16558	29031	2.2	0.0E+00	4505078	NT	Homo sapiens glutamate receptor, metabotropic 3 (GRM3) mRNA
3964	16562	29043	1.02	0.0E+00	AF149412.1	NT	Homo sapiens melanoma antigen, family B, 1 (MAGEB1) mRNA
3975	16573	29047	1.92	0.0E+00	4508753	NT	Homo sapiens HBP17 heparin-binding and FGF-binding protein gene, complete cds
3978	16577	29047	1.81	0.0E+00	4585642	NT	Homo sapiens ryanodine receptor 3 (RYR3) mRNA
3988	16586	29057	1.88	0.0E+00	BF355295.1	EST_HUMAN	Homo sapiens zinc finger protein (KIA040412) mRNA
3990	16588	29059	1.04	0.0E+00	AW888221.1	EST_HUMAN	RC3-H10860-170800-011-a12 H10860 Homo sapiens cDNA
3990	16588	29060	1.04	0.0E+00	AW888221.1	EST_HUMAN	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1986728 similar to MXRA5
3998	16596	29068	2.84	0.0E+00	AF129533.1	NT	MXRA5 Human matrix tissue expression library Homo sapiens cDNA clone Incyte 1986728 similar to MXRA5
4001	16599	29071	1.08	0.0E+00	U86281.1	NT	Matrix remodeling associated gene 5
4001	16599	29072	1.06	0.0E+00	U86281.1	NT	Homo sapiens F-box protein Fbl3b (FBL3B) mRNA, partial cds
4006	16604	29078	4.1	0.0E+00	BE378802.1	EST_HUMAN	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4014	16612	29085	1.28	0.0E+00	AW580740.1	EST_HUMAN	Homo sapiens olfactory receptor (OR7-141) gene, partial cds
4047	16644	29110	13.52	0.0E+00	AF116195.1	NT	601236968F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608800 5'
4047	16644	29111	13.52	0.0E+00	AF116195.1	NT	PM3-L70031-100100-003-H09 L70031 Homo sapiens cDNA
4057	16654		4.5	0.0E+00	M23910.1	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
4059	16656		6.04	0.0E+00	AL163303.2	NT	Homo sapiens cancer-testis antigen CT10 (CT10) gene, complete cds
							Human MHC class II lymphocyte antigen DPw4-beta-2 pseudogene, exon 2
							Homo sapiens chromosome 21 segment HS21C103

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4065	16662	29124	1.23	0.0E+00	AL118494.1	NT	Novel human gene mapping to chromosome 20
4069	16665	29126	3.49	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4077	16673	29134	2.12	0.0E+00	AL163288.2	NT	Homo sapiens chromosome 21 segment HS21C088
4090	16686		60.86	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4099	16693	29150	1.89	0.0E+00	U09306.1	NT	Human zinc finger protein ZNF133
4120	16713	29169	10.72	0.0E+00	AB015610.1	NT	Chlorococcus aethiops mRNA for ribosomal protein S4X, complete cds
4130	16722	29185	3.27	0.0E+00	AJ238617.1	NT	Homo sapiens mRNA for UGA suppressor tRNA-associated antigenic protein (RNA48 gene)
4140	16732	29186	1.81	0.0E+00	AL163203.2	NT	Homo sapiens chromosome 21 segment HS21C003
4141	16733	29188	2.96	0.0E+00	AJ272726.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4141	16733	29187	2.96	0.0E+00	AJ272726.1	NT	Homo sapiens mRNA for rapa-2 (rapa gene)
4148	16740	29193	8.52	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4148	16740	29194	8.52	0.0E+00	5032026	NT	Homo sapiens retinoblastoma-binding protein 4 (RBBP4) mRNA
4158	16750	29203	0.98	0.0E+00	4503914	NT	Homo sapiens phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminimidazole synthetase (GART) mRNA
4164	16755	29207	7.55	0.0E+00	4885306	NT	Homo sapiens G protein-coupled receptor 21 (GPR21), mRNA
4165	16756	29208	4.94	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
4168	16759	29209	0.68	0.0E+00	4758807	NT	Homo sapiens ras GTPase activating protein-like (NGAP) mRNA
4169	16760	29210	6.82	0.0E+00	11419287	NT	Homo sapiens IMP (inosine monophosphate) dehydrogenase 1 (IMPDH1), mRNA
4170	16761	29211	2.88	0.0E+00	AL096857.1	NT	Novel human mRNA from chromosome 1, which has similarities to BAT2 genes
4171	16762		1.11	0.0E+00	AA018975.1	EST_HUMAN	ze55a09.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:362920 5' similar to contains Alu repetitive element;
4178	16769	29218	3.61	0.0E+00	AF165527.1	NT	Homo sapiens DGCR8 (DGCR8) mRNA, complete cds
4189	13773	26282	0.76	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4189	13773	26283	0.76	0.0E+00	4826947	NT	Homo sapiens protein kinase, X-linked (PRKX) mRNA
4195	16785	29233	2.14	0.0E+00	5901905	NT	Homo sapiens butyrophilin, subfamily 3, member A2 (BTN3A2), mRNA
4196	16786	29234	1.21	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60KD) (GABPA), mRNA
4196	16786	29235	1.21	0.0E+00	4503854	NT	Homo sapiens GA-binding protein transcription factor, alpha subunit (60KD) (GABPA), mRNA
4198	16789	29237	0.57	0.0E+00	4506884	NT	Homo sapiens semenogelin II (SEMG2) mRNA
4200	16789	29237	1.35	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4200	16789	29238	1.35	0.0E+00	8922391	NT	Homo sapiens hypothetical protein FLJ10379 (FLJ10379), mRNA
4206	16795	29242	0.59	0.0E+00	AB020702.1	NT	Homo sapiens mRNA for KIAA0895 protein, partial cds
4213	16802	29251	18.39	0.0E+00	AJ982597.1	EST_HUMAN	wu04d04.x1 NCJ CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4213	16802	29252	18.39	0.0E+00	AJ982597.1	EST_HUMAN	wu04d04.x1 NCJ CGAP GC8 Homo sapiens cDNA clone IMAGE:2515975 3'
4216	16804	29254	1.08	0.0E+00	BE184856.1	EST_HUMAN	MR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Database Source	Top Hit Descriptor
4216	16804	29255	1.08	0.0E+00	BE184898.1	NR1-HT0707-100500-001-a02 HT0707 Homo sapiens cDNA
4221	16808		3.97	0.0E+00	BE274217.1	60112078F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2987630 5'
4227	16815	29262	1.12	0.0E+00	AB032951.1	Homo sapiens mRNA for KIAA1125 protein, partial cds
4227	16815	29263	1.12	0.0E+00	AB032951.1	Homo sapiens mRNA for KIAA1125 protein, partial cds
4229	16817	29265	2.51	0.0E+00	5728725	Homo sapiens nuclear receptor coactivator 3 (NCOA3), mRNA
4236	16824		5.9	0.0E+00	AW675699.1	ba51f04.x1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2900095 3' similar to SW:TH12_BOVIN
4241	16829	29279	1.14	0.0E+00	AW408798.1	Q95108 MITOCHONDRIAL THIOREDOXIN PRECURSOR
4242	16830	29280	1.64	0.0E+00	8922466	UI-HF-BMD-edx-c-02-0-JUL1 NIH_MGC_38 Homo sapiens cDNA clone IMAGE:3063147 5'
4242	16830	29281	1.64	0.0E+00	8922466	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4251	16839		2.08	0.0E+00	5174632	Homo sapiens hypothetical protein FLJ10498 (FLJ10498), mRNA
4263	16849	29297	1.06	0.0E+00	AB037739.1	Homo sapiens polycystic kidney disease (polycystin) and REJ (sperm receptor for egg jelly, sea urchin homolog)-like (PKDREJ) mRNA
4270	16858	29303	10.06	0.0E+00	AA401438.1	Homo sapiens mRNA for KIAA1318 protein, partial cds
4270	16858	29304	10.06	0.0E+00	AA401438.1	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;
4273	16859	29308	1.01	0.0E+00	AF157476.1	zu68h07.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:743197 3' similar to contains Alu repetitive element; contains element MER35 repetitive element;
4286	16872	29319	1.02	0.0E+00	4507720	Homo sapiens DNA polymerase zeta catalytic subunit (REV3) mRNA, complete cds
4286	16872	29320	1.02	0.0E+00	4507720	Homo sapiens titin (TTN) mRNA
4301	16887	29331	1.09	0.0E+00	7681989	Homo sapiens titin (TTN) mRNA
4305	16891	29333	1.6	0.0E+00	4758199	Homo sapiens KIAA0173 gene product (KIAA0173), mRNA
4305	16891	29334	1.6	0.0E+00	4758199	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4314	16900		0.72	0.0E+00	AL163303.2	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA
4344	16931	29372	1.17	0.0E+00	AJ003145.1	Homo sapiens chromosome 21 segment HS21G103
4346	16933	29374	0.96	0.0E+00	AJ010770.1	Homo sapiens mRNA for olfactory receptor protein, pseudogene
4360	16947	29389	17.92	0.0E+00	J02610.1	Homo sapiens hyperion gene, exons 1-50
4375	16962	29408	0.84	0.0E+00	AW636889.1	Human apolipoprotein B-100 mRNA, complete cds
4381	16968	29415	0.59	0.0E+00	4828827	PM2-D10023-080300-004-e08 D10023 Homo sapiens cDNA
4381	16968	29416	0.59	0.0E+00	4828827	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4383	16970	29418	4.39	0.0E+00	AF174590.1	Homo sapiens myelodysplasia syndrome 1 (MDS1) mRNA
4391	16977		2.19	0.0E+00	AI189844.1	Homo sapiens F-box protein Fbl4 (FBL4) mRNA, partial cds
4395	16980		4.49	0.0E+00	U14520.1	q023f08.x1 Soares_placenta_8to9weeks_2NbtIP8t08W Homo sapiens cDNA clone IMAGE:1724579 3' similar to contains MER20 b2 MER20 repetitive element;
						Human CBFA3 (Cbfa3) gene, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4399	16984	29429	0.84	0.0E+00	5174574	NT	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 4 (MLLT4) mRNA
4418	17003	29446	0.9	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4418	17003	29447	0.9	0.0E+00	6563384	NT	Homo sapiens protein kinase C, nu (PRKCN), mRNA
4425	17010	29453	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4425	17010	29454	1.16	0.0E+00	U10991.1	NT	Human G2 protein mRNA, partial cds
4433	17019	29459	11.1	0.0E+00	6912281	NT	Homo sapiens COMPLEMENT COMPONENT C1q RECEPTOR (C1QR), mRNA
4451	17037		1.13	0.0E+00	AF153047.2	NT	Homo sapiens gap junction protein connexin-36 (CX36) gene, complete cds
4460	17046	29489	4.6	0.0E+00	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
4464	17050	29494	5.78	0.0E+00	Z60780.1	NT	H. sapiens H2B/h gene
4464	17050	29495	5.78	0.0E+00	Z60780.1	NT	H. sapiens H2B/h gene
4470	17056	29501	1.97	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4470	17056	29502	1.97	0.0E+00	X60483.1	NT	H. sapiens H4/d gene for H4 histone
4475	17060	29508	10.17	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4475	17060	29509	10.17	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4484	17069	29519	1.11	0.0E+00	X82338.1	NT	Homo sapiens Menkes disease gene, exon 4
4487	17072	29523	16.07	0.0E+00	4885126	NT	Homo sapiens caudal type homeo box transcription factor 4 (CDX4), mRNA
4488	17073	29524	1.73	0.0E+00	AJ271738.1	NT	Homo sapiens Xq pseudautosomal region; segment 2/2
4491	17076	29526	1.14	0.0E+00	AB037781.1	NT	Homo sapiens myosin regulatory light chain interacting protein (MIR), mRNA
4528	17110	29554	1.43	0.0E+00	7019458	NT	Homo sapiens mRNA for KIAA1360 protein, partial cds
4537	17121		7.31	0.0E+00	AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
4545	17129	29572	1.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4545	17129	29573	1.27	0.0E+00	AJ249765.1	NT	Homo sapiens ACTN2 gene for alpha-Actinin 2, exon 10
4549	17132	29579	0.58	0.0E+00	W26178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4549	17132	29580	0.58	0.0E+00	W26178.1	EST_HUMAN	24g7 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA
4555	17138	29585	6.07	0.0E+00	4506782	NT	Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1) (SCA1), mRNA
4555	17138	29586	6.07	0.0E+00	4506782	NT	Homo sapiens spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1) (SCA1), mRNA
4567	17150		2.3	0.0E+00	AF200828.1	NT	Homo sapiens HPS1 gene, intron 5
4585	17168	28611	0.59	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA CoB-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft205 5'
4585	17168	28612	0.59	0.0E+00	T10233.1	EST_HUMAN	seq1329 b4HB3MA CoB-HAP-Ft Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft205 5'
4588	17171		0.65	0.0E+00	M14123.1	NT	Human endogenous retrovirus HERV-K10

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4589	17172	29616	1.48	0.0E+00	AA228126.1	EST_HUMAN	z58c04.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
4589	17172	29617	1.48	0.0E+00	AA228126.1	EST_HUMAN	z58c04.1 Soares_NHMPu_S1 Homo sapiens cDNA clone IMAGE:667590 5' similar to TR:G222811 G222811 ALPHA 1 CHAIN OF TYPE XII COLLAGEN.;
4598	17183	29630	6.46	0.0E+00	AWD084964.1	EST_HUMAN	xc68e08.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2589446 3' similar to SW:AHNK_HUMAN Q06666 NEUROBLAST DIFFERENTIATION ASSOCIATED PROTEIN AHNAK.;
4601	18007		2.1	0.0E+00	B051619	NT	Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA
4603	17186	29633	0.92	0.0E+00	AI696698.1	EST_HUMAN	wc56b02.x1 NCI_CGAP_P728 Homo sapiens cDNA clone IMAGE:2322603 3' similar to contains MER22.b2 PTR5 repetitive element.;
4607	17190		8.58	0.0E+00	AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
4609	17192	29638	2.41	0.0E+00	AW381570.1	EST_HUMAN	PM1-HT0305-101169-002-003 HT0305 Homo sapiens cDNA
4615	17198	29645	1.43	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4615	17198	29646	1.43	0.0E+00	AJ278120.1	NT	Homo sapiens mRNA for putative ankyrin-repeat containing protein (ORF1)
4617	17200	29648	2.01	0.0E+00	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
4618	17201	29649	3.28	0.0E+00	AF108830.1	NT	Homo sapiens serine-threonine protein kinase (MNBH) mRNA, complete cds
4623	17206	29655	1.19	0.0E+00	4506952	NT	Homo sapiens sialyltransferase 8 (alpha-N-acetylneuraminase: alpha-2,8-sialyltransferase, GD3 synthase) (SIAT8) mRNA
4628	17211	29661	1.16	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4628	17211	29662	1.16	0.0E+00	AF111163.1	NT	Homo sapiens pyrin (MEFV) gene, complete cds
4637	18008	29673	2.92	0.0E+00	6005973	NT	Homo sapiens zinc finger protein 195 (ZNF195), mRNA
4642	17224	29678	4.04	0.0E+00	AF208181.1	NT	Homo sapiens syncytin precursor, mRNA, complete cds
4647	17228	29685	1.66	0.0E+00	AF152337.1	NT	Homo sapiens probocadherin gamma C3 (PCDH-gamma-C3) mRNA, complete cds
4650	17232	29688	1.5	0.0E+00	5454175	NT	Homo sapiens zinc finger protein 211 (ZNF211), mRNA
4662	17244	29698	32.6	0.0E+00	4503470	NT	Homo sapiens eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) mRNA
4671	17253	29705	0.79	0.0E+00	4505016	NT	Homo sapiens low density lipoprotein receptor-related protein 6 (LRP6) mRNA, and translated products
4676	17257	29708	1.02	0.0E+00	4503098	NT	Homo sapiens chondroitin sulfate proteoglycan 4 (melanoma-associated) (CSPG4), mRNA
4679	17261	29713	1.14	0.0E+00	4502356	NT	Homo sapiens calcium/calmodulin-dependent protein kinase IV (CAMK4) mRNA
4684	17266		3.03	0.0E+00	L35485.1	NT	Homo sapiens iduronate sulphate sulphatase (IDS) gene, complete cds
4686	17268	29716	9.75	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4686	17268	29717	9.75	0.0E+00	7662091	NT	Homo sapiens KIAA0390 gene product (KIAA0390), mRNA
4707	17289	29733	3.17	0.0E+00	AF143314.1	NT	Homo sapiens PTEN (PTEN) gene, exons 3 through 5
4710	17292	29736	11.37	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4710	17282	29737	11.37	0.0E+00	AJ245418.1	NT	Homo sapiens mRNA for G7c protein (G7c gene located in the class III region of the major histocompatibility complex)
4712	17284	29738	0.64	0.0E+00	AB018338.1	NT	Homo sapiens mRNA for KIAA0705 protein, partial cds
4718	17288		0.65	0.0E+00	D87875.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
4730	17311		1.68	0.0E+00	AA174072.1	EST_HUMAN	zfp18g08.s1 Strategene fetal retina 937202 Homo sapiens cDNA clone IMAGE:609854 3'
4732	17313		1.97	0.0E+00	7657410	NT	Homo sapiens cdz (odd Oz/ten-m, Drosophila) homolog 1 (ODZ1), mRNA
4734	17316		2.45	0.0E+00	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4735	17318	29758	1.89	0.0E+00	AF184110.1	NT	Homo sapiens cyclophilin-related protein (NKTFR) gene, complete cds
4736	17317	29759	5.45	0.0E+00	AL163300.2	NT	Homo sapiens chromosome 21 segment HS21C100
4737	17318		1.94	0.0E+00	AB037521.1	NT	Homo sapiens gene for natriuretic protein, partial cds
4739	17320	29760	0.62	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
4747	17328	29770	8.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4747	17328	29771	8.77	0.0E+00	4557887	NT	Homo sapiens keratin 18 (KRT18) mRNA
4748	17328	29772	1.57	0.0E+00	AF187441.1	NT	Mus musculus E-cadherin binding protein E7 mRNA, complete cds
4757	17338	29783	1.13	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4757	17338	29784	1.13	0.0E+00	AB028970.1	NT	Homo sapiens mRNA for KIAA1047 protein, partial cds
4763	17344	29792	12.17	0.0E+00	Y18890.1	NT	Human endogenous retrovirus type K (HERV-K), gag, pol and env genes
4772	17353	29805	1.21	0.0E+00	BE081527.1	EST_HUMAN	QV2-BT0635-160400-142-h05 BT0635 Homo sapiens cDNA
4773	17354	29806	1.04	0.0E+00	AA418246.1	EST_HUMAN	z196b07.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:767605 3'
4779	17360		2.04	0.0E+00	AF086841.1	NT	Homo sapiens truncated tenascin XB (TNXB) gene, partial cds and TNXA gene recombination breakpoint region
4785	17365	29816	1.09	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4785	17365	29817	1.09	0.0E+00	AL163278.2	NT	Homo sapiens chromosome 21 segment HS21C078
4786	17366	29818	2.54	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4786	17366	29819	2.54	0.0E+00	AB037820.1	NT	Homo sapiens mRNA for KIAA1399 protein, partial cds
4787	17367	29820	2.04	0.0E+00	M74099.1	NT	Human displacement protein (CCAAT) mRNA
4792	17371	29824	2	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4792	17371	29825	2	0.0E+00	6453812	NT	Homo sapiens butyrophilin, subfamily 2, member A2 (BTN2A2), mRNA
4794	12809	25297	1.8	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Strategene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:68310 5'
4794	12809	25298	1.8	0.0E+00	T56945.1	EST_HUMAN	ya83g04.12 Strategene fetal spleen (#637205) Homo sapiens cDNA clone IMAGE:68310 5'
4797	17375	29831	1.1	0.0E+00	BE278730.1	EST_HUMAN	601158935F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505521 5'
4803	17381	29849	0.84	0.0E+00	BE390050.1	EST_HUMAN	601285248F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607087 5'
4818	17398	29849	0.83	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA
4818	17398	29850	0.93	0.0E+00	5729817	NT	Homo sapiens ecotropic viral integration site 2B (EVI2B), mRNA

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4819	17397	29851	1.01	0.0E+00	U56651.1	NT	Mus musculus neurophilin 1 (Nxp1) gene, large exon and 3' end of the intron, and partial cds
4823	17401	29854	5.32	0.0E+00	M80902.1	NT	Human AHNK nucleoprotein mRNA, 5' end
4826	17404	29857	133.49	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4828	17404	29858	133.49	0.0E+00	M69197.1	NT	Human haptoglobin and haptoglobin-related protein (HP and HPR) genes, complete cds
4829	17407	29861	1.32	0.0E+00	AF184110.1	NT	Human haptoglobin-related protein (NKR) gene, complete cds
4832	17410	29863	1.26	0.0E+00	7662181	NT	Homo sapiens KIAA0563 gene product (KIAA0563), mRNA
4851	17429		1.08	0.0E+00	X58467.1	NT	Human CYP2D7AP pseudogene for cytochrome P450 2D6
4861	17439	29868	0.83	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4861	17439	29869	0.83	0.0E+00	7304922	NT	Homo sapiens bromodomain adjacent to zinc finger domain, 2B (BAZ2B), mRNA
4873	17448	29899	1.3	0.0E+00	AF028801.1	NT	Homo sapiens alpha-3 type IX collagen (COL9A3) gene, promoter region, and exons 1-28
4876	17451	29902	0.91	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4876	17451	29903	0.91	0.0E+00	6677700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
4879	17454	29906	0.83	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4879	17454	29907	0.83	0.0E+00	7019320	NT	Homo sapiens proteinx0008 (AD013), mRNA
4900	17475	29931	1.61	0.0E+00	AW444637.1	EST_HUMAN	UI-H-B13-qlw-c-04-Q-U1.s1 NCI CGAP Sub5 Homo sapiens cDNA clone IMAGE:2733284 3'
4907	17482	29940	1.36	0.0E+00	AF303134.1	NT	Homo sapiens aldehyde dehydrogenase 12 (ALDH12) mRNA, complete cds
4910	17485		1.51	0.0E+00	AF083242.1	NT	Homo sapiens HSP0024-iso mRNA, complete cds
4923	17498		0.59	0.0E+00	AW339253.1	EST_HUMAN	xz88d08.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2871371 3'
4968	17542		3.61	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
4971	17545	29987	1.76	0.0E+00	X87205.1	NT	M fascicularis mRNA for metalloprotease-like, disintegrin-like protein, IVa
4973	17547	29989	1.19	0.0E+00	AF084479.1	NT	Homo sapiens Williams-Buren syndrome deletion transcript 9 (WBSCR9) mRNA, complete cds
4974	17548	29990	1.36	0.0E+00	AF097416.1	NT	Mus musculus zinc finger transcription factor Kaiso mRNA, complete cds
4975	17549	29991	4.69	0.0E+00	4503766	NT	Homo sapiens fragile X mental retardation 2 (FMR2) mRNA
4977	17551	29993	12.25	0.0E+00	4895048	NT	Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA
4978	17552	29994	1.19	0.0E+00	P52740	SWISSPROT	ZINC FINGER PROTEIN 132
4980	17554	29996	1.7	0.0E+00	8922180	NT	Homo sapiens hypothetical protein DKFZp762E1312 (DKFZp762E1312), mRNA
4983	17557	30000	5.09	0.0E+00	8923080	NT	Homo sapiens hypothetical protein FLJ20073 (FLJ20073), mRNA
4987	17561	30004	1.8	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- J61 segments; and Tcr-C-alpha gene, exons 1-4
4987	17561	30005	1.8	0.0E+00	M94081.1	NT	Human Tcr-C-delta gene, exons 1-4; Tcr-V-delta gene, exons 1-2; T-cell receptor alpha (Tcr-alpha) gene, J1- J61 segments; and Tcr-C-alpha gene, exons 1-4
4989	17563	30007	1.78	0.0E+00	X94628.1	NT	H sapiens MeCP-2 gene
4989	17563	30008	1.78	0.0E+00	X94628.1	NT	H sapiens MeCP-2 gene

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4992	17568	30011	2.79	0.0E+00	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
4994	17568	30012	0.98	0.0E+00	7706604	NT	Homo sapiens MAGE-C2 (MAGEC2), mRNA
5005	17578	30022	0.95	0.0E+00	5032150	NT	Homo sapiens TATA box binding protein (TBP)-associated factor, RNA polymerase II, 1, 28kD (TAF2I) mRNA
5015	17589	30032	1.75	0.0E+00	4585642	NT	Homo sapiens zinc finger protein (KIAA0412), mRNA
5016	17590	30033	0.84	0.0E+00	AB037864.1	NT	Homo sapiens mRNA for KIAA1443 protein, partial cds
5017	17591	30034	1.32	0.0E+00	AB014533.1	NT	Homo sapiens mRNA for KIAA0633 protein, partial cds
5018	17592	30035	2.53	0.0E+00	6677648	NT	Mus musculus zinc finger protein interacting with K protein 1 (Zfk1), mRNA
5019	17593	30036	2.01	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5021	17595	30038	2.81	0.0E+00	4758199	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP), mRNA
5023	17597	30040	0.98	0.0E+00	Y16729.1	NT	Homo sapiens gene encoding filensin, exon 8
5024	17598	30041	1.26	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5024	17598	30042	1.26	0.0E+00	5174560	NT	Homo sapiens meningioma expressed antigen 6 (coiled-coil proline-rich) (MGEA6), mRNA
5026	17600	30045	16.3	0.0E+00	AF050566.1	NT	Homo sapiens MHC class 1 region
5028	17602		2.87	0.0E+00	4505508	NT	Homo sapiens opicoid receptor, delta 1 (OPRD1), mRNA
5029	17603	30048	3.33	0.0E+00	AF091711.1	NT	Homo sapiens splice variant AKAP350 mRNA, partial cds
5041	17614	30058	2.27	0.0E+00	4503684	NT	Homo sapiens farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase) (FDP5), mRNA
5043	17616	30060	3.9	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5), mRNA
5043	17616	30061	3.9	0.0E+00	4557472	NT	Homo sapiens chloride channel 5 (nephrolithiasis 2, X-linked, Dent disease) (CLCN5), mRNA
5058	17631		0.59	0.0E+00	AI291129.1	EST_HUMAN	qm15105.x1 NCI CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881921 3' similar to TR-Q61632 Q61632
5061	17634	30076	2.85	0.0E+00	AB006625.1	NT	EN-2/LACZ FUSION PROTEIN ;
5061	17634	30077	2.85	0.0E+00	AB006625.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5072	17645	30087	0.92	0.0E+00	AB026898.1	NT	Homo sapiens mRNA for KIAA0287 gene, partial cds
5088	17661	30101	1.38	0.0E+00	AL163284.2	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)
5093	17666	30105	0.57	0.0E+00	7662319	NT	Homo sapiens chromosome 21 segment HS21C084
5103	17675	30115	2.12	0.0E+00	4502398	NT	Homo sapiens KIAA0806 gene product (KIAA0806), mRNA
5108	17680		7.33	0.0E+00	U14987.1	NT	Homo sapiens beaded filament structural protein 1, filensin (BFSP1), mRNA
5116	17690	30128	1.25	0.0E+00	M10976.1	NT	Human ribosomal protein L21 mRNA, complete cds
5121	17693		2.86	0.0E+00	BE408963.1	EST_HUMAN	Human endogenous retroviral DNA (4-1), complete retroviral segment
5124	17698	30133	3.82	0.0E+00	4758199	NT	601303729FT NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3638118 5'
5135	17707	30139	1.19	0.0E+00	AB028966.1	NT	Homo sapiens desmoplakin (DPI, DPL) (DSP), mRNA
							Homo sapiens mRNA for KIAA1043 protein, partial cds

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5152	17722	30152	1.89	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5152	17722	30153	1.89	0.0E+00	8923441	NT	Homo sapiens hypothetical protein FLJ20477 (FLJ20477), mRNA
5170	17738	30165	1.07	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5170	17738	30166	1.07	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5170	17738	30167	1.07	0.0E+00	AA601246.1	EST_HUMAN	no14g09.s1 NCL_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100704 3' similar to TR:E239140
5172	17739	30168	0.96	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5172	17739	30169	0.96	0.0E+00	AF161463.1	NT	Homo sapiens HSPC114 mRNA, complete cds
5183	12887	25374	0.58	0.0E+00	AF195658.1	NT	Homo sapiens DNA mismatch repair protein (MLH3) gene, complete cds
5188	17753		1.72	0.0E+00	4758225	NT	Homo sapiens E2F transcription factor 2 (E2F2) mRNA
5199	17764	30188	0.94	0.0E+00	AF016705.1	NT	Homo sapiens E6-AP ubiquitin-protein ligase (UBE3A) gene, exon 3
5204	17769	30192	0.87	0.0E+00	U53588.1	NT	Homo sapiens MHC class I region
5211	17776		1.3	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
5214	17778		29.82	0.0E+00	D50857.1	NT	Homo sapiens gamma-cytoplasmic actin (ACTGP3) pseudogene
5245	17809	30231	3.36	0.0E+00	X52988.1	NT	Bacillus amyloqueliciens sacB gene for levansucrase (EC 2.4.1.10)
5266	17828	30252	1.23	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5266	17828	30253	1.23	0.0E+00	AF240635.1	NT	Homo sapiens vascular endothelial cadherin 2 mRNA, complete cds
5267	17828	30254	0.96	0.0E+00	5454153	NT	Homo sapiens cyclophilin (USA-CYP) mRNA
5282	17844	30271	0.95	0.0E+00	6877700	NT	Homo sapiens G-protein coupled receptor (RE2), mRNA
5298	17860	30285	0.77	0.0E+00	5902055	NT	Homo sapiens ring finger protein (RNF), mRNA
5300	17862	30286	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5300	17862	30287	1.03	0.0E+00	M10905.1	NT	Human cellular fibronectin mRNA
5301	17863	30288	0.93	0.0E+00	U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRet gene, and sodium phosphate transporter (NPT3) gene, complete cds
5308	17870	30292	0.84	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
5326	17888	30304	0.87	0.0E+00	5802091	NT	Homo sapiens solute carrier family 5 (nositol transporters), member 3 (SLC5A3), mRNA
5333	17884	30308	1.1	0.0E+00	L35475.1	NT	Human offactory receptor-like gene, complete cds
5333	17884	30309	1.1	0.0E+00	L35475.1	NT	Human offactory receptor-like gene, complete cds
5340	17901	30316	0.81	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5340	17901	30317	0.81	0.0E+00	7706245	NT	Homo sapiens 4F2 light chain (LOC51597), mRNA
5341	17902	30318	0.6	0.0E+00	7662421	NT	Homo sapiens KIAA0971 protein (KIAA0971), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5347	17907	30322	25.99	0.0E+00	J02810.1	NT	Human apolipoprotein B-100 mRNA, complete cds
5355	17915	30330	0.98	0.0E+00	U71601.1	NT	Human zinc finger protein zfp47 (z47) mRNA, partial cds
5357	17917	30332	1.06	0.0E+00	P51523	SWISSPROT	ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2)
5365	17925	30339	9.37	0.0E+00	M19828.1	NT	Human apolipoprotein B-100 (apoB) gene, exons 22 through 29
5373	17932	30346	11.28	0.0E+00	5380213	NT	Human sapiens glypican 3 (GPC3) mRNA
5374	17933	30347	1.1	0.0E+00	4826777	NT	Human sapiens lumajil (mouse) homolog (JMU) mRNA
5377	17936	30349	0.88	0.0E+00	AE000327.1	NT	Escherichia coli K-12 MG1655 section 217 of 400 of the complete genome
5385	17944	30357	8.06	0.0E+00	4502152	NT	Human sapiens apolipoprotein B (including Ag(x) antigen) (APOB) mRNA
5389	17957	30368	1.01	0.0E+00	4885474	NT	Human sapiens melanoma antigen, family C, 1 (MAGEC1), mRNA
5430	17987	30391	1.56	0.0E+00	4826877	NT	Human sapiens resin (RELN) mRNA
5451	18020		3.55	0.0E+00	AF093093.1	NT	Human sapiens acotinase (ACO2) gene, nuclear gene encoding mitochondrial protein, exon 15
5459	18094	30411	2.28	0.0E+00	AF137286.1	NT	Human sapiens keratin 12 (KRT12) gene, complete cds
5459	18094	30412	2.28	0.0E+00	AF137286.1	NT	Human sapiens keratin 12 (KRT12) gene, complete cds
5478	18112	30521	1.27	0.0E+00	A1934964.1	EST_HUMAN	wp06g08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2464094 3'
5481	18115	30524	2.18	0.0E+00	9256579	NT	Human sapiens protocadherin alpha 13 (PCDHA13), mRNA
5495	18129	30537	3.75	0.0E+00	BE931080.1	EST_HUMAN	RC3-GN0076-310800-013-p03 GN0076 Homo sapiens cDNA
5499	18133	30541	3.31	0.0E+00	AF182034.1	NT	Human sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5499	18133	30542	3.31	0.0E+00	AF182034.1	NT	Human sapiens polycystic kidney disease-like 2 protein (PKDL2) mRNA, complete cds
5506	18139	30550	2.08	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5508	18139	30551	2.08	0.0E+00	X56163.1	NT	H. sapiens immunoglobulin heavy chain gene, variable region
5584	18215	30864	5.94	0.0E+00	BE875488.1	EST_HUMAN	7110008.x1 NCI_CGAP_CELL1 Homo sapiens cDNA clone IMAGE:3284250 3'
5585	18216						h196a02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3165104 3' similar to SW:Y054_HUMAN
5588	18217	30666	1.58	0.0E+00	BE794412.1	EST_HUMAN	P42694 HYPOTHETICAL PROTEIN KIAA0084 ;
5588	18217	30667	1.58	0.0E+00	BE794412.1	EST_HUMAN	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5589	18220	30670	7.35	0.0E+00	M29808.1	NT	601589422F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943804 5'
5600	24746	30678	4.43	0.0E+00	11421038	NT	Human sapiens eosinophil peroxidase (EPP) gene, exon 7
5609	18238		1.98	0.0E+00	BF665962.1	EST_HUMAN	Human sapiens Sp4 transcription factor (SP4), mRNA
5614	18243	30694	0.8	0.0E+00	BE538857.1	EST_HUMAN	602118928F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4276254 5'
5622	18251	30719	1.49	0.0E+00	BE292784.1	EST_HUMAN	601081489F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3447839 5'
5628	18255	30724	2.5	0.0E+00	BF526328.1	EST_HUMAN	601105891F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2988310 5'
5628	18255	30725	2.5	0.0E+00	BF526328.1	EST_HUMAN	602071372F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5645	19006	32325	2.91	0.0E+00	4557384	NT	602071372F1 NCI_CGAP_Bn64 Homo sapiens cDNA clone IMAGE:4214272 5'
5648	18276	30751	0.9	0.0E+00	AB007935.1	NT	Human sapiens Bloom syndrome (BLM) mRNA
							Human sapiens mRNA for KIAA0466 protein, partial cds

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5648	18276	30752	0.9	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0468 protein, partial cds
5652	18278	30756	4.93	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5652	18278	30757	4.93	0.0E+00	AF257737.1	NT	Homo sapiens ciliary dynein heavy chain 9 (DNAH9) mRNA, complete cds
5665	18292	30771	1.42	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5665	18292	30772	1.42	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
5680	18307	30803	1.98	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5686	18312	30809	0.86	0.0E+00	Z38133.1	NT	H. sapiens mRNA for myosin
5704	18330	30833	0.89	0.0E+00	D61564.1	EST_HUMAN	HUM418D05B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-418D05
5704	18330	30834	0.89	0.0E+00	D61564.1	EST_HUMAN	5'
5707	18333	30838	5.12	0.0E+00	BF528931.1	EST_HUMAN	5'
5707	18333	30839	5.12	0.0E+00	BF528931.1	EST_HUMAN	602042322F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4179888 5'
5712	18338	30843	2.7	0.0E+00	BF313139.1	EST_HUMAN	602042322F1 NCI_CGAP_Bm87 Homo sapiens cDNA clone IMAGE:4179888 5'
5723	18349	31052	4.03	0.0E+00	11434392	NT	601897659F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4128815 5'
5753	18379	31090	1.49	0.0E+00	BE260777.1	EST_HUMAN	Homo sapiens calcium channel, voltage-dependent, alpha 1G subunit (CACNA1G), mRNA
5762	18388	31114	4.06	0.0E+00	AW867318.1	EST_HUMAN	601150252F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502909 5'
5775	18400	31114	2.42	0.0E+00	BE292899.1	EST_HUMAN	MRQ-SN0037-030400-001-h07 SN0037 Homo sapiens cDNA
5775	18400	31115	2.42	0.0E+00	BE292899.1	EST_HUMAN	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987803 5'
5783	18418	31133	1.67	0.0E+00	11420819	NT	601105291F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987803 5'
5793	18418	31134	1.67	0.0E+00	11420819	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5800	18425	31142	4.39	0.0E+00	AF064254.1	NT	Homo sapiens olfactory receptor, family 2, subfamily F, member 1 (OR2F1), mRNA
5800	18425	31143	4.39	0.0E+00	AF064254.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5806	18431	31151	2.56	0.0E+00	AJ224639.1	NT	Homo sapiens very long-chain acyl-CoA synthetase homolog 1 mRNA, complete cds
5806	18431	31152	2.56	0.0E+00	AJ224639.1	NT	Homo sapiens Surf-5 and Surf-6 genes
5833	18457	31178	0.72	0.0E+00	A1988515.1	EST_HUMAN	Homo sapiens Surf-5 and Surf-6 genes
5837	18461	31184	6.38	0.0E+00	M85719.1	EST_HUMAN	qf94g10.x1 Soares_Placenta_86c9weeks_2NHHP86c9W Homo sapiens cDNA clone IMAGE:1757730 3'
5844	18488	31193	6.29	0.0E+00	AW405472.1	EST_HUMAN	similar to SW:CADC_HUMAN P55266 BRAIN-CADHERIN PRECURSOR ;
5856	18479	31202	1.35	0.0E+00	Z26269.1	NT	EST02238 Fetal brain, Striatum (catf836206) Homo sapiens cDNA clone HFCM48
5866	18488	31212	1.78	0.0E+00	AW361877.1	EST_HUMAN	U-HF-BLG-eth-4-02-0-JUL1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061658 5'
5866	18488	31213	1.78	0.0E+00	AW361877.1	EST_HUMAN	H. sapiens isoform 1 gene for L-type calcium channel, exon 14 adnd 15
5866	18488	31214	1.78	0.0E+00	AW361877.1	EST_HUMAN	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
5870	18492	31219	1.91	0.0E+00	U36261.1	NT	PM3-CT0263-091289-007-h05 CT0263 Homo sapiens cDNA
							Human beta-prime-adaptin (BAM22) gene, exon 13

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5897	18519	31244	1.02	0.0E+00	AB046861.1	NT	Homo sapiens mRNA for KIAA1641 protein, partial cds
5951	18573	31305	1.46	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5951	18573	31306	1.46	0.0E+00	AJ006345.1	NT	Homo sapiens KVLQT1 gene
5958	18580	31315	1.28	0.0E+00	AJ207616.1	EST_HUMAN	HA2881 Human fetal liver cDNA library Homo sapiens cDNA
5975	18595	31330	4.88	0.0E+00	1141680.1	NT	Homo sapiens protocadherin beta 2 (PCDH22), mRNA
5980	18600	31333	1.09	0.0E+00	BE791173.1	EST_HUMAN	601584032F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3838551 5'
5987	18607	31341	1.29	0.0E+00	9988943	NT	Homo sapiens amiloride-sensitive cation channel 1, neuronal (degenerin) (ACCN1), mRNA
5988	18608	31342	6.36	0.0E+00	BE560082.1	EST_HUMAN	601345141F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3677843 5'
5989	18609	31343	1.48	0.0E+00	10048478	NT	Mus musculus ezrin (Ac2), mRNA
5990	18610	31344	3.25	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
5990	18610	31345	3.25	0.0E+00	U86961.1	NT	Human L-type calcium channel beta-1 subunit (CACNLB1) gene, exon 13B and isoform beta-1B, complete cds
6008	18628	31363	2.23	0.0E+00	BF338835.1	EST_HUMAN	602036272F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4184321 5'
6010	18630	31365	0.88	0.0E+00	AF142821.1	NT	Homo sapiens calcium channel gamma 5 subunit (CACNG5) gene, exon 4 and complete cds
6011	18631	31366	3.17	0.0E+00	BE273983.1	EST_HUMAN	601104462F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3347463 5'
6020	18639	31379	1.22	0.0E+00	BE503086.1	EST_HUMAN	h283d11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3214581 3' similar to TR:Q62084 Q62084 PHOSPHOLIPASE C NEIGHBORING
6024	18643	31385	2.27	0.0E+00	BF569805.1	EST_HUMAN	602185832F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310076 5'
6028	18647	31388	1.14	0.0E+00	AA454842.1	EST_HUMAN	z699d06.s1 Soares_NhhMPu_S1 Homo sapiens cDNA clone IMAGE:811883 3'
6060	18677	31419	3.11	0.0E+00	AF217289.1	NT	Homo sapiens cadherin 20 (CDH20) mRNA, complete cds
6062	18679	31421	2.35	0.0E+00	BE828144.1	EST_HUMAN	RC5-ET0027-210600-022-G10 ET0027 Homo sapiens cDNA
6066	18683	31425	1.25	0.0E+00	BE958636.1	EST_HUMAN	601645287F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930453 5'
6083	18700	31447	0.9	0.0E+00	AW276760.1	EST_HUMAN	xp65f03.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745245 3' similar to TR:P78335 P78335 GUANYLATE KINASE ASSOCIATED PROTEIN ;
6093	18709	31457	0.96	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6093	18709	31458	0.96	0.0E+00	BF031742.1	EST_HUMAN	601558060F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:3827775 5'
6104	18720	31473	1.03	0.0E+00	AW470846.1	EST_HUMAN	hs34d06.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2875595 3' similar to TR:Q9Z1N3 Q9Z1N3 MYOSIN-RHO GAP PROTEIN, MYR 7 ;
6115	18731	31483	1.1	0.0E+00	BF155870.1	EST_HUMAN	QV4-HT0894-280900-399-a10 HT0894 Homo sapiens cDNA
6115	18731	31484	1.1	0.0E+00	BF155870.1	EST_HUMAN	QV4-HT0894-280900-399-a10 HT0894 Homo sapiens cDNA
6123	18738	31490	1.38	0.0E+00	W33069.1	EST_HUMAN	z608d06.r1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:321755 5'
6123	18738	31491	1.38	0.0E+00	W33069.1	EST_HUMAN	z608d06.r1 Soares_parathyroid_tumor_NHHPA Homo sapiens cDNA clone IMAGE:321755 5'
6124	18739		2.2	0.0E+00	AF012618.1	NT	Homo sapiens (familial mental retardation protein 2 (FMR2) gene, exon 14

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6127	18742	31495	3.14	0.0E+00	BE280197.1	EST_HUMAN	601159515F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3505323 5'
6133	18747	31503	1.88	0.0E+00	BE889810.1	EST_HUMAN	601512630F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3914238 5'
6148	18761	31520	1.46	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6148	18761	31521	1.46	0.0E+00	11433071	NT	Homo sapiens KIAA0735 gene product; synaptic vesicle protein 2B homolog (KIAA0735), mRNA
6149	18762	31522	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6149	18762	31523	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6149	18762	31524	1.15	0.0E+00	BE901608.1	EST_HUMAN	601677735F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3960200 5'
6164	24758	31540	10.16	0.0E+00	9789988	NT	Homo sapiens potassium voltage-gated channel, Shal-related subfamily, member 2 (KCNB2), mRNA
6167	18779	31543	1.38	0.0E+00	AA183506.1	EST_HUMAN	zr40h01.1 Soares NIHIMPu S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42684 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6167	18779	31544	1.38	0.0E+00	AA183506.1	EST_HUMAN	zr40h01.1 Soares NIHIMPu S1 Homo sapiens cDNA clone IMAGE:665905 5' similar to SW:YY05_HUMAN P42684 HYPOTHETICAL MYELOID CELL LINE PROTEIN 5. ;
6189	18789	31568	12.83	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6189	18789	31569	12.83	0.0E+00	U34625.1	NT	Human T cell surface glycoprotein CD-6 mRNA, complete cds
6229	18838	31611	1.35	0.0E+00	BE258330.1	EST_HUMAN	601114823F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3355565 5'
6238	18847	31618	1.64	0.0E+00	BE156561.1	EST_HUMAN	QV0-HT0368-090200-098-e09 HT0368 Homo sapiens cDNA
6280	18888	31657	1.54	0.0E+00	BE379007.1	EST_HUMAN	601236278F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608490 5'
6286	18894	31663	1.23	0.0E+00	AU137772	EST_HUMAN	AU137772 PLACE1 Homo sapiens cDNA clone PLACE1007201 5'
6306	18913	31687	3.42	0.0E+00	U45982.1	NT	Human G protein-coupled receptor GPR-9-6 gene, complete cds
6334	18940	31717	4.13	0.0E+00	AA204740.1	EST_HUMAN	zq81d03.1 Stratagene HNT neuron (#837233) Homo sapiens cDNA clone IMAGE:648005 5' similar to TR:G854195 G854195 LEUKOCYTE SURFACE PROTEIN. ;
6335	18941	31718	3.66	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6335	18941	31719	3.68	0.0E+00	11545913	NT	Homo sapiens xylosyltransferase II (XT2), mRNA
6354	18959	31737	0.7	0.0E+00	U07223.1	NT	Human beta2-chimerin mRNA, complete cds
6371	18975	31753	1.87	0.0E+00	11426387	NT	Homo sapiens carcinoembryonic antigen-related cell adhesion molecule 8 (CEACAM8), mRNA
6375	18979	31758	3.62	0.0E+00	BE257173.1	EST_HUMAN	601106532F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3350622 5'
6388	18991		0.94	0.0E+00	A1686048.1	EST_HUMAN	t91f10.x1 NCL CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2248939 3' similar to TR:Q14839 Q14839
6392	18995	31774	1.39	0.0E+00	L35930.1	NT	Human anion exchanger (AE1) gene, exons 1-20
6401	19004	31782	1.03	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6401	19004	31783	1.03	0.0E+00	BE797385.1	EST_HUMAN	601587971F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942329 5'
6411	19014	31786	0.96	0.0E+00	BF357123.1	EST_HUMAN	MR0-HT0923-220800-102-b05 HT0923 Homo sapiens cDNA
6419	19022	31806	1.53	0.0E+00	11435630	NT	Homo sapiens peptide transporter 3 (LOC51296), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6428	19031	31814	0.96	0.0E+00	D55649.1	NT	Human mRNA for alpha mannosidase II isozyme, complete cds
6442	19044	31832	1.11	0.0E+00	AW178142.1	EST_HUMAN	IL3-HT0082-010998-014-A04 HT0082 Homo sapiens cDNA
6462	19063	31848	0.78	0.0E+00	BE674544.1	EST_HUMAN	7602c12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3281302.3' similar to SW:Y176_HUMAN
6488	19067	31853	0.96	0.0E+00	7662039	NT	Q14681 HYPOTHETICAL PROTEIN KIAA0176 ; Homo sapiens KIAA0285 gene product (KIAA0285), mRNA
6490	19081		8.14	0.0E+00	AV650020.1	EST_HUMAN	AV650020 GLC Homo sapiens cDNA clone GLC0409.3'
6487	19088	31871	3.19	0.0E+00	AW575598.1	EST_HUMAN	UI-HF-BL0-acc-g-12-Q-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3058751.3'
6490	19091	31874	5.26	0.0E+00	H01255.1	EST_HUMAN	y27b03.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:149933.5'
6501	19101	31886	3.3	0.0E+00	X15377.1	NT	Human gene for the light and heavy chains of myeloperoxidase
6503	19103	31888	1.02	0.0E+00	AI612841.1	EST_HUMAN	t257408.x1 NCI_CGAP_Ov45 Homo sapiens cDNA clone IMAGE:2292687.3' similar to SW:NTCS_HUMAN
6509	19109	31894	4.19	0.0E+00	BE735989.1	EST_HUMAN	P53798 SODIUM- AND CHLORIDE-DEPENDENT CREATINE TRANSPORTER 2 ;
6509	19109	31895	4.19	0.0E+00	BE735989.1	EST_HUMAN	601305338F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639816.5'
6513	19113	31901	0.83	0.0E+00	AW748596.1	EST_HUMAN	601305338F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639816.5'
6513	19113	31902	0.83	0.0E+00	AW748596.1	EST_HUMAN	MR0-BT0264-221199-002-F11 BT0264 Homo sapiens cDNA
6515	19115	31904	167.16	0.0E+00	AU119245.1	EST_HUMAN	MR0-BT0264-221199-002-F11 BT0264 Homo sapiens cDNA
6515	19115	31905	167.16	0.0E+00	AU119245.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360.5'
6519	19119	31910	0.83	0.0E+00	BE780453.1	EST_HUMAN	AU119245 HEMBA1 Homo sapiens cDNA clone HEMBA1005360.5'
6520	19120	31911	0.89	0.0E+00	X92217.1	NT	601468712F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:3871899.5'
6531	19131	31925	1.98	0.0E+00	AI689483.1	EST_HUMAN	Hi.sapiens germ-line immunoglobulin heavy chain, variable region, (13-2)
6543	19142	31934	2.84	0.0E+00	BE283153.1	EST_HUMAN	ws25c07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2408220.3'
6543	19142	31935	2.84	0.0E+00	BE283153.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963.5'
6606	19203	32009	1.05	0.0E+00	AW406348.1	EST_HUMAN	601105344F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987963.5'
6606	19203	32010	1.05	0.0E+00	AW406348.1	EST_HUMAN	UI-HF-BL0-acc-h-02-Q-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931.5'
6634	19230	32034	5.36	0.0E+00	AV719444.1	EST_HUMAN	UI-HF-BL0-acc-h-02-Q-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059931.5'
6642	19238	32040	1.02	0.0E+00	BE888340.1	EST_HUMAN	AV719444 GLC Homo sapiens cDNA clone GLOEHC06.5'
6642	19238	32041	1.02	0.0E+00	BE888340.1	EST_HUMAN	601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301.5'
							601681150F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951301.5'
							Homo sapiens low voltage-activated T-type calcium channel alpha 1G splice variant CavT.1a (CACNA1G) mRNA, complete cds
6645	19241	32044	2.16	0.0E+00	AF190860.1	NT	mRNA, complete cds
6648	19244	32046	1.05	0.0E+00	11420658	NT	Homo sapiens transcription factor domain-associated protein (TRRAP), mRNA
6655	19251	32053	3.35	0.0E+00	AW163640.1	EST_HUMAN	au98h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159.5' similar to TR:O15390 O15390 GT24. [3] TR:O43940 TR:O43208 ;
6655	19251	32054	3.35	0.0E+00	AW163640.1	EST_HUMAN	au98h08.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2784159.5' similar to TR:O15390 O15390 GT24. [3] TR:O43940 TR:O43208 ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6859	19255	32057	0.97	0.0E+00	W37163.1	EST_HUMAN	zb20e08.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW:ZN45 HUMAN Q02386 ZINC FINGER PROTEIN 45 ;
6859	19255	32058	0.97	0.0E+00	W37163.1	EST_HUMAN	zb20e08.r1 Soares_fetal_lung_NHL19W Homo sapiens cDNA clone IMAGE:302628 5' similar to SW:ZN45 HUMAN Q02386 ZINC FINGER PROTEIN 45 ;
6871	19267	32071	1.08	0.0E+00	BE704853.1	EST_HUMAN	601589371F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943504 5'
6878	19274	32078	4.45	0.0E+00	BE799873.1	EST_HUMAN	601587561F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3941847 5'
6882	19278	32081	7.35	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6882	19278	32082	7.35	0.0E+00	BE889813.1	EST_HUMAN	601512058F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3913311 5'
6889	19285	32088	3.81	0.0E+00	L24493.1	NT	Human antigen CD27 gene, exons 1-2
6894	19290	32092	2.03	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6894	19290	32093	2.03	0.0E+00	AL163204.2	NT	Homo sapiens chromosome 21 segment HS21C004
6700	19296	32100	3.54	0.0E+00	6005983	NT	Homo sapiens zona pellucida glycoprotein 3A (sperm receptor) (ZP3A), mRNA
6703	19288	32102	3.88	0.0E+00	AI639412.1	EST_HUMAN	t331f1.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2242413 3' similar to SW:WNT3_MOUSE P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR ;
6704	19289	32103	1.36	0.0E+00	L32832.1	NT	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
6714	19308	32112	0.78	0.0E+00	AW505430.1	EST_HUMAN	UI-HF-BND-ame-c-01-0-U1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3081217 5'
6716	19310	32113	3.78	0.0E+00	AA434584.1	EST_HUMAN	zw52c03.r1 Soares_fetal_fetus_NB2HF8_9w Homo sapiens cDNA clone IMAGE:773668 5'
6730	19324		1.08	0.0E+00	BF217200.1	EST_HUMAN	601885317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103683 5'
6734	19328	32133	1.72	0.0E+00	BE925875.1	EST_HUMAN	QV3-BN0047-300800-278-c08 BN0047 Homo sapiens cDNA
6774	19368	32178	1.98	0.0E+00	AU125928.1	EST_HUMAN	AU125928 NT2RM4 Homo sapiens cDNA clone NT2RM4002430 5'
6776	19368	32180	0.73	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-H10 NN0174 Homo sapiens cDNA
6778	19368	32181	0.73	0.0E+00	BE701434.1	EST_HUMAN	PM2-NN0174-260700-001-H10 NN0174 Homo sapiens cDNA
6795	19388	32202	1.28	0.0E+00	BE142363.1	EST_HUMAN	CMO-HT0143-270999-082-d08 HT0143 Homo sapiens cDNA
6815	19408	32222	0.81	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-280300-032-a04 BN0121 Homo sapiens cDNA
6815	19408	32223	0.81	0.0E+00	BE006012.1	EST_HUMAN	RCO-BN0121-280300-032-a04 BN0121 Homo sapiens cDNA
6835	19425	32241	7.25	0.0E+00	BE169131.1	EST_HUMAN	PM3-HT0520-230200-002-c08 HT0520 Homo sapiens cDNA
6837	19427	32243	1.62	0.0E+00	BF085687.1	EST_HUMAN	IL5-GN0032-180900-145-d07 GN0032 Homo sapiens cDNA
6873	19507	32441	3.11	0.0E+00	AA180755.1	EST_HUMAN	zp88e03.r1 Strategene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:627292 5'
6882	19617	32452	0.99	0.0E+00	U30573.1	NT	Human salivary peroxidase mRNA, complete cds
6885	19620	32454	0.72	0.0E+00	BE871987.1	EST_HUMAN	7e49b07.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:3222037 3' similar to TR:Q9Z285 Q9Z285 TEKIN ;
6892	19626	32462	6.2	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6892	19628	32463	6.2	0.0E+00	AI940621.1	EST_HUMAN	IL3-ST0024-230799-001-B01 ST0024 Homo sapiens cDNA
6902	19638	32474	2.67	0.0E+00	11435626	NT	Homo sapiens CD6 antigen (CD6), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6913	19572	32401	0.94	0.0E+00	AL024443.1	EST_HUMAN	DKFZp434D2021_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2021 5'
6916	19575	32404	0.84	0.0E+00	AI168270.1	EST_HUMAN	oo10d01.x1 Scores_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1565761 3' similar to
6921	19580	32409	0.89	0.0E+00	BE734087.1	EST_HUMAN	TR:Q28623 Q28623 TEKTIN C1.1
6936	18044	30466	1.22	0.0E+00	BE566391.1	EST_HUMAN	601567370F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842080 5'
6943	18051	30473	13.34	0.0E+00	BE867889.1	EST_HUMAN	601339977F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3682287 5'
6943	18051	30473	13.34	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6943	18051	30474	13.34	0.0E+00	BE867889.1	EST_HUMAN	601443667F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3847697 5'
6948	19525	32347	1.75	0.0E+00	BE550162.1	EST_HUMAN	7b49f03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6948	19525	32348	1.75	0.0E+00	BE550162.1	EST_HUMAN	Q86379 GOLGIN-95.1
6970	19547	32371	2.55	0.0E+00	BF098376.1	EST_HUMAN	7b49f03.x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3231581 3' similar to SW:GG95_HUMAN
6977	19553	32378	2.01	0.0E+00	AA195106.1	EST_HUMAN	Q86379 GOLGIN-95.1
6984	19482		10.79	0.0E+00	11034810	NT	Q86379 GOLGIN-95.1
6986	19484	32305	1.11	0.0E+00	11431474	NT	Q86379 GOLGIN-95.1
7001	19490	32316	2.35	0.0E+00	BF569905.1	EST_HUMAN	Q86379 GOLGIN-95.1
7008	19506	32325	0.75	0.0E+00	4557364	NT	Q86379 GOLGIN-95.1
7016	19514		2.49	0.0E+00	103069.1	NT	Q86379 GOLGIN-95.1
7024	19558	32383	4.16	0.0E+00	AF217289.1	NT	Q86379 GOLGIN-95.1
7024	19558	32384	4.16	0.0E+00	AF217289.1	NT	Q86379 GOLGIN-95.1
7025	19559	32385	1	0.0E+00	M38113.1	NT	Q86379 GOLGIN-95.1
7036	18056	30479	2.94	0.0E+00	11420775	NT	Q86379 GOLGIN-95.1
7039	18059	30481	0.69	0.0E+00	BE266708.1	EST_HUMAN	Q86379 GOLGIN-95.1
7057	18076	30428	1.11	0.0E+00	AL118478.1	EST_HUMAN	Q86379 GOLGIN-95.1
7059	18078	30432	4.93	0.0E+00	BE262941.1	EST_HUMAN	Q86379 GOLGIN-95.1
7060	18079	30433	2.1	0.0E+00	Z37978.1	NT	Q86379 GOLGIN-95.1
7060	18079	30434	2.1	0.0E+00	Z37978.1	NT	Q86379 GOLGIN-95.1
7061	18080	30435	2.68	0.0E+00	AF257737.1	NT	Q86379 GOLGIN-95.1
7061	18080	30436	2.68	0.0E+00	AF257737.1	NT	Q86379 GOLGIN-95.1
7066	18085	30441	1.44	0.0E+00	AF310105.1	NT	Q86379 GOLGIN-95.1
7071	19643	32480	0.68	0.0E+00	BE762770.1	EST_HUMAN	Q86379 GOLGIN-95.1
7075	19647	32485	2.59	0.0E+00	BF569905.1	EST_HUMAN	Q86379 GOLGIN-95.1
7079	19651	32490	3.92	0.0E+00	LO1978.1	NT	Q86379 GOLGIN-95.1

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7089	19660	32499	0.82	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7089	19660	32500	0.82	0.0E+00	AL039581.1	EST_HUMAN	DKFZp434D2211_1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D2211 5'
7095	19668	32505	8.1	0.0E+00	BF306896.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7100	19670	32509	2.1	0.0E+00	U41302.1	NT	Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds
7132	19472	32292	1.1	0.0E+00	AL049784.1	NT	Novel human gene mapping to chromosome 13
7167	19699	32646	0.89	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7167	19699	32547	0.89	0.0E+00	AU137738.1	EST_HUMAN	AU137738 PLACE1 Homo sapiens cDNA clone PLACE1007120 5'
7173	19705	32553	1.43	0.0E+00	AW954806.1	EST_HUMAN	EST366876 IMAGE resequences, MAGC Homo sapiens cDNA
7174	19706	32554	1.05	0.0E+00	BE254103.1	EST_HUMAN	601113958F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3354566 5'
7187	19719	32566	1.23	0.0E+00	L01973.1	NT	Human type VI sodium channel alpha polypeptide (SCN4A) gene, exon 14
7195	19726	32576	0.71	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7195	19728	32577	0.71	0.0E+00	AB007935.1	NT	Homo sapiens mRNA for KIAA0466 protein, partial cds
7201	19732	32584	1.97	0.0E+00	AU133213.1	EST_HUMAN	AU133213 NT2RP4 Homo sapiens cDNA clone NT2RP4001556 5'
7216	19747	32603	0.86	0.0E+00	11428081	NT	Homo sapiens membrane protein CH1 (CH1), mRNA
7221	19752	32608	2.39	0.0E+00	AU143706.1	EST_HUMAN	AU143706 Y78AA1 Homo sapiens cDNA clone Y78AA1002365 5'
7222	19753	32608	1.2	0.0E+00	4758539	NT	Homo sapiens netrin 1 (NTN1), mRNA
7231	19762	32617	1.83	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7231	19762	32618	1.83	0.0E+00	BE891286.1	EST_HUMAN	601431819F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917164 5'
7252	18094	30411	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7252	18094	30412	2.27	0.0E+00	AF137286.1	NT	Homo sapiens keratin 12 (KRT12) gene, complete cds
7263	19791	32646	0.78	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7263	19791	32647	0.78	0.0E+00	BE747231.1	EST_HUMAN	601580948F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3929722 5'
7274	19802	32659	4.67	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
7274	19802	32660	4.67	0.0E+00	11436699	NT	Homo sapiens vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR), mRNA
							qc67a07.x1 Soares_placenta_8to9weeks_2NHP8t09W Homo sapiens cDNA clone IMAGE:1714644 3'
							similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR; contains element HGR
7302	19830	32688	28.85	0.0E+00	AI128344.1	EST_HUMAN	similar to SW:ARSD_HUMAN P51689 ARYL SULFATASE D PRECURSOR; contains element HGR
7302	19830	32689	28.85	0.0E+00	AI128344.1	EST_HUMAN	repetitive element;
7304	19832	32691	4.05	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7304	19832	32692	4.05	0.0E+00	11426392	NT	Homo sapiens myosin, heavy polypeptide 8, skeletal muscle, perinatal (MYH8), mRNA
7307	19835		14.08	0.0E+00	BF337375.1	EST_HUMAN	602035089F1 NCI_CGAP_Brn64 Homo sapiens cDNA clone IMAGE:4182839 5'

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7309	19837	32695	3.39	0.0E+00	AA128453.1	EST_HUMAN	zn60f09.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562601 5' similar to TR:G806562 G806562 NEBULIN ;
7314	19841	32701	0.9	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7314	19841	32702	0.9	0.0E+00	AL079497.1	EST_HUMAN	DKFZp434B0226_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B0226 5'
7349	19875	32741	1.2	0.0E+00	BE295499.1	EST_HUMAN	601174576F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3528794 5'
7351	19877	32742	0.86	0.0E+00	11427965	NT	Homo sapiens hypothetical protein (FLJ20281), mRNA
7354	19880		2.37	0.0E+00	AU118607.1	EST_HUMAN	AU118607 HEMBA1 Homo sapiens cDNA clone HEMBA1003969 5'
7355	19881	32745	1.77	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7355	19881	32746	1.77	0.0E+00	AF005213.1	NT	Homo sapiens ankyrin 1 (ANK1) mRNA, complete cds
7365	19891	32754	0.99	0.0E+00	AF245505.1	NT	Homo sapiens adican mRNA, complete cds
7371	19897	32758	8.87	0.0E+00	X70172.1	NT	H. sapiens DNA for ZNGP2 pseudogene, exon 4
7373	19899	32760	8.18	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7373	19899	32761	8.18	0.0E+00	U45448.1	NT	Human P2x1 receptor mRNA, complete cds
7385	19911	32775	0.98	0.0E+00	AW956503.1	EST_HUMAN	EST368573 IMAGE resequences, MAGD Homo sapiens cDNA
7387	19913	32777	3.25	0.0E+00	AW950516.1	EST_HUMAN	EST362588 IMAGE resequences, MAGA Homo sapiens cDNA
7408	19933	32797	1.04	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa, S.C.) Homo sapiens cDNA clone kappa_200
7408	19933	32798	1.04	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa, S.C.) Homo sapiens cDNA clone kappa_200
7408	19933	32799	1.04	0.0E+00	AF001543.1	EST_HUMAN	AF001543 Human cDNA (Chandrasekharappa, S.C.) Homo sapiens cDNA clone kappa_200
7425	19949		0.78	0.0E+00	M90354.1	NT	Human BTF3 protein homologue gene, complete cds
7426	19950	32815	0.71	0.0E+00	BE408293.1	EST_HUMAN	601302679F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3637434 5'
7451	19975		1.16	0.0E+00	R87430.1	EST_HUMAN	xb39a05.y1 NC1 CGAP Lu31 Homo sapiens cDNA clone IMAGE:166051 5'
7452	19976	32841	2.37	0.0E+00	AW239326.1	EST_HUMAN	HNFB3/FH TRANSCRIPTION FACTOR GENESIS ;
7468	19990		1.19	0.0E+00	AU117553.1	EST_HUMAN	AU117553 HEMBA1 Homo sapiens cDNA clone HEMBA1001691 5'
7470	19992	32855	3.61	0.0E+00	11427135	NT	Homo sapiens glucagon-like peptide 2 receptor (GLP2R), mRNA
7482	20004	32869	0.68	0.0E+00	AA211683.1	EST_HUMAN	zn56102.r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:562203 5' similar to gb:X03740
7488	20011	32877	0.82	0.0E+00	L32832.1	NT	MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
7509	20030	32894	0.98	0.0E+00	BF306998.1	EST_HUMAN	Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
7509	20030	32895	0.98	0.0E+00	BF306998.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7517	20037	32905	1.48	0.0E+00	AU118787.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
7561	20078	32952	4.53	0.0E+00	AU118787.1	EST_HUMAN	AU118787 HEMBA1 Homo sapiens cDNA clone HEMBA1004314 5'
							cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_en17d05 random

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7561	20078	32953	4.53	0.0E+00	AI752561.1	EST_HUMAN	cn17d05.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn17d05 random
7631	20143	33023	1.45	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7631	20143	33024	1.45	0.0E+00	AF064205.1	NT	Homo sapiens dynactin 1 (DCTN1) gene, alternatively spliced products, exons 7 through 32 and complete cds
7639	20151	33035	1.03	0.0E+00	U74315.1	EST_HUMAN	HSU74315 Human chromosome 14 Homo sapiens cDNA clone 1-4
7653	20165	33052	0.87	0.0E+00	BE439545.1	EST_HUMAN	HTM1-183F1 HTM1 Homo sapiens cDNA
7654	20168	33053	1.08	0.0E+00	11417342	NT	Homo sapiens sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A (SEMA5A), mRNA
7681	20192	33081	2.91	0.0E+00	6912735	NT	Homo sapiens transient receptor potential channel 5 (TRPC5), mRNA
7687	20198	33084	1	0.0E+00	N76126.1	EST_HUMAN	zab6e05.st Soares_fetal_lung_NHFL19W Homo sapiens cDNA clone IMAGE:298455 3'
7691	20200	33087	5.26	0.0E+00	BF217905.1	EST_HUMAN	6071885465F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103728 5'
7698	20208	33095	4.27	0.0E+00	AU129622.1	EST_HUMAN	AU129622 NT2RP2 Homo sapiens cDNA clone NT2RP2005913 5'
7715	24789	33111	1.1	0.0E+00	AW069274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7715	24789	33112	1.1	0.0E+00	AW069274.1	EST_HUMAN	cr42e09.x1 Jia bone marrow stroma Homo sapiens cDNA clone HBMSC_cr42e09 3'
7718	20226	33114	6.48	0.0E+00	4501848	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
7725	20233	33121	1.01	0.0E+00	AV758467.1	EST_HUMAN	AV758467 BM Homo sapiens cDNA clone BMFBGG05 5'
7726	20234	33122	6.72	0.0E+00	BE739870.1	EST_HUMAN	6071593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7726	20234	33123	6.72	0.0E+00	BE739870.1	EST_HUMAN	6071593156F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3947365 5'
7727	20235	33124	0.81	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7727	20235	33125	0.81	0.0E+00	6912461	NT	Homo sapiens atrophin-1 interacting protein 1; activin receptor interacting protein 1 (KIAA0705), mRNA
7728	20236	33126	1.02	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7728	20236	33127	1.02	0.0E+00	AU120424.1	EST_HUMAN	AU120424 HEMBB1 Homo sapiens cDNA clone HEMBB1000655 5'
7757	20265	33160	1.73	0.0E+00	BE767610.1	EST_HUMAN	6071481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7757	20265	33161	1.73	0.0E+00	BE767610.1	EST_HUMAN	6071481713F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3884258 5'
7767	20275	33173	0.8	0.0E+00	AW402189.1	EST_HUMAN	UI-HF-BK0-eat-c-07-UJ.1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3054733 5'
7776	20285	33182	0.9	0.0E+00	AW968044.1	EST_HUMAN	EST380119 IMAGE resequences, MAGJ Homo sapiens cDNA
7795	20338	33246	1.97	0.0E+00	AU133167.1	EST_HUMAN	AU133167 NT2RP4 Homo sapiens cDNA clone NT2RP4001507 5'
7840	20382		0.51	0.0E+00	BF217200.1	EST_HUMAN	6071895317F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4103693 5'
7853	20395	33300	0.85	0.0E+00	BE313013.1	EST_HUMAN	6071150347F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503050 5'
7864	20408	33313	1.18	0.0E+00	AA149791.1	EST_HUMAN	z601c06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:566410 5'

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7877	20419	33327	0.8	0.0E+00	BF026628.1	EST_HUMAN	601672310F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3955131 5'
7890	20432	33341	0.51	0.0E+00	AA017021.1	EST_HUMAN	za33108.1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:360831 5'
7907	20449	33358	2.32	0.0E+00	BE736046.1	EST_HUMAN	601305658F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3639603 5'
7923	20465	33372	3.32	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7923	20465	33373	3.32	0.0E+00	M34872.1	NT	Human amyloid-beta protein (APP) gene, exon 11
7953	20495	33404	0.77	0.0E+00	AW674581.1	EST_HUMAN	b63402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652
7953	20495	33405	0.77	0.0E+00	AW674581.1	EST_HUMAN	F17K2.26 PROTEIN ; b63402.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:2985123 5' similar to TR:O64652 O64652
7960	20502	33411	3.05	0.0E+00	AA397551.1	EST_HUMAN	z81b04.1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:728719 5' similar to TR:G3000482
7962	20504	33412	0.83	0.0E+00	AW387131.1	EST_HUMAN	G3000482 POL-REVERSE TRANSCRIPTASE HOMOLOG (RETROVIRAL ELEMENT) ; MRO-ST0031-061099-003-a11 ST0031 Homo sapiens cDNA
7965	20507		0.53	0.0E+00	AB020661.1	NT	Homo sapiens mRNA for KIAA0894 protein, partial cds
7966	20508	33414	7.21	0.0E+00	AU142402.1	EST_HUMAN	AU142402 Y79AA1 Homo sapiens cDNA clone Y79AA1000277 5'
7970	20512	33418	0.97	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7970	20512	33419	0.97	0.0E+00	BE388421.1	EST_HUMAN	601285550F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3607237 5'
7985	20527	33433	0.52	0.0E+00	7657276	NT	Homo sapiens Killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1 (KIR2DS1), mRNA
7987	20529	33435	0.87	0.0E+00	W95278.1	EST_HUMAN	ze05d01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7987	20529	33438	0.87	0.0E+00	W95278.1	EST_HUMAN	ze05d01.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:358081 5'
7989	20531		17.03	0.0E+00	BF673096.1	EST_HUMAN	602153008F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4204128 5'
7993	20535		1.38	0.0E+00	AU134114	EST_HUMAN	AU134114 OVARC1 Homo sapiens cDNA clone OVARC1001286 5'
8007	20549	33453	2.35	0.0E+00	BF525534.1	EST_HUMAN	602089632F1 NCI_CGAP_Brt64 Homo sapiens cDNA clone IMAGE:4212727 5'
8007	20549	33454	2.35	0.0E+00	BF525534.1	EST_HUMAN	602089632F1 NCI_CGAP_Brt64 Homo sapiens cDNA clone IMAGE:4212727 5'
8037	20579	33484	1.88	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8037	20579	33485	1.88	0.0E+00	AL120124.1	EST_HUMAN	DKFZp761P092.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761P092 5'
8077	20619		1.82	0.0E+00	BE877693.1	EST_HUMAN	601485254F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887773 5'
8098	20639	33550	2.09	0.0E+00	AW500549.1	EST_HUMAN	U1HF-BN0-alk4-01-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077498 5'
8106	20647	33558	11.19	0.0E+00	AW157233.1	EST_HUMAN	au83b08.x1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783799 3' similar to TR:O60463 O60463 TYPE-2 PHOSPHATIDIC ACID PHOSPHOHYDROLASE [1]; xa07d12.x1 Soares NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2567639 3' similar to contains element OFR repetitive element ;
8123	20664	33574	0.65	0.0E+00	AW072395.1	EST_HUMAN	Homo sapiens centrosomal protein 2 (CEP2), mRNA
8141	20682	33594	1.05	0.0E+00	11421722	NT	z836d03.r1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:294633 5'
8144	20685	33597	0.75	0.0E+00	W01616.1	EST_HUMAN	

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8146	20887	33599	1.55	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8146	20887	33600	1.55	0.0E+00	BE745597.1	EST_HUMAN	601578195F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3926998 5'
8158	20899	33613	1.32	0.0E+00	AJ271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
8178	20719	33634	6.51	0.0E+00	D45032.1	NT	Human DNA for ceruloplasmin, exon 5
8198	20739	33651	1.47	0.0E+00	A1367350.1	EST_HUMAN	q95c12.x1 NCI_CGAP_U2 Homo sapiens cDNA clone IMAGE:1989334 3' similar to TR:Q14673 Q14873 KIAA0164 PROTEIN ;
8211	20752	33666	3.14	0.0E+00	BE674157.1	EST_HUMAN	7876a04.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278862 3' similar to TR:O95783 O95793 STAUFEN PROTEIN ;
8213	20754	33668	1.31	0.0E+00	A1885671.1	EST_HUMAN	w60b10.x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2429275 3' similar to SW:COGT_HUMAN P50281 MATRIX METALLOPROTEINASE-14 PRECURSOR ;
8224	20765	33682	1.38	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8224	20765	33683	1.38	0.0E+00	BE563650.1	EST_HUMAN	601334790F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688655 5'
8231	20772	33692	1.63	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8231	20772	33693	1.63	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
8233	20774	33695	1.7	0.0E+00	AA403192.1	EST_HUMAN	z66802.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD ;
8233	20774	33696	1.7	0.0E+00	AA403192.1	EST_HUMAN	z66802.r1 Soares_tetal_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:758619 5' similar to TR:G1304132 G1304132 TPRD ;
8275	20816		4.36	0.0E+00	AA398511.1	EST_HUMAN	z73a08.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:727958 3' similar to gb:S85655 PROHIBITIN (HUMAN);
8283	20824	33745	0.5	0.0E+00	BE837593.1	EST_HUMAN	RC2-FN0094-120600-013-h07 FN0094 Homo sapiens cDNA
8284	20825	33746	1.22	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221298-048-c07 DT0045 Homo sapiens cDNA
8284	20825	33747	1.22	0.0E+00	AW364874.1	EST_HUMAN	QV3-DT0045-221298-048-c07 DT0045 Homo sapiens cDNA
8303	20844	33766	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3866179 6'
8303	20844	33767	1.24	0.0E+00	BE612586.1	EST_HUMAN	601452412F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3866179 5'
8318	20859	33784	1.26	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8318	20859	33785	1.26	0.0E+00	AL163209.2	NT	Homo sapiens chromosome 21 segment HS21C009
8326	20867	33790	0.76	0.0E+00	A1884477.1	EST_HUMAN	wm33a11.x1 NCI_CGAP_U14 Homo sapiens cDNA clone IMAGE:2437724 3' similar to TR:O75457 O75457 CYTOSOLIC PHOSPHOLIPASE A2-GAMMA ;
8333	20874	33798	0.93	0.0E+00	AA502294.1	EST_HUMAN	ne25d10.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:882259 3' similar to TR:G1136434 G1136434 KIAA0187 PROTEIN ;
8338	20878		0.64	0.0E+00	11416799	NT	Homo sapiens protocadherin beta 3 (PCDH3), mRNA
8345	20886	33807	1.33	0.0E+00	A1580780.1	EST_HUMAN	ta04f11.x1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:2043117 3'
8348	20889		1.86	0.0E+00	BE890797.1	EST_HUMAN	601431238F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916569 5'

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8374	20914	33833	0.81	0.0E+00	AW245785.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8374	20914	33834	0.61	0.0E+00	AW245785.1	EST_HUMAN	2822701.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822701 5'
8375	20915	33835	2.27	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8375	20915	33836	2.27	0.0E+00	4758695	NT	Homo sapiens mitogen-activated protein kinase kinase 13 (MAP3K13), mRNA
8378	20918	33838	0.6	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8378	20918	33839	0.6	0.0E+00	U88084.1	NT	Human zinc finger protein (ZNF165), gene, exons 2 and 3
8443	20983	33839	0.7	0.0E+00	AJ251780.1	NT	Homo sapiens NESP55, GNAS1 antisense (partial) and Xlaiphas (partial) genes
8448	20988	33904	3.77	0.0E+00	X89922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8448	20988	33905	3.77	0.0E+00	X89922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8448	20988	33906	3.77	0.0E+00	X89922.1	NT	H. sapiens mRNA for gamma-glutamyltransferase
8463	21003	33920	1.07	0.0E+00	U82679.1	NT	Human immunoglobulin-like transcript-3 mRNA, complete cds
8502	21041	33962	0.88	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8502	21041	33963	0.88	0.0E+00	AF022655.1	NT	Homo sapiens cep250 centrosome associated protein mRNA, complete cds
8505	21044	33965	0.89	0.0E+00	AU131871.1	EST_HUMAN	AU131871 NT2RP3 Homo sapiens cDNA clone NT2RP3003016 5'
8520	21059	33982	0.6	0.0E+00	11428572	NT	Homo sapiens immunoglobulin superfamily, member 2 (IGSF2), mRNA
8524	21063		1.84	0.0E+00	AW513513.1	EST_HUMAN	xc46a01.x1 NCI_CGAP_L11 Homo sapiens cDNA clone IMAGE:2707032 3' similar to gb:M14123_cds4
8528	21065		0.84	0.0E+00	BE783232.1	EST_HUMAN	RETROVIRUS-RELATED POLYPROTEIN (HUMAN);
8527	21068	33985	16.45	0.0E+00	D52650.1	EST_HUMAN	HUM084C02B Clontech human fetal brain polyA+ mRNA (#6535) Homo sapiens cDNA clone GEN-084C02 5'
8557	21096	34017	3.98	0.0E+00	BE378495.1	EST_HUMAN	601238488F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3608708 5'
8563	21102	34021	2.84	0.0E+00	AA410545.1	EST_HUMAN	Z32e04.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:724082 5'
8565	21104		2.44	0.0E+00	BF313946.1	EST_HUMAN	601900571F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4129744 5'
8572	21111	34030	0.85	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
8576	21115	34034	1.28	0.0E+00	AW139873.1	EST_HUMAN	UI-H-B11-adr-φ-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8576	21115	34035	1.28	0.0E+00	AW139873.1	EST_HUMAN	UI-H-B11-adr-φ-12-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2717687 3'
8581	21120		0.82	0.0E+00	A1640190.1	EST_HUMAN	ws30b10 x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2299579 3' similar to TR-O15044
8600	21139	34053	1.78	0.0E+00	BF377897.1	EST_HUMAN	O15044 KIAA0335 ;
8608	21147	34063	0.55	0.0E+00	AL163301.2	NT	CM1-TN0141-250800-439-b08 TN0141 Homo sapiens cDNA
8614	21153	34067	2.14	0.0E+00	BE260272.1	EST_HUMAN	Homo sapiens chromosome 21 segment HS21C101
8619	21158	34071	2.58	0.0E+00	BF700165.1	EST_HUMAN	601150051F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3502836 5'
8619	21158	34072	2.58	0.0E+00	BF700165.1	EST_HUMAN	602127694F1 NIH_MGC_58 Homo sapiens cDNA clone IMAGE:4284542 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8619	21158	34073	2.58	0.0E+00	BF700165.1	EST_HUMAN	602127684F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4284542 5'
8633	21172	34090	0.63	0.0E+00	AK458722.1	EST_HUMAN	tk13h11.x1 NCI CGAP Lu24 Homo sapiens cDNA clone IMAGE:2150949 3'
8660	21199	34117	2.45	0.0E+00	AL449770.1	EST_HUMAN	AL449770 Homo sapiens fetal brain (Stavrides GS) Homo sapiens cDNA
8667	21206	34123	18.43	0.0E+00	AA962527.1	EST_HUMAN	α -80g02 s1 NCI CGAP Lu5 Homo sapiens cDNA clone IMAGE:1602194 3' similar to gb:M36072 60S
8673	21212	34131	4.67	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8673	21212	34132	4.67	0.0E+00	10947037	NT	Homo sapiens ankyrin 1, erythrocytic (ANK1), transcript variant 1, mRNA
8697	21236	34159	1.28	0.0E+00	Y11107.3	NT	Homo sapiens ITGB4 gene for integrin beta 4 subunit, exons 3-41
8699	21238	34161	1.76	0.0E+00	BE278917.1	EST_HUMAN	601156330F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3139734 5'
8708	21247		4.02	0.0E+00	AV718377.1	EST_HUMAN	AV718377 FHTB Homo sapiens cDNA clone FHTBAF11 5'
8715	21254	34175	3.11	0.0E+00	AW337277.1	EST_HUMAN	xw73c07.x1 NCI CGAP_Par1 Homo sapiens cDNA clone IMAGE:2833844 3' similar to gb:X63587
8721	21260	34180	1.42	0.0E+00	AU124051.1	EST_HUMAN	INTEGRIN BETA-4 SUBUNIT PRECURSOR (HUMAN);
8766	21335	34260	0.9	0.0E+00	AU140704.1	EST_HUMAN	AU124051 NT2RM2 Homo sapiens cDNA clone NT2RM2001575 5'
8806	21345	34269	0.54	0.0E+00	AB007923.1	NT	AU140704 PLACE4 Homo sapiens cDNA clone PLACE4000088 5'
8810	21349	34272	0.6	0.0E+00	R17132.1	EST_HUMAN	Homo sapiens mRNA for KIAA0454 protein, partial cds
8810	21349	34273	0.6	0.0E+00	R17132.1	EST_HUMAN	yg09a09.t1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:31674 5'
8814	21353	34276	3.85	0.0E+00	AW592233.1	EST_HUMAN	yg09a09.t1 Soares Infant brain TNIB Homo sapiens cDNA clone IMAGE:31674 5'
8849	21388	34311	0.5	0.0E+00	AU128804.1	EST_HUMAN	h448a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2835096 3'
8859	21398	34321	1.27	0.0E+00	AV714764.1	EST_HUMAN	h448a09.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2835096 3'
8874	21413	34335	2.6	0.0E+00	AL040428.1	EST_HUMAN	AU128804 NT2RP2 Homo sapiens cDNA clone NT2RP2004245 5'
8874	21413	34336	2.6	0.0E+00	AL040428.1	EST_HUMAN	AV714764 DCB Homo sapiens cDNA clone DCBAUA08 5'
8880	21418	34342	1.55	0.0E+00	AF133901.1	NT	DKFZp434C1814_s1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434C1814 3'
8882	21420	34345	1.68	0.0E+00	AB040945.1	NT	DKFZp434C1814_s1 434 (synonym: hbs3) Homo sapiens cDNA clone DKFZp434C1814 3'
8889	21427	34352	0.54	0.0E+00	BF675505.1	EST_HUMAN	Homo sapiens Killer inhibitory receptor 2-2-1 (KIR221) and killer inhibitory receptor 2-2-2 (KIR222) genes, partial cds
8891	21428		0.97	0.0E+00	BF058289.1	EST_HUMAN	Homo sapiens mRNA for KIAA1512 protein, partial cds
8921	21459	34377	6.2	0.0E+00	11422857	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
8930	21468	34386	1.15	0.0E+00	K01241.1	NT	Homo sapiens tumor protein p73 (TP73), mRNA
8937	21475	34395	4.14	0.0E+00	AB020630.1	NT	Human Ig rearranged H-chain epsilon-3 pseudogene, constant region
8937	21475	34396	4.14	0.0E+00	AB020630.1	NT	Homo sapiens mRNA for KIAA0823 protein, partial cds
8942	21480	34402	1.61	0.0E+00	AV660739.1	EST_HUMAN	Homo sapiens mRNA for KIAA0823 protein, partial cds
							AV660739 GLC Homo sapiens cDNA clone GLOGKG12 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8948	21486	34408	3.39	0.0E+00	7706638	NT	Homo sapiens polycystin-L (PKDL), mRNA
8953	21491	34413	2.58	0.0E+00	BE793326.1	EST_HUMAN	601598304F1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:3942563 5'
8954	21492	34414	0.56	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8954	21492	34415	0.56	0.0E+00	AB033077.1	NT	Homo sapiens mRNA for KIAA1251 protein, partial cds
8966	21504	34437	1.07	0.0E+00	H73937.1	EST_HUMAN	yu0308.11 Scarsa fetal liver spleen 1NPLS Homo sapiens cDNA clone IMAGE:232767 5'
8976	21514	34437	4.52	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC.9 Homo sapiens cDNA clone IMAGE:3140740 5'
8976	21514	34438	4.52	0.0E+00	BE315402.1	EST_HUMAN	601141119F1 NIH_MGC.9 Homo sapiens cDNA clone IMAGE:3140740 5'
8986	21524	34453	0.63	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3856100 5'
8986	21524	34454	0.63	0.0E+00	BE612721.1	EST_HUMAN	601452582F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3856100 5'
8989	21527		0.58	0.0E+00	M8986.1	NT	Human polymorphic loci in Xq28
8991	21529	34458	1.84	0.0E+00	X14768.1	NT	Human mRNA for GABA-A receptor, alpha 1 subunit
9011	21548	34477	2.5	0.0E+00	A1061395.1	EST_HUMAN	an29a04.x1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:1700094 3'
9016	21553	34481	1.82	0.0E+00	A1654607.1	EST_HUMAN	wq34a12.x1 NCI_CGAP_GCB Homo sapiens cDNA clone IMAGE:2473150 3' similar to SW:MG83_HUMAN
9021	21558	34486	4.57	0.0E+00	9256595	NT	O15480 MELANOMA-ASSOCIATED ANTIGEN B3
9031	21568	34497	2.1	0.0E+00	AW958311.1	EST_HUMAN	Homo sapiens protocadherin alpha 8 (PCDH8), mRNA
9041	21578	34507	2.81	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
9056	21593	34523	1.13	0.0E+00	AU142662.1	EST_HUMAN	AU142662 Y79AA1 Homo sapiens cDNA clone Y79AA1000678 5'
9070	21607	34538	1.25	0.0E+00	11436995	NT	Homo sapiens MAP-kinase activating death domain (MADD), mRNA
9071	21608		0.9	0.0E+00	BE410768.1	EST_HUMAN	601301676F1 NIH_MGC.21 Homo sapiens cDNA clone IMAGE:3636163 5'
9085	21621	34557	1.69	0.0E+00	BF002024.1	EST_HUMAN	7g97h12.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3314471 3' similar to TR:Q9UJH62
9099	21635	34573	0.83	0.0E+00	AB011150.1	NT	Q9UJH62 HYPOPHYSAL 42.5 KD PROTEIN
9100	21636	34574	7.17	0.0E+00	BE794923.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9104	21640	34579	0.52	0.0E+00	BE810292.1	EST_HUMAN	Homo sapiens mRNA for KIAA0578 protein, partial cds
9104	21640	34580	0.52	0.0E+00	BE810292.1	EST_HUMAN	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA
9107	21643	34583	1.17	0.0E+00	AU136229.1	EST_HUMAN	RC3-PT0151-290600-011-c05 PT0151 Homo sapiens cDNA
9112	21648	34588	1.18	0.0E+00	BE83843.1	EST_HUMAN	AU136229 PLACE1 Homo sapiens cDNA clone PLACE1003804 5'
9112	21648	34589	1.18	0.0E+00	BE83843.1	EST_HUMAN	601510247F1 NIH_MGC.71 Homo sapiens cDNA clone IMAGE:3911986 5'
9130	21665	34605	0.79	0.0E+00	AB011166.1	NT	Homo sapiens mRNA for KIAA0594 protein, partial cds
9133	21668	34609	1.64	0.0E+00	AA344801.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9133	21668	34610	1.64	0.0E+00	AA344801.1	EST_HUMAN	EST50505 Gall bladder I Homo sapiens cDNA 5' end
9188	21705	34647	0.85	0.0E+00	AW673469.1	EST_HUMAN	ba54408.y0 NIH_MGC.10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9188	21705	34848	0.85	0.0E+00	AW673469.1	EST_HUMAN	ba54408.y3 NIH_MGC.10 Homo sapiens cDNA clone IMAGE:2900367 5' similar to TR:O60275 O60275 KIAA0522 PROTEIN.;
9222	21738	34890	3.48	0.0E+00	BE207063.1	EST_HUMAN	bc0905.y1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9222	21738	34881	3.48	0.0E+00	BE207063.1	EST_HUMAN	bc0905.y1 NIH_MGC.7 Homo sapiens cDNA clone IMAGE:2823873 5' similar to gb:L35049 Mus musculus Bcl-xL mRNA, complete cds (MOUSE);
9233	21955	34804	2.35	0.0E+00	BF348013.1	EST_HUMAN	BC2023150F1 NCJ CGAP_Brt87 Homo sapiens cDNA clone IMAGE:4158300 5'
9268	21784	34743	2.8	0.0E+00	BE712515.1	EST_HUMAN	QV2-HT0698-250700-282-b08 HT0698 Homo sapiens cDNA
9289	21899	34846	0.98	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3859035 5'
9289	21899	34847	0.98	0.0E+00	BF034377.1	EST_HUMAN	601455116F1 NIH_MGC.66 Homo sapiens cDNA clone IMAGE:3859035 5'
9305	21805	34854	0.53	0.0E+00	AI068351.1	EST_HUMAN	RC-BT108-040399-032 BT108 Homo sapiens cDNA
9308	21908	34856	1.54	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9308	21908	34857	1.54	0.0E+00	5803069	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5 (LILRB5), mRNA
9317	21831	34782	1.96	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
9352	21866	34816	2.17	0.0E+00	AI088043.1	EST_HUMAN	ow60h01.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:1651249 3' similar to TR:Q14677 Q14677 KIAA0171 PROTEIN.;
9359	20298	33196	0.93	0.0E+00	BF309962.1	EST_HUMAN	601892245F1 NIH_MGC.17 Homo sapiens cDNA clone IMAGE:4138066 5'
9361	20300	33199	2.26	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9361	20300	33200	2.28	0.0E+00	11560151	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
9363	20302	33203	18.79	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCJ CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9363	20302	33204	18.79	0.0E+00	AI290909.1	EST_HUMAN	qm09a06.x1 NCJ CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1881298 3' similar to SW:RL2B_HUMAN
9364	20303	33205	6.56	0.0E+00	AW953836.1	EST_HUMAN	P29316 60S RIBOSOMAL PROTEIN L23A. ;
9391	21814	34763	3.79	0.0E+00	AF153468.1	NT	EST366028 MAGC resequences, MAGC Homo sapiens cDNA
9394	21817	34767	0.81	0.0E+00	BE885128.1	EST_HUMAN	Homo sapiens polycystic kidney disease 2-like protein (PKD2L) gene, exon 8
9394	21817	34768	0.81	0.0E+00	BE885128.1	EST_HUMAN	601510882F1 NIH_MGC.71 Homo sapiens cDNA clone IMAGE:3912165 5'
9403	21912		19.73	0.0E+00	BE255829.1	EST_HUMAN	601510882F1 NIH_MGC.71 Homo sapiens cDNA clone IMAGE:3912165 5'
9406	21915	34864	1.36	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC.67 Homo sapiens cDNA clone IMAGE:3870007 5'
9406	21915	34865	1.36	0.0E+00	BE781382.1	EST_HUMAN	601466828F1 NIH_MGC.67 Homo sapiens cDNA clone IMAGE:3870007 5'
9408	21917	34866	29.88	0.0E+00	AW163779.1	EST_HUMAN	au86c04.y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:2783142 5' similar to gb:M36072 60S RIBOSOMAL PROTEIN L7A (HUMAN);

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9428	21937	34886	3	0.0E+00	BE263191.1	EST_HUMAN	601145054F2 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3160477 5'
9446	21972	34922	4.5	0.0E+00	C08158.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9446	21972	34923	4.5	0.0E+00	C08158.1	EST_HUMAN	C08158 Human pancreatic islet Homo sapiens cDNA clone hbc5605
9448	21974	34926	2.7	0.0E+00	BE746215.1	EST_HUMAN	601578683F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3927548 5'
9458	21984	34936	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9458	21984	34937	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9458	21984	34938	2.92	0.0E+00	11437282	NT	Homo sapiens solute carrier family 21 (organic anion transporter), member 9 (SLC21A9), mRNA
9478	21877	34824	1.89	0.0E+00	BE900549.1	EST_HUMAN	601673425F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3956238 5'
9498	21993	34952	0.76	0.0E+00	AV701829.1	EST_HUMAN	AV701829 ADB Homo sapiens cDNA clone ADBBY401 5'
9508	22008	34965	2.38	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9508	22008	34966	2.38	0.0E+00	AF019084.1	NT	Homo sapiens keratin 2a (KRT2E) gene, complete cds
9540	22040	35001	1.32	0.0E+00	BE082977.1	EST_HUMAN	RC2-BT0842-130300-017-g01 BT0842 Homo sapiens cDNA
9559	22059	35021	1.86	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BN0-akg-b-12-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9559	22059	35022	1.86	0.0E+00	AW500293.1	EST_HUMAN	UI-HF-BN0-akg-b-12-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3076943 5'
9568	22068	35028	1.75	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9568	22068	35029	1.75	0.0E+00	AF029308.1	NT	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
9570	22070	35030	0.72	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9570	22070	35031	0.72	0.0E+00	BE783272.1	EST_HUMAN	601470824F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874037 5'
9579	22079	35043	1.14	0.0E+00	W56629.1	EST_HUMAN	zd16a11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9579	22079	35044	1.14	0.0E+00	W56629.1	EST_HUMAN	zd16a11.1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:340844 5'
9591	22091	35055	1.05	0.0E+00	AB035366.1	NT	Homo sapiens mRNA for neurexin I-alpha protein, complete cds
9595	22095	35060	0.64	0.0E+00	A1124780.1	EST_HUMAN	am56a11.xt Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539548 3'
9597	22097	35060	2.65	0.0E+00	AW500526.1	EST_HUMAN	UI-HF-BN0-akj-c-07-Q-UJ.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077364 5'
9640	22140	35107	1.46	0.0E+00	AF009668.1	NT	Multiple sclerosis associated retrovirus polyprotein (pol) mRNA, partial cds
9666	22165	35138	2.21	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9666	22165	35139	2.21	0.0E+00	S78468.1	NT	AIGF=androgen-induced growth factor AIGF [human, placenta, Genomic/mRNA, 498 nt, segment 5 of 5]
9669	22168	35144	2.54	0.0E+00	BE563320.1	EST_HUMAN	601334603F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3688680 5'
9689	22188	35161	1.5	0.0E+00	AW363135.1	EST_HUMAN	CM2-CT0311-301199-043-h11 CT0311 Homo sapiens cDNA
9708	22208	35179	0.91	0.0E+00	11438432	NT	Homo sapiens multimetric (MMRN), mRNA

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9709	22207	35180	0.74	0.0E+00	11424387	NT	Homo sapiens leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 (LILRB3), mRNA
9718	22216	35190	0.83	0.0E+00	BE208710.1	EST_HUMAN	bb28c01.x1 NIH_MGC_5 Homo sapiens cDNA clone IMAGE:2964000 3'
9733	22231	35208	2.41	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9733	22231	35209	2.41	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9742	22240	35221	1.45	0.0E+00	AW500936.1	EST_HUMAN	UI-HF-BP0P-4ir-f05-0-U1 r1 NIH_MGC_51 Homo sapiens cDNA clone IMAGE:3072897 5'
9748	22246	35227	19.66	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9748	22246	35228	19.66	0.0E+00	BE740490.1	EST_HUMAN	601595558F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3949383 5'
9761	22259	35242	2.32	0.0E+00	7862067	NT	Homo sapiens KIAA0345 gene product (KIAA0345), mRNA
9779	22277	35262	1.98	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434L0120 5'
9784	22282	35268	0.71	0.0E+00	AL041084.2	EST_HUMAN	DKFZp434B2416_r1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434B2416 5'
9794	22292	35275	2.32	0.0E+00	AU132349.1	EST_HUMAN	AU132349 NT2RP3 Homo sapiens cDNA clone NT2RP3004260 5'
9795	22293	35278	2.48	0.0E+00	AF152308.1	NT	Homo sapiens protocadherin alpha 12 (PCDH-alpha12) mRNA, complete cds
9822	22320	35304	2.61	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9822	22320	35305	2.61	0.0E+00	AF009220.1	NT	Homo sapiens leukocyte immunoglobulin-like receptor-1 mRNA, complete cds
9838	22336	35318	3.23	0.0E+00	BF002898.1	EST_HUMAN	MR4-TN0114-110900-101-e04 TN0114 Homo sapiens cDNA
9855	22362	35342	2.74	0.0E+00	BE280793.1	EST_HUMAN	601155227F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3138798 5'
9874	22371	35348	8.19	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
9874	22371	35349	8.19	0.0E+00	BE388700.1	EST_HUMAN	601286351F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3613045 5'
							xm72b01.x1 NCL_CGAP_CML1 Homo sapiens cDNA clone IMAGE:2698977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
9883	22380	35355	9.02	0.0E+00	AW236269.1	EST_HUMAN	EST46740 Fetal kidney II Homo sapiens cDNA 5' end
9884	22381	35356	0.92	0.0E+00	AA341305.1	EST_HUMAN	EST46740 Fetal kidney II Homo sapiens cDNA 5' end
9883	22390	35368	0.5	0.0E+00	11427235	NT	Homo sapiens Chediak-Higashi syndrome 1 (CHS1), mRNA
9916	22412	35387	0.79	0.0E+00	AW964113.1	EST_HUMAN	EST376186 MAGG resequences, MAGH Homo sapiens cDNA
9929	22425	35398	6.82	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
9929	22425	35399	6.82	0.0E+00	AU143673.1	EST_HUMAN	AU143673 Y79AA1 Homo sapiens cDNA clone Y79AA1002307 5'
9932	22428	35402	3.44	0.0E+00	AFD72408.1	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9935	22430	35404	2.52	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
9935	22430	35405	2.52	0.0E+00	11421001	NT	Homo sapiens HEF like Protein (HEFL), mRNA
9968	22463	35447	3.55	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9968	22463	35448	3.55	0.0E+00	AU136637.1	EST_HUMAN	AU136637 PLACE1 Homo sapiens cDNA clone PLACE1004737 5'
9984	22479	35462	2.1	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin7 and partial ZNF143 gene
9984	22479	35463	2.1	0.0E+00	AJ295844.1	NT	Homo sapiens partial RANBP7 gene for RANBP7/importin7 and partial ZNF143 gene
9988	22484	35470	0.92	0.0E+00	AV695712.1	EST_HUMAN	AV695712 GKCC Homo sapiens cDNA clone GKCDXA07 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Database Source	Top Hit Descriptor
9989	22484	35471	0.92	0.0E+00	EST_HUMAN	AV695712 GKC Homo sapiens cDNA clone GKCDXA07 5'
9995	22490	35478	0.57	0.0E+00	NT	Homo sapiens killer cell inhibitory receptor KIRCI gene, exons 2, 3, and 4
9997	22492	35481	2.78	0.0E+00	EST_HUMAN	Zp97h11.1r1 Stratogene muscle 937209 Homo sapiens cDNA clone IMAGE:628197 5'
10020	22515	35508	1.81	0.0E+00	EST_HUMAN	Z31f01.1r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10020	22515	35509	1.81	0.0E+00	EST_HUMAN	Z31f01.1r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:503545 5'
10061	22556	35551	1.56	0.0E+00	NT	Homo sapiens KIF4 (KIF4) mRNA, complete cds
10102	22597	35560	0.75	0.0E+00	EST_HUMAN	601491565F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3803657 5'
10113	22608	35598	11.65	0.0E+00	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10113	22608	35598	11.65	0.0E+00	EST_HUMAN	601570712F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3845403 5'
10118	22613	35603	1.05	0.0E+00	EST_HUMAN	AU127403 NT2RP2 Homo sapiens cDNA clone NT2RP2001212 5'
10127	22622	35612	0.99	0.0E+00	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10127	22622	35613	0.99	0.0E+00	EST_HUMAN	601645134F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3930177 5'
10142	22637	35628	0.79	0.0E+00	EST_HUMAN	601432317F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917453 5'
10163	22648	35642	0.79	0.0E+00	EST_HUMAN	EST182353 Jurkat T-cells VI Homo sapiens cDNA 5' end
10154	22649	35643	0.57	0.0E+00	NT	Homo sapiens neuroxin III (NRXN3) mRNA
10167	22662	35657	0.81	0.0E+00	EST_HUMAN	601432228F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917598 5'
10170	22665	35660	1.29	0.0E+00	NT	Homo sapiens hypothetical C2H2 zinc finger protein FLJ22504 (FLJ22504), mRNA
10179	22674	35666	1.47	0.0E+00	NT	Homo sapiens mRNA for actin binding protein ABP620, complete cds
10180	22675	35667	0.53	0.0E+00	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10180	22675	35668	0.53	0.0E+00	EST_HUMAN	601105459F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2987918 5'
10187	22682	35673	6.03	0.0E+00	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10187	22682	35674	6.03	0.0E+00	NT	Homo sapiens mRNA for estrogen receptor beta, complete cds
10194	22689	35682	0.57	0.0E+00	EST_HUMAN	Zq06h11.1r1 Stratogene muscle 937209 Homo sapiens cDNA clone IMAGE:628965 5' similar to TR:G407097 G407097 168KD PROTEIN ;
10196	22691	35684	1.18	0.0E+00	EST_HUMAN	Z19h06.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:450707 3' similar to gb:M14123_cds1 RETROVIRUS-RELATED GAG POLYPROTEIN (HUMAN);
10198	22693	35685	1.31	0.0E+00	NT	Homo sapiens beta 1,4-galactosyltransferase mRNA, complete cds
10200	22695	35688	5.5	0.0E+00	EST_HUMAN	602037045F1 NCI CGAP Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'
10200	22695	35689	5.5	0.0E+00	EST_HUMAN	602037045F1 NCI CGAP Bm84 Homo sapiens cDNA clone IMAGE:4184939 5'
10227	22722	35713	0.93	0.0E+00	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10227	22722	35714	0.93	0.0E+00	EST_HUMAN	601439713F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924578 5'
10256	22751	35739	0.53	0.0E+00	EST_HUMAN	AV716271 DCB Homo sapiens cDNA clone DCBBDC08 5'
10256	22751	35740	0.53	0.0E+00	EST_HUMAN	AV716271 DCB Homo sapiens cDNA clone DCBBDC08 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10285	22780	35770	0.77	0.0E+00	AI631818.1	EST_HUMAN	wa36e03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10285	22780	35771	0.77	0.0E+00	AI631818.1	EST_HUMAN	Q61204 NOTCH2-LIKE 1
10298	22792	35782	1.32	0.0E+00	TO3078.1	EST_HUMAN	wa36e03.x1 NCI CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2300188 3' similar to TR:Q61204
10321	22815	35811	0.83	0.0E+00	AU122429.1	EST_HUMAN	FB23A4 Fetal brain, Stratogene Homo sapiens cDNA clone FB23A4 3'end
10348	22842	35838	2.69	0.0E+00	BF436218.1	EST_HUMAN	AU122429 MAMMA1 Homo sapiens cDNA clone MAMMA1002368 5'
10349	22843		1.61	0.0E+00	AV654765.1	EST_HUMAN	nab45e12.x1 Soares_NSF_FB_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3265271 3'
							AV654765 GLC Homo sapiens cDNA clone GLODZC07 3'
							xu74b01.x1 NCI CGAP_Kid8 Homo sapiens cDNA clone IMAGE:2607401 3' similar to gb:M69066 MOESIN (HUMAN)
10387	22861	35854	3.53	0.0E+00	AW517980.1	EST_HUMAN	
10371	22865	35858	21.07	0.0E+00	BE549213.1	EST_HUMAN	601078764F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3484703 5'
10386	22880	35874	0.55	0.0E+00	11438005	NT	Homo sapiens hypothetical protein DKFZp781P1010 (DKFZp781P1010). mRNA
10410	22904	35901	1.22	0.0E+00	X69893.1	NT	H. sapiens mRNA for NK receptor (183 Act)
10411	22905	35902	3	0.0E+00	BE781742.1	EST_HUMAN	601467419F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3870700 5'
10430	22924	35928	2.88	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0842 Homo sapiens cDNA
10430	22924	35930	2.88	0.0E+00	BE082720.1	EST_HUMAN	RC2-BT0642-150200-012-403 BT0842 Homo sapiens cDNA
10437	22931	35938	0.6	0.0E+00	Y08032.1	NT	Human endogenous retrovirus-K, LTR U5 and gag gene
10443	22937	35947	0.66	0.0E+00	AI656890.1	EST_HUMAN	tt54e07.x1 NCI CGAP_GC8 Homo sapiens cDNA clone IMAGE:2244612 3'
10450	22944	35954	5.46	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10450	22944	35955	5.46	0.0E+00	BE743215.1	EST_HUMAN	601573895F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3835198 5'
10453	22947	35956	1.83	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10453	22947	35957	1.83	0.0E+00	BE617655.1	EST_HUMAN	601441723T1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3845956 3'
10458	22952	35960	0.49	0.0E+00	D29954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10458	22952	35961	0.49	0.0E+00	D29954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10474	22968	35977	0.66	0.0E+00	H39805.1	EST_HUMAN	yp01a10.11 Soares breast 3NbH18t Homo sapiens cDNA clone IMAGE:186138 5'
10474	22968	35989	0.46	0.0E+00	AW748117.1	EST_HUMAN	QV0-BT0107-230799-007-c06 BT0107 Homo sapiens cDNA
10498	22980	35999	1.14	0.0E+00	D87675.1	NT	Homo sapiens DNA for amyloid precursor protein, complete cds
10508	23002	36010	0.8	0.0E+00	D29954.1	NT	Human mRNA for KIAA0056 gene, partial cds
10515	23053	36064	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
10517	23053	36066	2.76	0.0E+00	AV711075.1	EST_HUMAN	AV711075 Cu Homo sapiens cDNA clone CuAAKG05 5'
10525	23062	36073	6.05	0.0E+00	AW813783.1	EST_HUMAN	RC3-ST0197-120200-015-a03 ST0197 Homo sapiens cDNA
10538	23075	36088	7.48	0.0E+00	AW963563.1	EST_HUMAN	EST375636 MAGE resequences, MAGH Homo sapiens cDNA
10538	23075	36088	1.91	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA
10538	23075	36089	1.91	0.0E+00	11431124	NT	Homo sapiens ATP-binding cassette, sub-family A (ABC1), member 3 (ABCA3), mRNA

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10540	23077	36091	1.82	0.0E+00	AW057621.1	EST_HUMAN	wy61f09.x1 Soares_NSF_F8_gw_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:2553065 3' similar to TR:Q60566 Q60566 VDX;
10549	23085	36096	2.26	0.0E+00	BE243270.1	EST_HUMAN	TCAAAP3D0917 Pediatric acute myelogenous leukemia cell (FAB M1) Baylor-HGSC project=TCAA Homo sapiens cDNA clone TCAAAP0917
10550	23086	36100	2.73	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
10550	23086	36101	2.73	0.0E+00	AI652239.1	EST_HUMAN	wb28a12.x1 NCL_CGAP_G08 Homo sapiens cDNA clone IMAGE:2306974 3' similar to contains element MSR1 MSR1 repetitive element;
10561	23097	36110	4.31	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10561	23097	36111	4.31	0.0E+00	11545911	NT	Homo sapiens NOD2 protein (NOD2), mRNA
10576	23111	36124	1.08	0.0E+00	AW404795.1	EST_HUMAN	UI-HF-BL0-acm-4-04-0-U1.1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3056983 5'
10580	23115	36128	5.92	0.0E+00	11424829	NT	Homo sapiens hypothetical protein FLJ20079 (FLJ20079), mRNA
10581	23116	36130	10.05	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10581	23116	36131	10.05	0.0E+00	4504536	NT	Homo sapiens 5-hydroxytryptamine (serotonin) receptor 1E (HTR1E) mRNA
10582	23117	36132	2.9	0.0E+00	AI981827.1	EST_HUMAN	wu32b06.x1 Soares_Dieckgraebe_colon_NHCD Homo sapiens cDNA clone IMAGE:2521715 3'
10585	23120	36136	2.57	0.0E+00	BE892109.1	EST_HUMAN	G01505204F2 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3906865 5'
10589	23124	36138	15.86	0.0E+00	BE891630.1	EST_HUMAN	G01434522F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919636 5'
10591	23126	36139	2.44	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10591	23126	36140	2.44	0.0E+00	8923839	NT	Homo sapiens myosin, heavy polypeptide 2, skeletal muscle, adult (MYH2), mRNA
10608	23140	36152	6.94	0.0E+00	BE903304.1	EST_HUMAN	G01674332F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3957343 5'
10609	18572	31304	2.31	0.0E+00	AA195905.1	EST_HUMAN	zp95b11.1 Stragene muscle 937209 Homo sapiens cDNA clone IMAGE:627993 5' similar to gb:X03740 MYOSIN HEAVY CHAIN, SKELETAL MUSCLE (HUMAN);
10630	23162	36174	1.99	0.0E+00	AA809080.1	EST_HUMAN	hw17c08.s1 NCL_CGAP_G080 Homo sapiens cDNA clone IMAGE:1240718 3' similar to gb:X57809 IG LAMBDA CHAIN C REGIONS (HUMAN);
10632	23164	36176	5.44	0.0E+00	BE793498.1	EST_HUMAN	G01588828F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943015 5'
10640	23172	36183	19.41	0.0E+00	AV727362.1	EST_HUMAN	G01727362F1 Homo sapiens cDNA clone HTCAOH08 5'
10640	23172	36184	19.41	0.0E+00	AV727362.1	EST_HUMAN	AV727362F1 Homo sapiens cDNA clone HTCAOH08 5'
10654	23186	36202	18.4	0.0E+00	AW518055.1	EST_HUMAN	xy04g10.x1 NCL_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2852226 3' similar to gb:M60854 40S RIBOSOMAL PROTEIN S16 (HUMAN);
10660	23192	36207	3.16	0.0E+00	AU135741.1	EST_HUMAN	AU135741F1 Homo sapiens cDNA clone PLACE1002784 5'
10665	23197	36210	2.88	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;
10685	23197	36211	2.88	0.0E+00	AW593333.1	EST_HUMAN	hg13d02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;

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10665	23197	36212	2.88	0.0E+00	AW593333.1	EST_HUMAN	hg13402.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2845475 3' similar to contains element MSR1 repetitive element;
10667	23199	36213	1.99	0.0E+00	Z34897.1	NT	H. sapiens mRNA for H1 histamine receptor
10668	23200	36214	3.18	0.0E+00	F13068.1	EST_HUMAN	HSC3IC031 normalized infant brain cDNA Homo sapiens cDNA clone c-3ic03
10678	23208	36220	3.91	0.0E+00	D10083.1	NT	Homo sapiens RGH1 gene, retrovirus-like element
10679	23211	36222	33.46	0.0E+00	11425570	NT	Homo sapiens pyridine receptor 1 (skaleia) (RYR1), mRNA
10695	23225	36239	3.59	0.0E+00	AW338094.1	EST_HUMAN	xw66701.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2832985 3' similar to gb:X17116 IG MU CHAIN C REGION (HUMAN);
10696	23226	36240	5.84	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-elt-a-01-0-U1.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
10698	23228	36241	5.84	0.0E+00	AW451230.1	EST_HUMAN	UI-H-B13-elt-a-01-0-U1.st NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736649 3'
10699	12891		16.23	0.0E+00	4506632	NT	Homo sapiens ribosomal protein L31 (RPL31) mRNA
10701	23230	36243	2.17	0.0E+00	AB014567.1	NT	Homo sapiens mRNA for KIAA0667 protein, partial cds
10714	23242	36259	2.26	0.0E+00	BE298449.1	EST_HUMAN	601119248F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3029219 5'
10730	23258	36272	1.99	0.0E+00	AB011117.1	NT	Homo sapiens mRNA for KIAA0545 protein, partial cds
10746	23270	36286	2.18	0.0E+00	BE792155.1	EST_HUMAN	601582046F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:3936539 5'
10747	23271		78.35	0.0E+00	BF684081.1	EST_HUMAN	602141405F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:4302432 5'
10749	23273	36288	4.66	0.0E+00	AU118386.1	EST_HUMAN	AU118386 HEMBA1 Homo sapiens cDNA clone HEMBA1003488 5'
10750	23274		8.15	0.0E+00	AW236269.1	EST_HUMAN	xn72b01.x1 NCI_CGAP_CWL1 Homo sapiens cDNA clone IMAGE:2699977 3' similar to gb:X02152_cds1 L-LACTATE DEHYDROGENASE M CHAIN (HUMAN);
10755	23279	36292	7.25	0.0E+00	A1149809.1	EST_HUMAN	qf43-c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10755	23279	36293	7.25	0.0E+00	A1149809.1	EST_HUMAN	qf43-c03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1752772 3'
10756	23280	36294	3.47	0.0E+00	AW391837.1	EST_HUMAN	QV4-ST0234-121193-032-b06 ST0234 Homo sapiens cDNA
10768	23292		1.54	0.0E+00	AU116908.1	EST_HUMAN	AU116908 HEMBA1 Homo sapiens cDNA clone HEMBA1000255 5'
10771	23295	36301	20.95	0.0E+00	11424728	NT	Homo sapiens insulin receptor (INSR), mRNA
10777	23301	36307	1.89	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-406 UM0093 Homo sapiens cDNA
10777	23301	36308	1.89	0.0E+00	AW804516.1	EST_HUMAN	QV0-UM0093-170400-191-406 UM0093 Homo sapiens cDNA
10778	23302	36309	2.04	0.0E+00	BF340308.1	EST_HUMAN	602037014F1 NCI_CGAP_Brn84 Homo sapiens cDNA clone IMAGE:4184979 5'
10779	23303	36310	39.28	0.0E+00	BE261209.1	EST_HUMAN	601148357F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3163310 5'
10790	23313	36321	3.78	0.0E+00	U50326.1	NT	Human protein kinase C substrate 80K-H (PRKCSH) gene, exon 15-17
10794	23317	36326	3.48	0.0E+00	BE773036.1	EST_HUMAN	RC1-FT0134-170700-012-r07 FT0134 Homo sapiens cDNA
10794	23317	36327	3.48	0.0E+00	BE773036.1	EST_HUMAN	rc32e07.st NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1325412 3' similar to contains element MSR1 repetitive element;
10816	23337	36350	55.63	0.0E+00	AA740782.1	EST_HUMAN	Homo sapiens signaling lymphocytic activation molecule (SLAM) gene, exon 2
10822	23343	36358	3.04	0.0E+00	AF25203.1	NT	

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
10835	23556	36371	1.92	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538667 5'
10835	23556	36372	1.92	0.0E+00	BE266478.1	EST_HUMAN	601192748F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538667 5'
10838	23559	36374	6.99	0.0E+00	C05089.1	EST_HUMAN	C05089 Human heart cDNA (YNAKamura) Homo sapiens cDNA clone 3NH4817
10845	23566	36382	2.16	0.0E+00	AA746375.1	EST_HUMAN	oa58h01.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10845	23566	36383	2.16	0.0E+00	AA746375.1	EST_HUMAN	oa58h01.r1 NCJ_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1309009 5'
10856	23377	36395	8.09	0.0E+00	AL157608.1	EST_HUMAN	DKFZp761J2116.1 761 (synonym: hamy2) Homo sapiens cDNA clone DKFZp761J2116 5'
10868	23389	36404	12.62	0.0E+00	AU116988.1	EST_HUMAN	AU116988 HEMBA1 Homo sapiens cDNA clone HEMBA1000424 5'
10881	23402	36419	2.07	0.0E+00	AV693656.1	EST_HUMAN	AV693656 GKC Homo sapiens cDNA clone GKCCNC03 5'
10913	23432	36453	3.17	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
10913	23432	36454	3.17	0.0E+00	BE182360.1	EST_HUMAN	PM0-HT0845-060500-002-E05 HT0845 Homo sapiens cDNA
10914	23433		1.8	0.0E+00	AV701152.1	EST_HUMAN	AV701152 ADA Homo sapiens cDNA clone ADAAD08 5'
10928	23446	36467	3.19	0.0E+00	BE896423.1	EST_HUMAN	601439032F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924142 5'
10935	23452	36474	1.69	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
10935	23452	36475	1.69	0.0E+00	AW500307.1	EST_HUMAN	UI-HF-BN0-akg-d-02-0-J1.r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077019 5'
							bb78c04.y1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3048488 5' similar to gb:Y00345 cds1 POLYADENYLATE-BINDING PROTEIN (HUMAN); gb:X65553 M.musculus mRNA for poly(A) binding protein (MOUSE);
10938	23455	36478	6.2	0.0E+00	BE018293.1	EST_HUMAN	601440446F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3925403 5'
10972	23487	36516	5.22	0.0E+00	BE897953.1	EST_HUMAN	ac86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10973	23488	36517	1.99	0.0E+00	A1459545.1	EST_HUMAN	ac86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10973	23488	36518	1.99	0.0E+00	A1459545.1	EST_HUMAN	ac86g11.x1 Schiller meningioma Homo sapiens cDNA clone IMAGE:1952804 3'
10986	23500	36530	1.82	0.0E+00	AL042278.1	EST_HUMAN	DKFZp434L0120.1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434L0120 5'
11018	23532	36568	3.57	0.0E+00	4758827	NT	Homo sapiens neuradin III (NRXN3) mRNA
11019	23533	36569	8.71	0.0E+00	BF206861.1	EST_HUMAN	601870902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4101433 5'
11023	23537	36573	20.4	0.0E+00	AW207734.1	EST_HUMAN	UI-H-B12-aga-h-01-0-U1.s1 NCJ_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724312 3'
11028	23542	36577	6.39	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
11028	23542	36578	6.39	0.0E+00	AB018260.1	NT	Homo sapiens mRNA for KIAA0717 protein, partial cds
							55KDA-ASSOCIATED PROTEIN ;
11028	23543	36579	3.29	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-
11029	23543	36580	3.29	0.0E+00	BE206846.1	EST_HUMAN	ba04d07.y1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-
11053	23566	36602	2.05	0.0E+00	BF083687.1	EST_HUMAN	55KDA-ASSOCIATED PROTEIN ;
11054	20011	32877	2.13	0.0E+00	L32832.1	NT	QV0-UM0091-120900-385-b12 UM0091 Homo sapiens cDNA
							Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds
11057	23569	36604	3.38	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA
11057	23569	36605	3.39	0.0E+00	BE148076.1	EST_HUMAN	RC3-HT0230-040500-110-h04 HT0230 Homo sapiens cDNA

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11092	23804	36844	5.37	0.0E+00	BF507876.1	EST_HUMAN	UI-H-B14-ack-b-10-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11092	23804	36845	5.37	0.0E+00	BF507876.1	EST_HUMAN	UI-H-B14-ack-b-10-Q-UI.s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085026 3'
11101	23811	36851	3.82	0.0E+00	AU135170.1	EST_HUMAN	AU135170 PLACE1 Homo sapiens cDNA clone IMAGE:4271630 5'
11105	23815	36855	1.61	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11105	23815	36856	1.61	0.0E+00	BF576138.1	EST_HUMAN	602132459F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271630 5'
11108	23816	36857	8.62	0.0E+00	BE878401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11108	23816	36858	8.62	0.0E+00	BE878401.1	EST_HUMAN	601486828F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3889207 5'
11113	23823	36864	1.85	0.0E+00	D87682.1	NT	Human mRNA for KIAA0241 gene, partial cds
11119	23828		5.3	0.0E+00	BF240536.1	EST_HUMAN	601875630F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4099710 5'
11132	23840	36880	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11132	23840	36881	3.05	0.0E+00	AB037737.1	NT	Homo sapiens mRNA for KIAA1316 protein, partial cds
11137	23845	36885	3.57	0.0E+00		NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11137	23845	36886	3.57	0.0E+00	11430868	NT	Homo sapiens retinoblastoma-like 2 (p130) (RBL2), mRNA
11154	23861	36706	9.12	0.0E+00	4503544	NT	Homo sapiens eukaryotic translation initiation factor 5A (EIF5A) mRNA
11162	23869	36714	1.66	0.0E+00	BF576287.1	EST_HUMAN	602134132F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4289502 5'
11165	23872	36718	6.44	0.0E+00	AW328173.1	EST_HUMAN	dr04g05.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2847177 5'
11168	23875		48.81	0.0E+00	M55083.1	NT	Human gamma actin-like pseudogene, complete cds
11173	23880	36725	5.47	0.0E+00	BF306696.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11173	23880	36728	5.47	0.0E+00	BF306696.1	EST_HUMAN	601889823F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4123948 5'
11180	23886	36733	45.22	0.0E+00	BF362462.1	EST_HUMAN	QV2-NN0054-230800-333-904 NN0054 Homo sapiens cDNA
11201	23706	36757	1.99	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11201	23706	36758	1.99	0.0E+00	U36284.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 16
11205	23710		6.26	0.0E+00	BE897051.1	EST_HUMAN	601439605F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924577 5'
11206	23711		1.61	0.0E+00	4503786	NT	Homo sapiens tyrosine-related kinase (FRK) mRNA
11217	23720	36774	2.82	0.0E+00	8923698	NT	Homo sapiens golgin-like protein (GLP), mRNA
11219	23722		2.56	0.0E+00	BF207662.1	EST_HUMAN	601861947F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4081715 5'
11220	23723		7.99	0.0E+00	BE257744.1	EST_HUMAN	601116705F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3957384 5'
11233	23764	36820	5.51	0.0E+00	BE206846.1	EST_HUMAN	ba04407.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN ;
11233	23764	36821	5.51	0.0E+00	BE206846.1	EST_HUMAN	ba04407.v1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2823373 5' similar to TR:O76022 O76022 E1B-55KDA-ASSOCIATED PROTEIN ;
11235	23766	36823	4.66	0.0E+00	AW753028.1	EST_HUMAN	QV0-CT0225-107299-071-106 CT0225 Homo sapiens cDNA
11240	23771		3.42	0.0E+00	AA558707.1	EST_HUMAN	n42c08.s1 NCI_CGAP_P14 Homo sapiens cDNA clone IMAGE:1043342 similar to gb:M95178 ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM (HUMAN);

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11241	18112	30521	6.08	0.0E+00	AI934954.1	EST_HUMAN	wp06g08.x1 NCL CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2484094 3'
11242	23772	36829	9.55	0.0E+00	AW327895.1	EST_HUMAN	dr02b08.x1 NIH_MGC_3 Homo sapiens cDNA clone IMAGE:2846919 5'
11260	24801	36847	1.56	0.0E+00	AW292776.1	EST_HUMAN	UI-H-BW0-ali-d-07-Q-U1.s1 NCL CGAP_Sub8 Homo sapiens cDNA clone IMAGE:2729509 3'
11266	23004	36012	2.1	0.0E+00	4758827	NT	Homo sapiens neuroxin III (NRXN3) mRNA
11274	23727	36781	1.59	0.0E+00	BE965909.2	EST_HUMAN	60165908R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11274	23727	36782	1.59	0.0E+00	BE965909.2	EST_HUMAN	60165908R1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895916 3'
11275	23728	36783	4.65	0.0E+00	BE185656.1	EST_HUMAN	IL5-HT0731-020900-077-105 HT0731 Homo sapiens cDNA
11288	23740	36796	5.82	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11288	23740	36797	5.82	0.0E+00	AL046540.1	EST_HUMAN	DKFZp434G178_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G178 5'
11298	23750	36807	18.85	0.0E+00	AI923116.1	EST_HUMAN	wn83g03.x1 NCL CGAP_U11 Homo sapiens cDNA clone IMAGE:2452468 3' similar to gb:S37431 LAMININ RECEPTOR (HUMAN);
11301	23794	36851	7	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11301	23794	36852	7	0.0E+00	AA760913.1	EST_HUMAN	nz11c07.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1287468 3' similar to TR:Q13686
11306	23799	36858	2.02	0.0E+00	BE910546.1	EST_HUMAN	Q13686 ALKB HOMOLOG PROTEIN.;
11314	23012	36021	7.16	0.0E+00	BE676347.1	EST_HUMAN	601501090F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3902928 5'
11323	23021	36030	1.89	0.0E+00	AV757420.1	EST_HUMAN	727112.x1 NCL CGAP_CLL1 Homo sapiens cDNA clone IMAGE:3295919 3' similar to TR:O00409 O00409 CHECKPOINT SUPPRESSOR 1.;
11352	23806	36865	3.55	0.0E+00	L39891.1	NT	AV757420 BM Homo sapiens cDNA clone BMFAGH03 5'
11352	23806	36866	3.55	0.0E+00	L39891.1	NT	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11386	23818	36879	4.02	0.0E+00	AU138211.1	EST_HUMAN	Homo sapiens polycystic kidney disease-associated protein (PKD1) gene, complete cds
11381	23833	36896	9.87	0.0E+00	BE622317.1	EST_HUMAN	AU138211 PLACE1 Homo sapiens cDNA clone PLACE1008077 5'
11386	23838	36900	11.61	0.0E+00	AI207425.1	EST_HUMAN	601441086F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3916270 5'
11386	23838	36901	11.61	0.0E+00	AI207425.1	EST_HUMAN	HA2767 Human fetal liver cDNA library Homo sapiens cDNA
11415	23866	36927	36.86	0.0E+00	BE748899.1	EST_HUMAN	HA2767 Human fetal liver cDNA library Homo sapiens cDNA
11415	23866	36928	36.86	0.0E+00	BE748899.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11425	23876	36940	2.19	0.0E+00	AU141882.1	EST_HUMAN	601572186T1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:3839012 3'
11425	23876	36941	2.19	0.0E+00	AU141882.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11428	23879	36944	2.52	0.0E+00	AW008022.1	EST_HUMAN	AU141882 THYRO1 Homo sapiens cDNA clone THYRO1001398 5'
11431	24802	36947	3.78	0.0E+00	BF002333.1	EST_HUMAN	wz91h01.x1 NCL CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2566225 3' similar to WP:F53H10.2
11450	23900	36987	3.81	0.0E+00	AW387776.1	EST_HUMAN	CE11040 ZINC FINGER, C2H2 TYPE ;
							7h22b10.x1 NCL CGAP_Cot16 Homo sapiens cDNA clone IMAGE:3316699 3' similar to TR:Q13458 Q13458 TRIO.;
							MR4-S1018-261069-012-b03 S10118 Homo sapiens cDNA

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11450	23800	36868	3.81	0.0E+00	AW387776.1	EST_HUMAN	MR4-ST0118-261099-012-b03 ST0118 Homo sapiens cDNA
11459	23809		2.48	0.0E+00	AW863777.1	EST_HUMAN	MR3-SN0010-310300-107-b03 SN0010 Homo sapiens cDNA
11471	23921	36960	3.38	0.0E+00		NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11471	23921	36961	3.38	0.0E+00	11435244	NT	Homo sapiens KIAA0247 gene product (KIAA0247), mRNA
11478	23926	36967	7.44	0.0E+00	U36253.1	NT	Human beta-prime-adaptin (BAM22) gene, exon 5
11479	23929	36969	12.8	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11479	23929	37000	12.8	0.0E+00	BE379254.1	EST_HUMAN	601237691F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3609623 5'
11492	23941	37012	2.5	0.0E+00	BE784758.1	EST_HUMAN	601590588F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3944708 5'
11493	23942	37013	115.96	0.0E+00	BE878633.1	EST_HUMAN	601491821F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894220 5'
11507	23956	37026	18.86	0.0E+00	BE409693.1	EST_HUMAN	601299403F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3829544 5'
11508	23957	37027	1.94	0.0E+00	BE148650.1	EST_HUMAN	MR0-HT0241-150500-011-102 HT0241 Homo sapiens cDNA
11509	23958	37028	3.08	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11509	23958	37028	3.08	0.0E+00	AF223391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced
11510	18292	30771	1.77	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11518	23966	37038	1.77	0.0E+00	D26535.1	NT	Human gene for dihydropyrimidine succinyltransferase, complete cds (exon 1-15)
11521	23969	37040	2.03	0.0E+00	AU132940.1	EST_HUMAN	AU132940 NT2RP4 Homo sapiens cDNA clone NT2RP4000929 5'
11533	23981	37051	4.44	0.0E+00	BE903372.1	EST_HUMAN	601676337F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3958835 5'
11533	23981	37052	1.84	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11535	23983	37054	1.84	0.0E+00	BF312552.1	EST_HUMAN	601897524F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4127069 5'
11535	23983	37055	3.01	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11544	23992	37055	3.01	0.0E+00	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
11544	23992	37055	4.03	0.0E+00	BE908402.1	EST_HUMAN	601498553F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900396 5'
11560	24007	37078	1.74	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
11574	24803		23.39	0.0E+00	BF309120.1	EST_HUMAN	601890534F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4131416 5'
11580	24026	37094	55.98	0.0E+00	BE297175.1	EST_HUMAN	601177407F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3532988 5'
11589	24032	37102	7.09	0.0E+00	AL040793.1	EST_HUMAN	DKFZp434D0415.t1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434D0415 5'
11652	25091	30499	6.23	0.0E+00	BE312542.1	EST_HUMAN	601150023F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503020 5'
11666	24925		1.78	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046
11668	24936		8.17	0.0E+00	AL180993.1	EST_HUMAN	qet17b12.x1 Soares fetal lung NBHL19W Homo sapiens cDNA clone IMAGE:1739231 3'
11678	24097		3.67	0.0E+00	AB011399.1	NT	Homo sapiens gene for AF-6, complete cds
11698	24112		4.16	0.0E+00	AL163246.2	NT	Homo sapiens chromosome 21 segment HS21C046

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Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
11701	24114		1.35	0.0E+00	AB018195.1	NT	Homo sapiens ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)
11709	24120		3.59	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
11728	24134		5.98	0.0E+00	5802973	NT	Homo sapiens antioxidant protein 1 (AOP1), nuclear gene encoding mitochondrial protein, mRNA
11763	24897	30711	1.49	0.0E+00	AF240786.1	NT	Homo sapiens glutathione S-transferase theta 2 (GSTT2) and glutathione S-transferase theta 1 (GSTT1) genes, complete cds
11774	24906		4.78	0.0E+00	AL041831.1	EST_HUMAN	DKFZp434K0819_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434K0819 5'
11803	25056		4.26	0.0E+00	11418318	NT	Homo sapiens G-2 and S-phase expressed 1 (GTSE1), mRNA
11812	24184		11.29	0.0E+00	AL046544.1	EST_HUMAN	DKFZp434G218_r1 434 (synonym: hies3) Homo sapiens cDNA clone DKFZp434G218 5'
11824	24941		2.62	0.0E+00	AI903497.1	EST_HUMAN	IL-BT030-271098-001 BT030 Homo sapiens cDNA
11862	25079		2.35	0.0E+00	NS4484.1	EST_HUMAN	yy40e08.s1 Scores fetal liver spleen 1NfLS Homo sapiens cDNA clone IMAGE:245222 3' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ;
11877	24227		4.72	0.0E+00	AF106656.1	NT	Homo sapiens adenylsuccinate lyase gene, complete cds
11880	13490	26007	5.46	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11880	13490	26008	5.46	0.0E+00	4507500	NT	Homo sapiens T-cell lymphoma invasion and metastasis 1 (TIAM1) mRNA
11889	24945		2.49	0.0E+00	10092587	NT	Homo sapiens nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 (NFATC2), mRNA
11917	13204		3.24	0.0E+00	AF003528.1	NT	Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions
11955	24720	30870	4.32	0.0E+00	11430460	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12017	24871	30708	24.36	0.0E+00	AW590082.1	EST_HUMAN	hg31e08.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2947234 3' similar to contains Alu repetitive element; contains element MER22 repetitive element ;
12028	24926		1.5	0.0E+00	BE090210.1	EST_HUMAN	RC6-BT0711-290300-011-D05 BT0711 Homo sapiens cDNA
12073	24938		2	0.0E+00	AF068757.1	NT	Homo sapiens somatostatin receptor subtype 3 (SSTR3) gene, 5' flanking region and partial cds
12112	24373		4.16	0.0E+00	9635487	NT	Human endogenous retrovirus, complete genome
12155	24931		1.93	0.0E+00	AI204914.1	EST_HUMAN	an05h04.x1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1684759 3'
12169	24927		1.52	0.0E+00	BE439792.1	EST_HUMAN	HTM1-654F HTM1 Homo sapiens cDNA
12244	14314	26855	4.92	0.0E+00	H30132.1	EST_HUMAN	yo59e08.r1 Scores breast 3NbIBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb.M64099
12244	14314	26856	4.92	0.0E+00	H30132.1	EST_HUMAN	GAMMA-GLUTAMYLTRANSEPTIDASE 5 PRECURSOR (HUMAN);
12256	24466		33.19	0.0E+00	D50659.1	NT	yo59e08.r1 Scores breast 3NbIBst Homo sapiens cDNA clone IMAGE:182246 5' similar to gb.M64099
12259	24469	30928	3.51	0.0E+00	11418189	NT	GAMMA-GLUTAMYLTRANSEPTIDASE 6 PRECURSOR (HUMAN);
12259	24469	30929	3.51	0.0E+00	11418189	NT	Human gamma-cytoplasmic actin (ACTGP9) pseudogene
							Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA
							Homo sapiens thyroid autoantigen 70kD (Ku antigen) (G22P1), mRNA

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Table 4
Single Exon Probes Expressed in Fetal Liver

Probe SEQ ID NO.	Exon SEQ ID NO.	ORF SEQ ID NO.	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
12279	14717	27289	1.42	0.0E+00	4758489	NT	Homo sapiens GTP binding protein 1 (GTPBP1), mRNA
12318	24508		1.61	0.0E+00	AW664999.1	EST_HUMAN	h186606.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2979154 3'
12401	15963	28440	5.09	0.0E+00	4855312	NT	Homo sapiens G protein-coupled receptor 24 (GPR24), mRNA
12409	18031	30492	2.86	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12412	24588		2.55	0.0E+00	AB029900.1	NT	Homo sapiens CST gene for cerebroside sulfotransferase, exon 1, 2, 3, 4, 5
12453	24587	30917	1.67	0.0E+00	9558724	NT	Homo sapiens cleavage and polyadenylation specific factor 1, 160kD subunit (CPSF1), mRNA
12481	25102		2.92	0.0E+00	AL183248.2	NT	Homo sapiens chromosome 21 segment HS21C046
12488	13277	25754	2.02	0.0E+00	6806918	NT	Homo sapiens low density lipoprotein-related protein 2 (LRP2), mRNA
12573	24670	30876	1.55	0.0E+00	11417862	NT	Homo sapiens calcineurin binding protein 1 (KIAA0330), mRNA
12576	24672		2.54	0.0E+00	AB002059.1	NT	Homo sapiens DNA for Human P2XM, complete cds
12580	24676		4.31	0.0E+00	7657020	NT	Homo sapiens DKFZp434P211 protein (DKFZP434P211), mRNA
12600	24686		2.35	0.0E+00	AB026898.1	NT	Homo sapiens DNA, DLEC1 to ORCTL4 gene region, section 1/2 (DLEC1, ORCTL3, ORCTL4 genes, complete cds)

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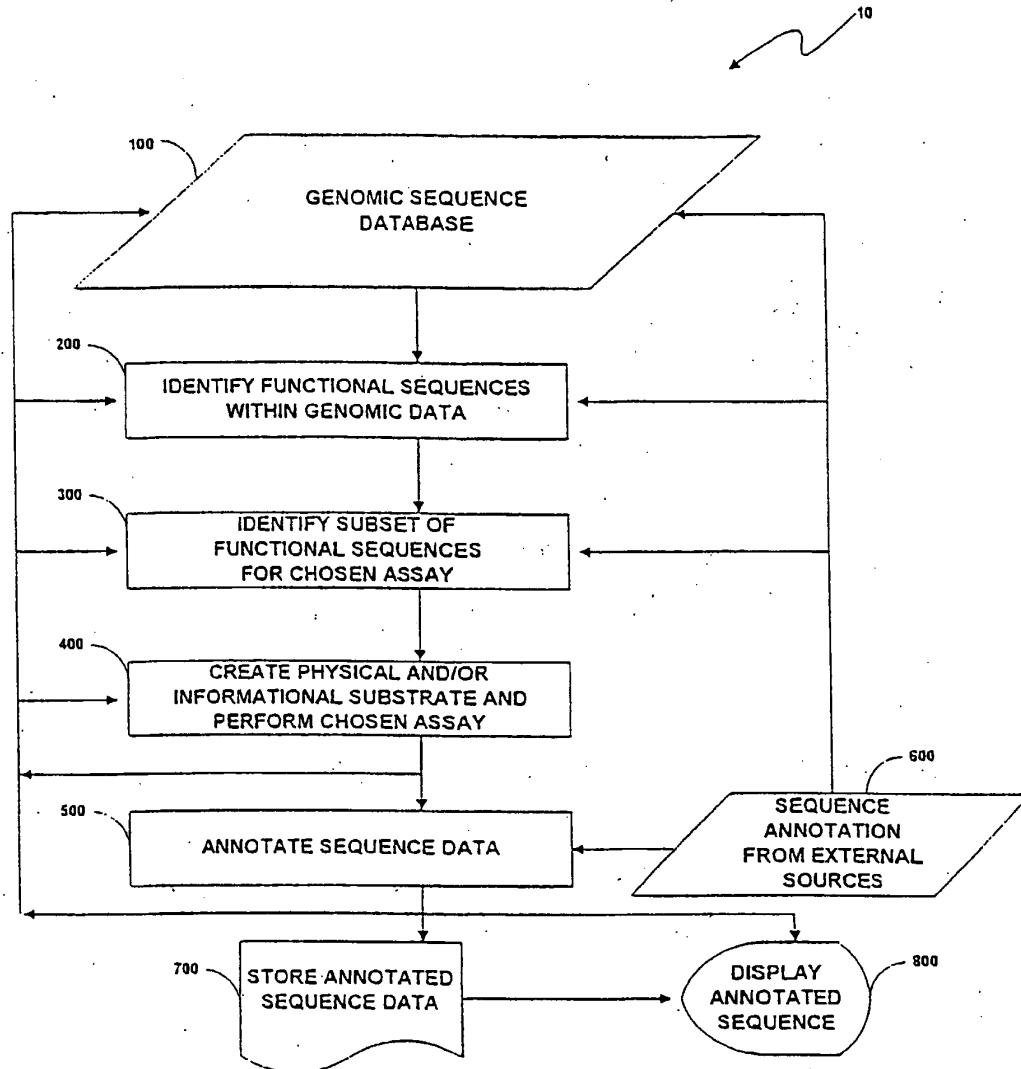


Fig. 1

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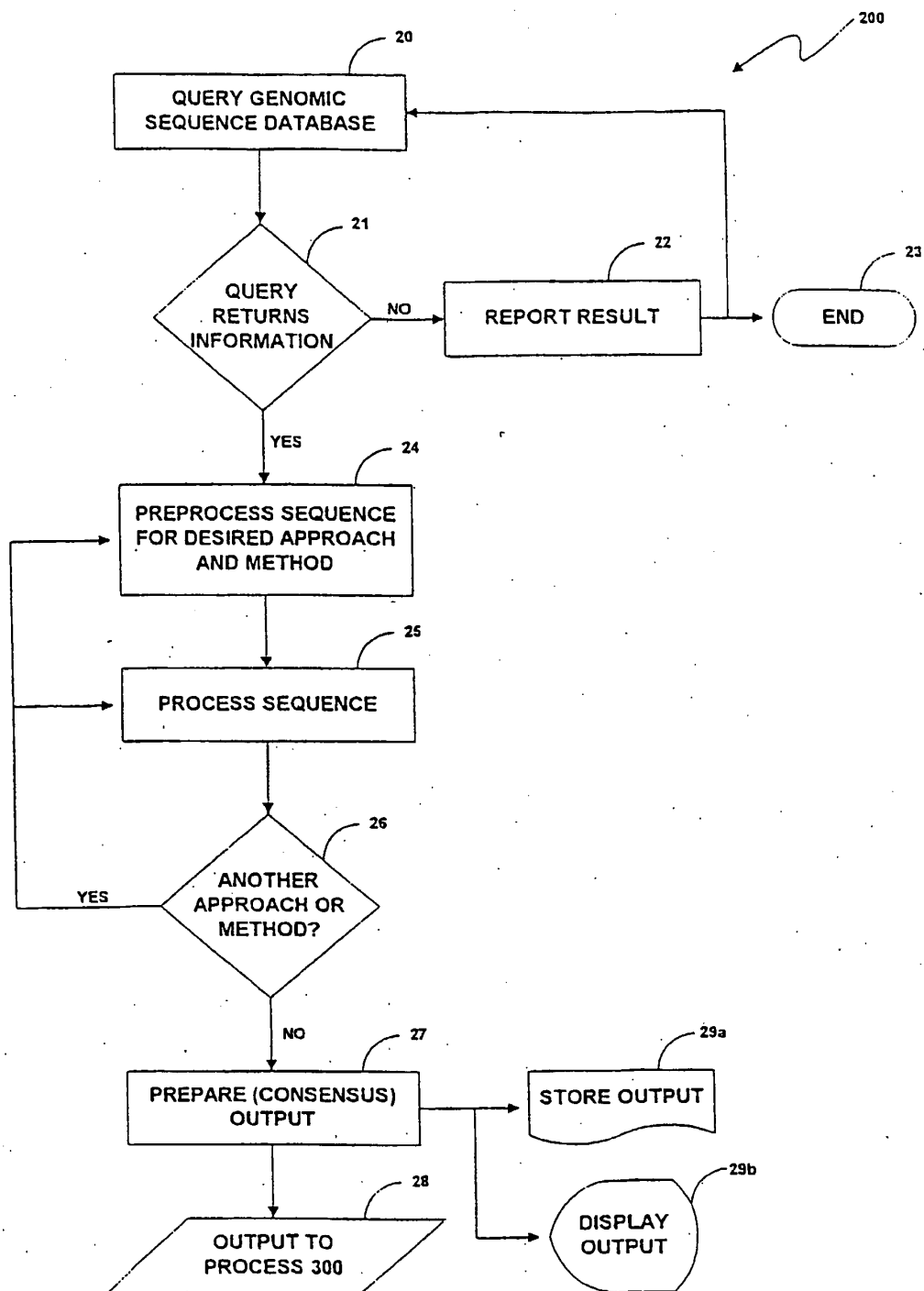


Fig. 2

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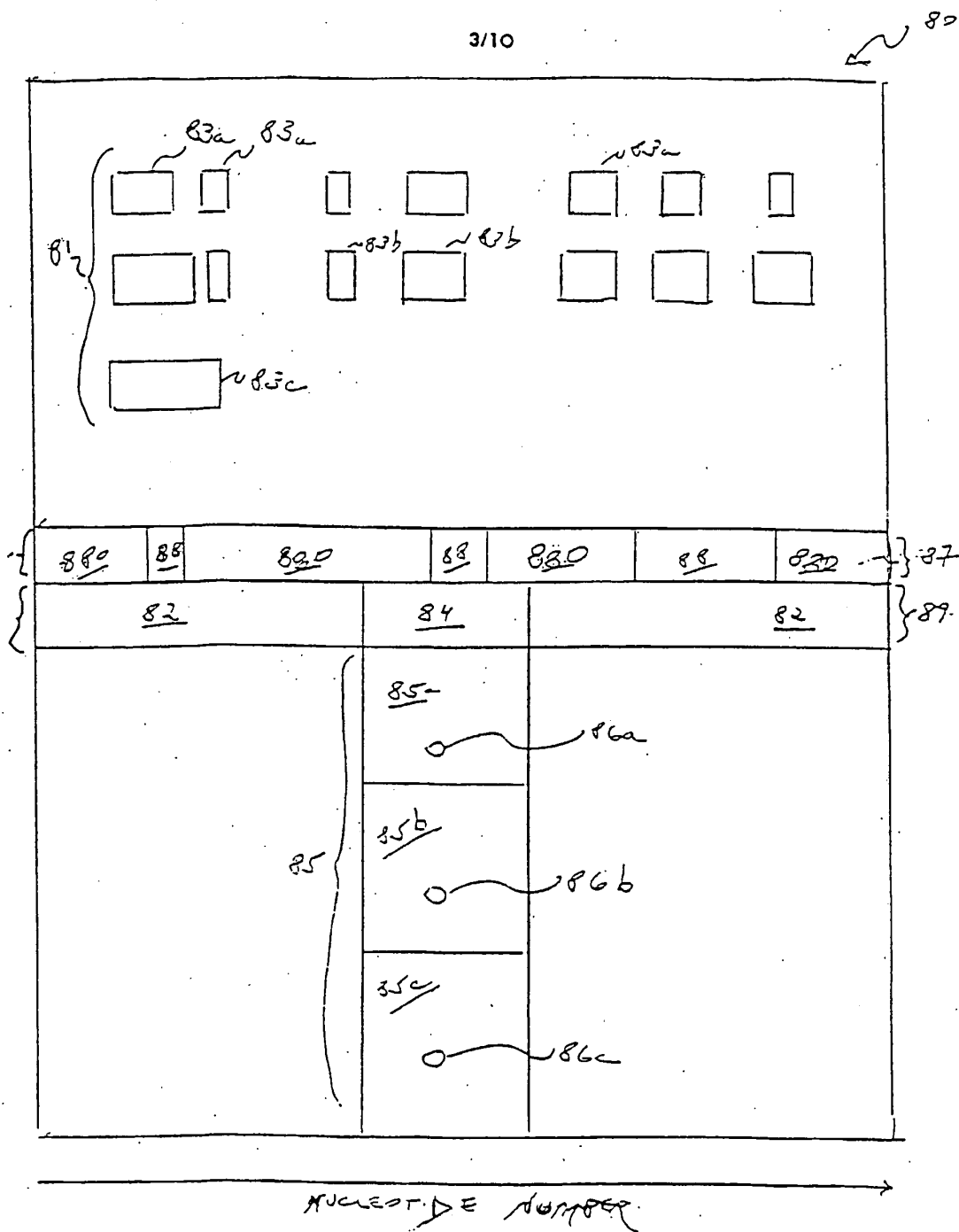


Fig. 3

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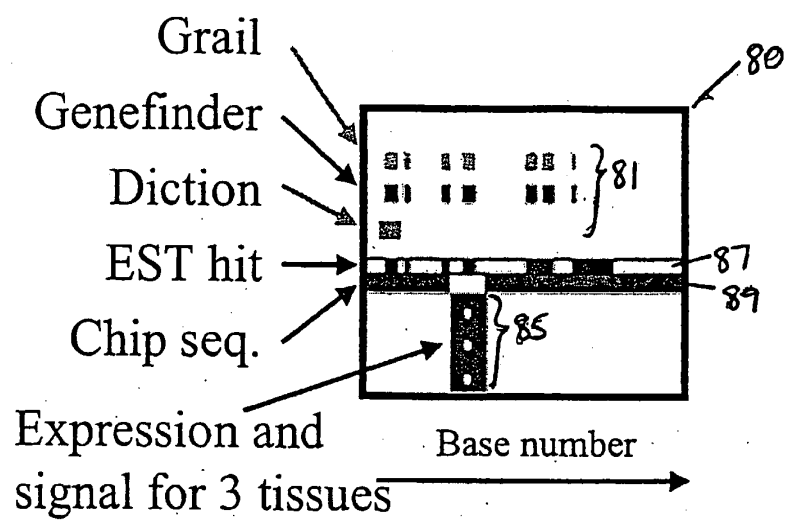


Fig. 4

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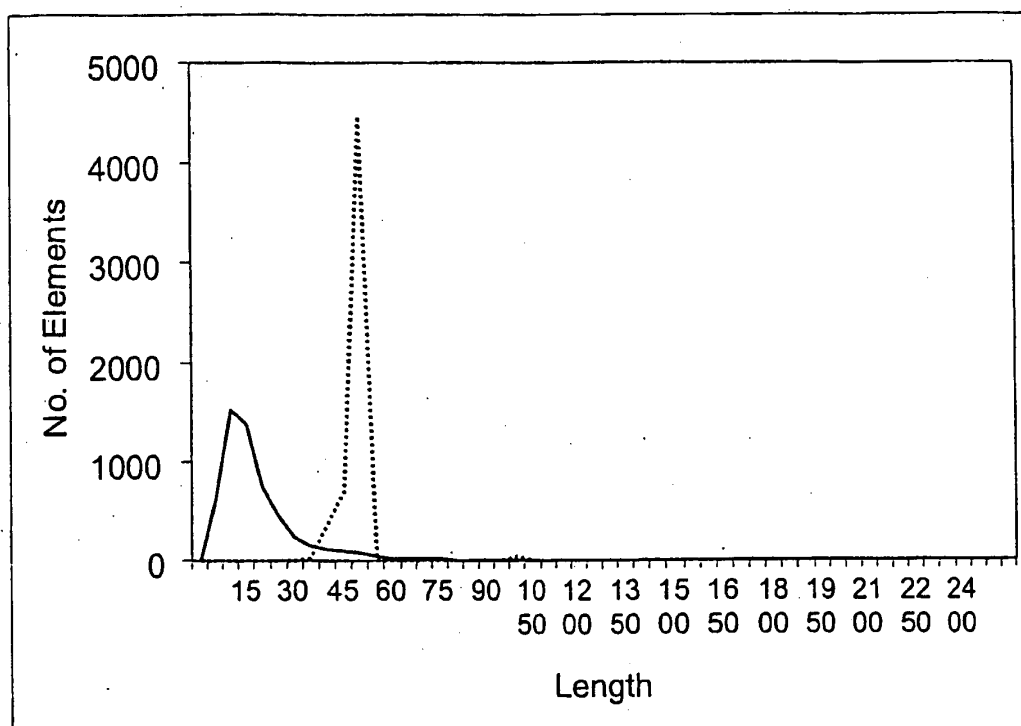


Fig. 5

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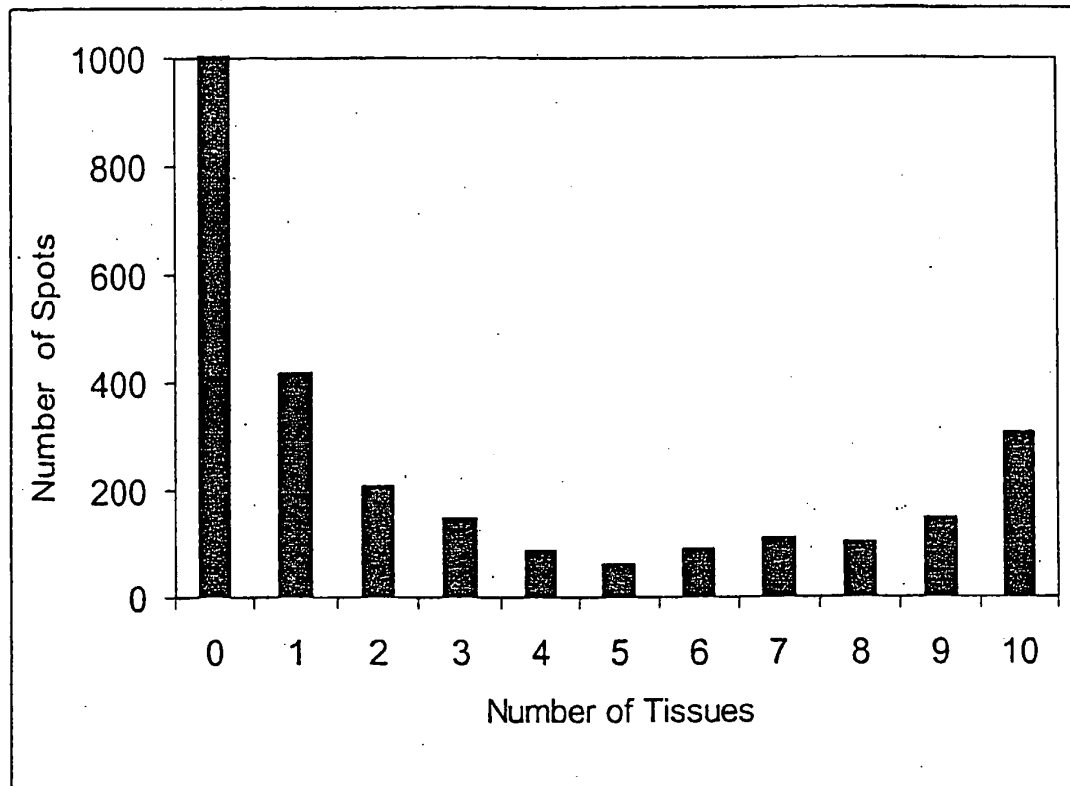


Fig. 6

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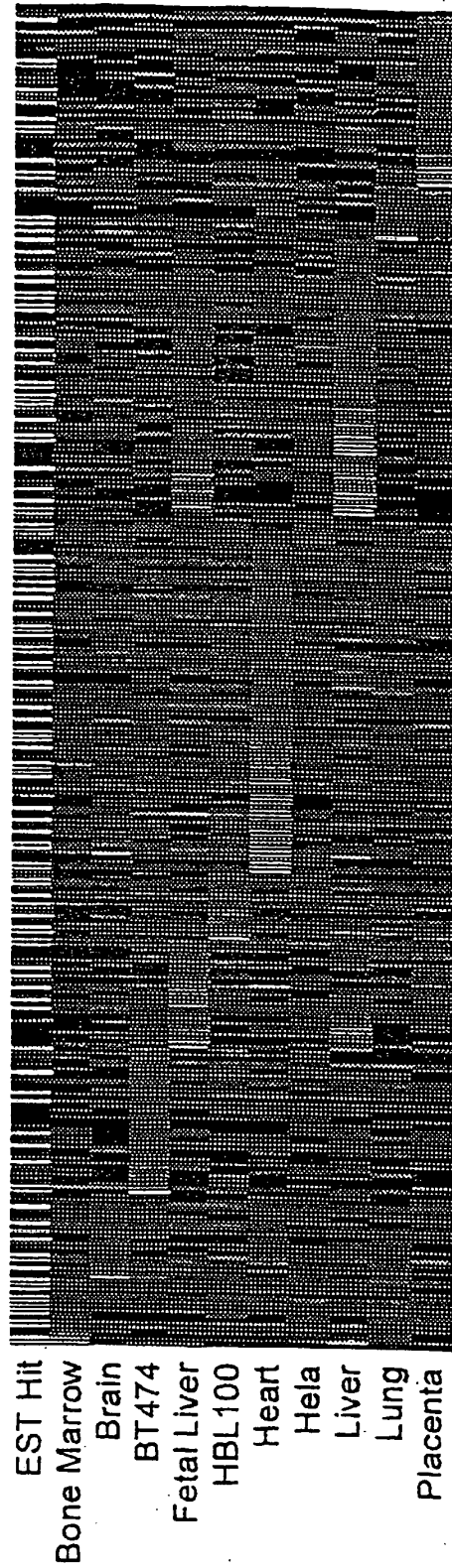


Fig. 7a

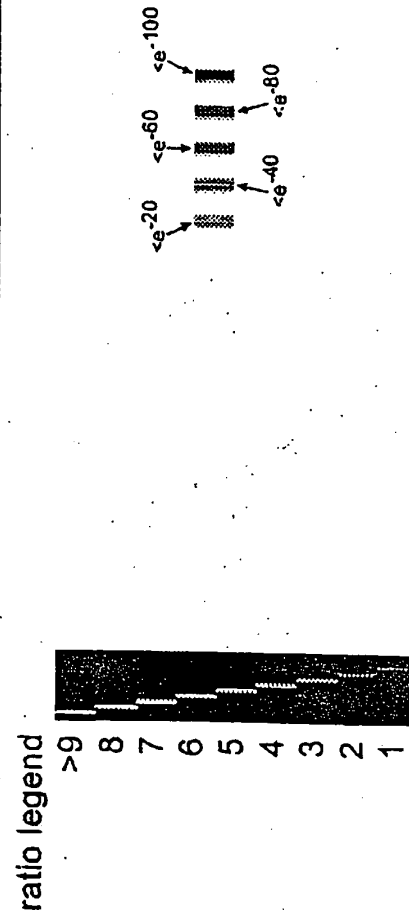


Fig. 7b

Fig. 7c

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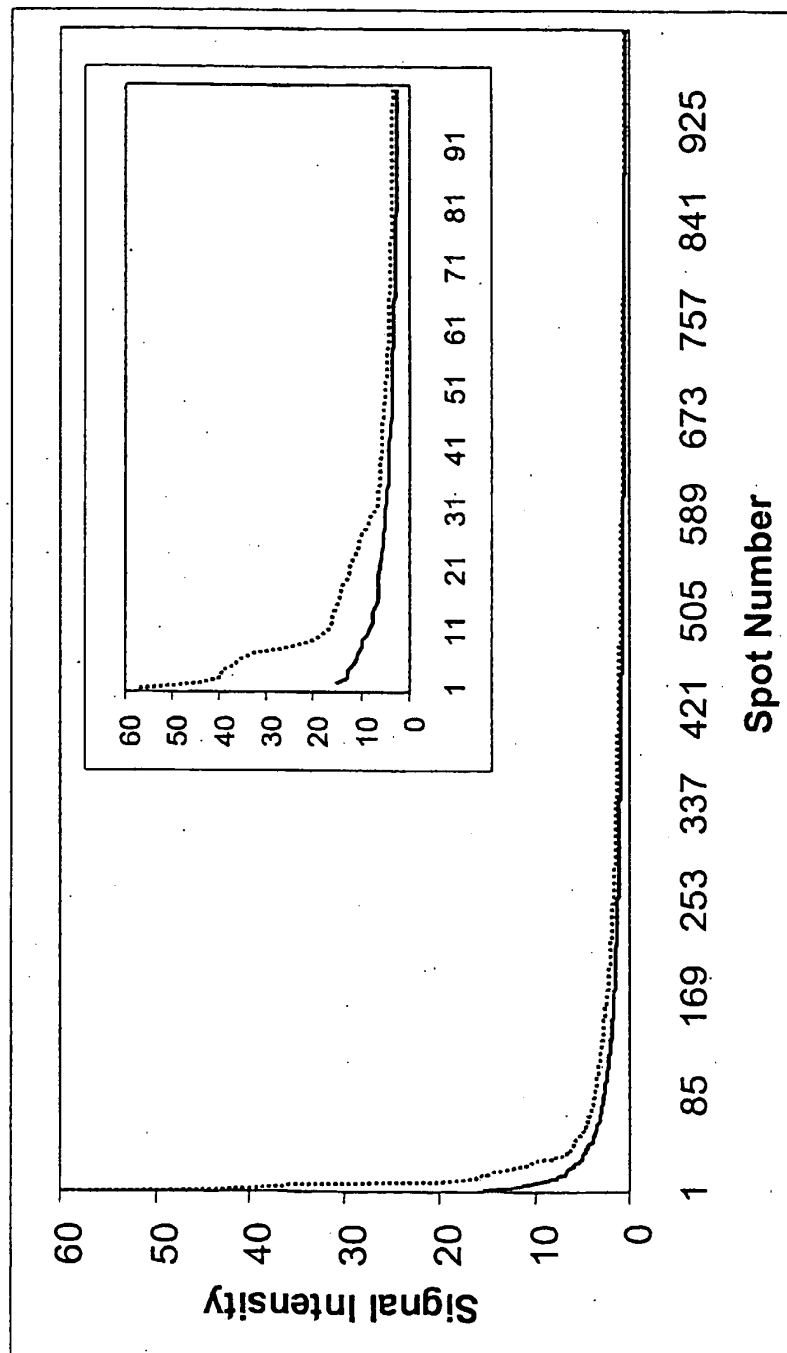


Fig. 8

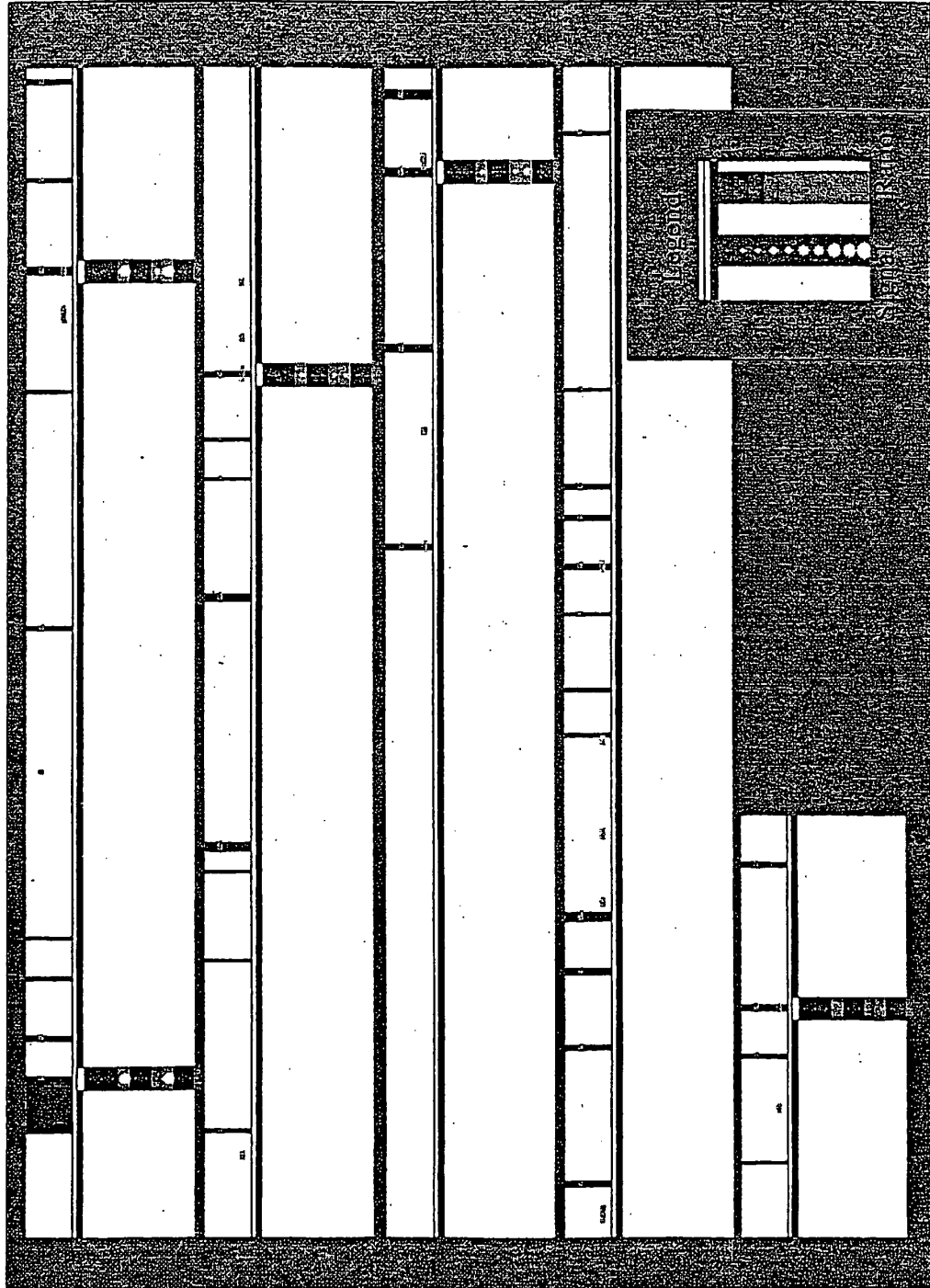


Fig. 9

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(74) Agent: RONNING, Royal, N., Jr.; Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ 08855 (US).

(21) International Application Number: PCT/US01/00669

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(30) Priority Data:

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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

(71) Applicant (*for all designated States except US*): AEOM-ICA, INC. [—/US]; 928 East Arques Avenue, Sunnyvale, CA 94085 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): PENN, Sharron, G. [GB/US]; 617 South Delaware Street, San Mateo, CA 94402 (US). HANZEL, David, K. [US/US]; 968 Loma Verde Avenue, Palo Alto, CA 94303 (US). CHEN, Wensheng [CN/US]; 210 Easy Street #25, Mountain View, CA 94043 (US). RANK, David, R. [US/US]; 117 El Dorado Commons, Fremont, CA 94539 (US).

Published:

- with international search report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

(88) Date of publication of the international search report:
13 February 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 01/057277 A3

(54) Title: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ANALYSIS OF GENE EXPRESSION IN HUMAN FETAL LIVER

(57) Abstract: A single exon nucleic acid microarray comprising a plurality of single exon nucleic acid probes for measuring gene expression in a sample derived from human Fetal liver is described. Also described are single exon nucleic acid probes expressed in the Fetal liver and their use in methods for detecting gene expression.

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 01/00669

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, EPO-Internal, SEQUENCE SEARCH, PAJ

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 99 23254 A (AFFYMETRIX INC ;NAIR ARCHANA (US); LOCKHART DAVID J (US); WARRINGT) 14 May 1999 (1999-05-14) the whole document	1-27
X	EP 0 321 362 A (PASTEUR INSTITUT) 21 June 1989 (1989-06-21) the whole document specially page 11, paragraph 1	1-27
X	PATENT ABSTRACTS OF JAPAN vol. 015, no. 373 (C-0869), 19 September 1991 (1991-09-19) & JP 03 147799 A (HOECHST JAPAN LTD), 24 June 1991 (1991-06-24) abstract	1-27
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

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- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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- *Z* document member of the same patent family

Date of the actual completion of the international search

11 July 2002

Date of mailing of the international search report

07.08.2002

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Molina Galan, E

INTERNATIONAL SEARCH REPORT

 International Application No
 PCT/US 01/00669

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	STEENBERGH P H ET AL: "COMPLETE NUCLEOTIDE SEQUENCE OF THE HIGH MOLECULAR WEIGHT HUMAN IGF-I MESSENGER RNA" BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 175, no. 2, 1991, pages 507-514, XP002185752 ISSN: 0006-291X the whole document ---	1-27
X	DATABASE EBI 'Online! EMBL; Accession Number AC007372, 27 April 1999 (1999-04-27) DICKHOFF ET AL: "Sequencing of human chromosome 14q31 region" XP002182131 sequence ---	13
X	DATABASE EBI 'Online! EMBL; ROBINS ET AL.: "2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries" Database accession no. AA078318 XP002185755 Sequence ---	13
X	DATABASE SWISSPROT 'Online! EMBL; AN: 002711, 1 July 1997 (1997-07-01) BENIT ET AL.: "Cloning of a new murine endogenous retrovirus" XP002037954 the whole document ---	13
X	DATABASE EBI 'Online! emb1; AN: AA414703, 9 May 1997 (1997-05-09) MARRA ET AL: "The Washu-HHMI mouse EST project" XP002205620 the whole document ---	13
A	US 5 618 671 A (LINDSTROEM PER) 8 April 1997 (1997-04-08) column 1, line 60 -column 2, line 19 column 4, line 36 -column 5, line 29; claims --- -/--	1-27

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 01/00669

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	EISEN M B ET AL: "Cluster analysis and display of genome-wide expression patterns" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 95, December 1998 (1998-12), pages 14863-14868, XP002140966 ISSN: 0027-8424 the whole document ----	1,12
P,X	PENN S G ET AL: "Mining the human genome using microarrays of open reading frames." NATURE GENETICS, (2000 NOV) 26 (3) 315-8., XP002183793 the whole document -----	1

INTERNATIONAL SEARCH REPORT

Information on patent family members

tional Application No

PCT/US 01/00669

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
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			DE 69330604 D1	20-09-2001
			DE 69330604 T2	04-07-2002
			EP 0647278 A1	12-04-1995
			JP 7508407 T	21-09-1995
			WO 9400597 A1	06-01-1994

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 01/00669

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 1-27 (partially)
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
see FURTHER INFORMATION sheet PCT/ISA/210
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-27 (partially)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-27 (partially)

The following statements about the impossibility of performing a meaningful search according to Art. 17(2) PCT are made for the subject matter for which a search has been performed and identified as the first and second inventions in form 206 PCT.

Present claims 1-12 and 22-24 relate to an extremely large number of possible sets of nucleic acid probes comprising Seq. Id. 1 or 2 as well as microarrays comprising said sets. In fact, the claims contain so many possible permutations that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search of the claims impossible. Consequently, the search for the sets of probes comprising Seq. Id. 1 or 2 has been limited to the Seq. Id. as such.

Claims 1-3, 5, 6, 8-15 and 18-24 relate to portions or fragments of nucleic acids defined by Seq. Id. 1 or 2. The length or other similar characterizing features of the portions or fragments is not disclosed, bringing the total number of possible prior art sequences to exceptionally high numbers. The shorter the length, the higher the possibility that an overflow of, in principle unrelated, sequences are retrieved, making the establishment of a meaningful International Search Report impossible. For this reason the search has been limited to portions or fragments of Seq. Id. 1 or 2 having a significant minimum length and being supported by the description, namely at least 15 contiguous nucleotides (see claim 16).

Claims 15-21 relate to an extremely large number of nucleic acid probes. The probes are defined solely by their potential to code for peptide Seq. Id. 25138. However, due to the degeneracy of the genetic code, every peptide is potentially coded by an extremely high number of nucleic acid sequences. In fact, the claims contain so many potential nucleic acid sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search over the whole scope of the claims impossible. The search has therefore been carried out for those parts of the claims which do appear to be clear and concise, namely the nucleic acid sequences disclosed in the application and identified as encoding the referred peptide in table 4 (Seq. Ids. 1 or 2 and 12682).

Likewise, claim 26, which refers to peptides encoded by Seq. Id. 1 or 2 and 12682, encompasses a high and undefined number of possible peptides. Besides three possible reading frames deriving from the encoding nucleic acid strand, as well as three additional reading frames deriving from the complementary nucleic acid strand, every possible fragment of these is being covered by the claim. This is due to the potential presence of stop codons within any of the six possible reading frames which can not be established a priori. Thus, claim 26 contains so many potential peptide sequences that a lack of clarity and conciseness within the meaning of Article 6 PCT arises to such an extent as to render a meaningful search

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

over the whole scope of the claim impossible. Consequently, the search has been carried out for those parts of the claim which do appear to be clear and concise, namely the peptide disclosed, identified by Seq. Id. 25138.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-27 (partially)

Invention 1

A nucleic acid probe comprising SEQ ID 1, complementary sequences or fragments thereof (in particular comprising Seq. Id. 12674). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. 1 (in particular the one defined by Seq. Id. 25130).

2. Claims: 1-27 (partially)

Invention 2

A nucleic acid probe comprising SEQ ID 2, complementary sequences or fragments thereof (in particular comprising Seq. Id. 12682). Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. 1 (in particular the one defined by Seq. Id. 25138).

3. Claims: 1-27 (partially)

Inventions 3-12673

A nucleic acid probe comprising SEQ ID n (where n ranges from 3-12673 according to the invention number above), complementary sequences or fragments thereof, in particular comprising the SEQ ID no. which is listed in the column "Exon Seq. Id. no." in the same row that contains Seq. Id. n in table 4. Spatially addressable sets of probes comprising said sequence, microarrays comprising said sets, a method for measuring gene expression, a method for identifying exons, a method for assigning exons to a single gene comprising the use of said arrays and peptides encoded by Seq. Id. n, in particular the one defined by the Seq. Id. no. in the column "ORF Seq. Id. no." of the same row where Seq. Id. n is listed.